

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 15:56:11 ; Search time 163 Seconds

(without alignments)  
4207.199 Million cell updates/sec

Title: US-10-642-248-2

Perfect score: 5108

Sequence: 1 MYTSLQAIKAYNSDYQLAL.....SARGENIPVKNFIINSITL 972

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05-80-\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	972	1 HAS_PASMU	Q7blv3 p hyaluron
2	4310.5	84.4	965	1 CHS_PASMU	Q9cmp0 p chondroit
3	2209	43.2	686	1 CHS_ECOLI	Q810v4 e chondroit
4	1306	25.6	253	2 Q847L4_PASMU	Q847l4 pasteurella
5	1303	25.5	253	2 Q847L2_PASMU	Q847l2 pasteurella
6	1148.5	22.5	220	2 Q847L3_PASMU	Q847l3 pasteurella
7	305	6.0	602	2 Q4UM29_RICFE	Q4um29 rickettsia
8	298.5	5.8	327	2 Q8Y828_LISMO	Q8y828 listeria mo
9	297	5.8	804	2 Q7U8H3_SYNPX	Q7u8h3 synchococcc
10	295	5.8	604	2 Q7PB12_RICSI	Q7pb12 rickettsia
11	293	5.7	604	2 Q92IF9_RICCN	Q92if9 rickettsia
12	289	5.7	337	2 Q9CLR9_PASMU	Q9clr9 pasteurella
13	287.5	5.6	836	2 Q831L3_ENTFA	Q831l3 enterococcu
14	282.5	5.5	350	2 Q9ALS8_CAMJE	Q9als8 campylobact
15	278.5	5.5	1127	2 Q7BG51_BACST	Q7bg51 bacillus st
16	276.5	5.4	326	2 Q8XN37_CLOPE	Q8xn37 clostridium
17	276.5	5.4	696	2 Q97P72_STRPN	Q97p72 streptococc
18	276.5	5.4	851	2 Q637U5_BACCCZ	Q637u5 bacillus ce
19	273.5	5.4	851	2 Q81YG7_BACAN	Q81yg7 bacillus an
20	273.5	5.4	851	2 Q6HFS0_BACHK	Q6hfs0 bacillus th
21	271	5.3	325	2 Q7N2R1_PHOLL	Q7n2r1 photorhabd
22	268.5	5.3	295	2 Q74BU3_GEOSL	Q74bu3 geobacter s
23	267.5	5.2	713	2 Q832P1_ENTFA	Q832p1 enterococcu
24	267	5.2	323	2 Q8ABR0_BACTN	Q8abr0 bacteroides
25	265.5	5.2	341	2 Q4K1L9_STRPN	Q4kl19 streptococc
26	264.5	5.2	319	2 Q5NGN8_FRATT	Q5ngn8 francisella
27	263.5	5.2	323	2 Q8YSL7_ANASP	Q8ysl7 anabaena sp
28	262	5.1	315	2 Q93T15_STRAG	Q93t15 streptococc
29	261.5	5.1	706	2 Q8B090_ENTFA	Q8b090 enterococcu
30	261	5.1	342	2 Q8XN57_CLOPE	Q8xn57 clostridium
31	260.5	5.1	324	2 Q8YSL1_ANASP	Q8ysl1 anabaena sp

## RESULT 1

HAS_PASMU	STANDARD;	PRT;	972 AA.
ID	Q7BLV3; O68389; O85457;		
AC	Q7BLV3; O68389; O85457;		
DT	10-MAY-2005 (Rel. 47, Created)		
DT	10-MAY-2005 (Rel. 47, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Hyaluronan synthase (EC 2.4.1.212) [Includes: Glucuronosyl-N-		
DE	acetylglucosaminyl-proteoglycan 4-beta-N-acetylglucosaminyltransferase		
DE	(UDP-GlcNAc transferase); N-acetylglucosaminyl-proteoglycan 3-beta-		
DE	glucuronosyltransferase (EC 2.4.1.226) (UDP-GlcUA transferase)].		
GN	Name=hyad;		
OS	Pasteurella multocida.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;		
OC	Pasteurellaceae; Pasteurella.		
OK	NCBI_taxID=747;		
RP	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Serogroup A:1 / X73;		
RC	MEDLINE=98442423; PubMed=9770287;		
RA	Chung J.Y., Zhang Y., Adler B.;		
RT	"The capsule biosynthetic locus of Pasteurella multocida A:1.";		
RL	FEMS Microbiol. Lett. 166:289-296(1998).		
RP	[2]		
RP	SEQUENCE REVISION TO 855-972.		
RA	Chung J.Y., Zhang Y., Adler B.;		
RL	Submitted (MAY-2000) to the ENBL/GenBank/DBJ databases.		
RP	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=P1059 / ATCC 15742;		
RC	MEDLINE=98192645; PubMed=9525958; DOI=10.1074/jbc.273.14.8454;		
RA	DeAngelis P.L., Jing W., Drake R.R., Achyuthan A.M.;		
RT	"Identification and molecular cloning of a unique hyaluronan synthase		
RL	from Pasteurella multocida.";		
RL	J. Biol. Chem. 273:8454-8458(1998).		
RP	[4]		
RP	SEQUENCE REVISION TO 43.		
RA	DeAngelis P.L., Jing W., Achyuthan A.M.;		
RL	Submitted (MAR-2004) to the ENBL/GenBank/DBJ databases.		
RP	[5]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Fuller T.E., Kennedy M.J., Lowery D.E.;		
RT	"Identification of Pasteurella multocida virulence genes in a		
RT	septicemic mouse model using signature-tagged mutagenesis.";		
RL	Submitted (FEB-2000) to the ENBL/GenBank/DBJ databases.		
RP	[6]		
RP	CHARACTERIZATION, AND MUTAGENESIS OF ASP-196 AND ASP-477.		
RC	STRAIN=P1059 / ATCC 15742;		
RC	PubMed=10988250; DOI=10.1093/glycob/10.9.883;		
RA	Jing W., DeAngelis P.L.;		
RT	"Dissection of the two transferase activities of the Pasteurella		
RT	multocida hyaluronan synthase: two active sites exist in one		
RT	polypeptide.";		
RL	Glycobiology 10:883-889(2000).		

Q8xn34 clostridium  
Q9k616 bacillus ha  
Q64w33 bacteroides  
Q4jyv4 streptococc  
Q93ti7 streptococc  
Q86893 streptococc  
Q9uz16 pyrococcus  
Q06035 lactococcus  
Q4jz64 streptococc  
Q81em5 bacillus ce  
Q9afh3 streptococc  
Q8d2e0 streptococc  
Q8xn54 clostridium  
Q4jz68 streptococc

## ALIGNMENTS

[7]  
 RP CHARACTERIZATION, AND MUTAGENESIS OF ASP-247; ASP-249; GLU-369;  
 RP ASP-370; ASP-527; ASP-529 AND ASP-563.  
 RX PubMed=12799342; DOI=10.1093/glycob/cwg085;  
 RA Jing W., DeAngelis P.L.;  
 RT "Analysis of the two active sites of the hyaluronan synthase and the  
 RT chondroitin synthase of *Pasteurella multocida*.";  
 RL Glycobiology 13:661-671 (2003).  
 CC -1- FUNCTION: Catalyzes the polymerization of hyaluronan, a  
 CC polyaccharide composed of a repeating disaccharide of N-  
 CC acetylglucosamine (GlcNAc) and glucuronic acid (GlcUA) units. Each  
 CC unit has the composition in beta-(1->3)-GlcUA-beta-(1->3)-GlcNAc.  
 CC -1- CATALYTIC ACTIVITY: n UDP-N-acetyl-D-glucosamine + n UDP-D-  
 CC glucuronate = (beta-N-acetyl-D-glucosaminyl(1->4)-beta-D-  
 CC glucuronosyl(1->3)) (n) + 2n UDP.  
 CC -1- COFACTOR: Magnesium or cobalt.  
 CC -1- BIOPHYSICOCHEMICAL PROPERTIES:  
 CC Kinetic parameters:  
 CC KM=160 uM for UDP-N-acetyl-D-glucosamine;  
 CC KM=140 uM for UDP-D-glucuronate;  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase 2 family. CS/HAS  
 C. subfamily.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC -----  
 CC EMBL; AF067175; AAC67250.2; -; Genomic DNA.  
 CC EMBL; AF036004; AAC38318.2; -; Genomic DNA.  
 CC EMBL; AF237926; AAF68412.1; -; Genomic DNA.  
 CC PIR; T09595; T09595.  
 CC HSSP; P39621; IQGQ.  
 CC InterPro; IPR001173; Glyco trans 2.  
 CC Pfam; PR00535; Glycos transf\_2; 2.  
 CC Glycosyltransferase; Membrane; Multifunctional enzyme; Repeat;  
 KW transferase.  
 KW REGION 152 325 A1.  
 FT REGION 432 604 A2.  
 FT MUTAGEN 196 196 D->E,K,N: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 247 247 D->E,K,N: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 249 249 D->E,K,N: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 369 369 E->D: Complete loss of GlcNAc transferase  
 FT activity. Regains 30% of wild type  
 FT activity at high UDP-GlcNAc  
 FT concentrations.  
 FT MUTAGEN 369 369 E->H,Q: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 370 370 D->E,K,N: Complete loss of GlcNAc  
 FT transferase activity.  
 FT MUTAGEN 477 477 D->E,K,N: Complete loss of GlcUA  
 FT transferase activity.  
 FT MUTAGEN 527 527 D->E,K,N: Complete loss of GlcUA  
 FT transferase activity.  
 FT MUTAGEN 529 529 D->E: 90% loss of GlcUA transferase  
 FT activity.  
 FT MUTAGEN 529 529 D->K,N: Complete loss of GlcUA  
 FT transferase activity.  
 FT MUTAGEN 563 563 D->E,K,N: No effect.  
 FT CONFLICT 17 17 Q -> E (in Ref. 1).  
 FT CONFLICT 43 43 K -> Q (in Ref. 5).  
 SQ SEQUENCE 972 AA; 111839 MW; D933BD8C1E923685 CRC64;

Query Match 100.0%; Score 5108; DB 1; Length 972;  
 Best Local Similarity 100.0%; Pred. No. 7,8e-272;  
 Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNTLSQAIKAYNSNDYQLALKLFEKSAEIIYGRKIVFQITKCKELSAHPSVNSAHL SVN 60

Db	1	MNTLSQAIKAYNSNDYQLALKLFEKSAEIIYGRKIVFQITKCKELSAHPSVNSAHL SVN	60
Qy	61	KEEKVNVCDSPDLDIATQLLLSNVKLVLSDSKXNTLNKWKLTETKSENAEYRAVALVP	120
Db	61	KEEKVNVCDSPDLDIATQLLLSNVKLVLSDSKXNTLNKWKLTETKSENAEYRAVALVP	120
Qy	121	KDPPKDLVLAPLDPHVNDFTWYKKRKRIGIKPEHQHVGLSIIIVTFNRPAILSLITACL	180
Db	121	KDPPKDLVLAPLDPHVNDFTWYKKRKRIGIKPEHQHVGLSIIIVTFNRPAILSLITACL	180
Qy	181	VNOKTHYPEVIVTDGSGDELSPIITROYENKLDIRYVQKONGFOASARNNGRLAKY	240
Db	181	VNOKTHYPEVIVTDGSGDELSPIITROYENKLDIRYVQKONGFOASARNNGRLAKY	240
Qy	241	DFIGLLDCDMPNPLMVHVSVAELLEDDDLTIIGPRKYIDTQHDIDPKDFLNNASLLES	300
Db	241	DFIGLLDCDMPNPLMVHVSVAELLEDDDLTIIGPRKYIDTQHDIDPKDFLNNASLLES	300
Qy	301	EVTNNNSVAAKGEGTVSLDWRLEQPEKTENLRSLSDSPFFFAAGNVAFAKKWLNKSGFFD	360
Db	301	EVTNNNSVAAKGEGTVSLDWRLEQPEKTENLRSLSDSPFFFAAGNVAFAKKWLNKSGFFD	360
Qy	361	EEFNHGGEDVEFGYRLFRYGSFFKTDIGTMAVHQBPCKENETDREAGKNITLDMREK	420
Db	361	EEFNHGGEDVEFGYRLFRYGSFFKTDIGTMAVHQBPCKENETDREAGKNITLDMREK	420
Qy	421	VPYIYRKLLPIEDSHINRVPLSVIYIPAYNCANYIQCVDLSALNQTVDLEVCINC	480
Db	421	VPYIYRKLLPIEDSHINRVPLSVIYIPAYNCANYIQCVDLSALNQTVDLEVCINC	480
Qy	481	DNTLEVINLKYGNPVRIMSKPENGIGASNAASVAFAGYIIGQLSDDDYLPDVELC	540
Db	481	DNTLEVINLKYGNPVRIMSKPENGIGASNAASVAFAGYIIGQLSDDDYLPDVELC	540
Qy	541	LKEFLDKTKLACVYTTNRNVDPGSLIANGYNWPEFSREKLTAMTAHPRMTTIRAWHL	600
Db	541	LKEFLDKTKLACVYTTNRNVDPGSLIANGYNWPEFSREKLTAMTAHPRMTTIRAWHL	600
Qy	601	TGDFNEKIENAVDYMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN	660
Db	601	TGDFNEKIENAVDYMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN	660
Qy	661	QSLNRQGIYYNYDEPDDLDESRRKYIFNKTAEQEEDILDKOIKIIONKDAKIAVSIFYP	720
Db	661	QSLNRQGIYYNYDEPDDLDESRRKYIFNKTAEQEEDILDKOIKIIONKDAKIAVSIFYP	720
Qy	721	NTLNGLVKKLNNIIYNNKNI FVILVHVDKNHLPDIIKKEILAFYHKHQNILLNNDISYY	780
Db	721	NTLNGLVKKLNNIIYNNKNI FVILVHVDKNHLPDIIKKEILAFYHKHQNILLNNDISYY	780
Qy	781	TSNRLIKTEAHLNINKLSQLNLCBYIIFDNHDSLFVRKNSYAYMKKYDVGMNFSALTH	840
Db	781	TSNRLIKTEAHLNINKLSQLNLCBYIIFDNHDSLFVRKNSYAYMKKYDVGMNFSALTH	840
Qy	841	DMTEKINAHPPPKKLKTYTFNDNDLKSMMVKASQGMFTYALAHELLITIIKEVITSQS	900
Db	841	DMTEKINAHPPPKKLKTYTFNDNDLKSMMVKASQGMFTYALAHELLITIIKEVITSQS	900
Qy	901	IDSVPYNTEDTWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNQIESAKGENI	960
Db	901	IDSVPYNTEDTWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNQIESAKGENI	960
Qy	961	PVNKFIINSITL 972	
Db	961	PVNKFIINSITL 972	

RESULT 2  
 CHS\_PASMU  
 ID CHS\_PASMU STANDARD; PRT; 965 AA.  
 AC Q9CMP0; Q6P0M8; Q9AHL6; Q9KJ99;  
 DT 10-MAY-2005 (Rel. 47, Created)



```
Db 294 ETATNNPSITSGNISLWRLHFKYTDNLRLCDSPRYFSCGNVAFSEKWLKNGWFD 353
Qy 361 EEFNHGGEDEVERGYLRFVSGSFKTDIGTMAYHQBPPEKNETDREAGKNTLIDIMREK 420
Db 354 EEFNHGGEDEVERGYLRFVSGSFKTDIGTMAYHQBPPEKNETDREAGKNTLIDIMREK 413
Qy 421 VPYIYKLLPIEDSHINRPLVSTIYIPAYNCANYIQCVDLSALNTQVVDLEVCINDGST 480
Db 414 VPYIYKLLPIEDSHINRPLVSTIYIPAYNCANYIQCVDLSALNTQVVDLEVCINDGST 473
Qy 481 DNTLEVINKLYGNPRVRINKSPKGGIASASNAVSPAKGYIYIGQLSDDDYLDPEDAVELC 540
Db 474 DNTLEVINKLYGNPRVRINKSPKGGIASASNAVSPAKGYIYIGQLSDDDYLDPEDAVELC 533
Qy 541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNPEFSREKLTAMTIAHFMFTIRAWHL 600
Db 534 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNPEFSREKLTAMTIAHFMFTIRAWHL 593
Qy 601 TDGFNEKIENAVDYDFELKSEVGFKHLNKI CYNRVLHGDNTSIKLGIOKQKHFPVYN 660
Db 594 TDGFNEKIENAVDYDFELKSEVGFKHLNKI CYNRVLHGDNTSIKLGIOKQKHFPVYN 653
Qy 661 QSLNRQGITVYNYDEFDLDESRYIFNKTAQYQEEIDILDKIIONKDKAKIATVSIYFP 720
Db 654 QSLNRQGVSNYNYDEFDLDESRYIFNKTAQYQEEIDILDKIIVQRDKAKVAISIFYP 713
Qy 721 NTUNGVLKLNIIIEYNNKIFVILVHVDKVNHLDPDIKKEILAFYKHQVNLNNDISYY 780
Db 714 NRDGLVKKLNIIIEYNNKLIIVLHDKNHLTSIDIKKEILEFHNKQINILLNNDVSY 773
Qy 781 TSNRLIKTEAHLNINKLSOLNCEYIIFDNHDSLFPKNDSYAYMKKYDVGNFNLSLTH 840
Db 774 TNNRLIKTKAHLNMMKRLQNLNLEYIIFDNHDSLFPKNDSYAYMKKYDVGNFNLSLTH 833
Qy 841 DWIEKINAHPPFKLTKTYFENDNLDKSMNVKASQGMFTYALAHELLTIIEKIVITSCQS 900
Db 834 DWINKINAHSPFKNLTKYFENDNLDKTIINNVKASQGMFIKYTLAHDIAITIMKEVITLQCS 893
Qy 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKSTLTLYMPWERKLQWNTQIESAKRGENT 960
Db 894 TDSVPEYNTEDIWQFALLILEKKTGHVFNKSTLTLYMPWERKLQWNTQIESAKRGENT 953
Qy 961 PVNKFIIINSITL 972
Db 954 PVNKFIIINSITL 965

RESULT 3
CHS_ECOLI STANDARD; PRT; 686 AA.
AC QBL0V4;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Chondroitin synthase (CS) (Chondroitin polymerase) [Includes:
DE Glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-beta-N-
DE acetylgalactosaminyltransferase (EC 2.4.1.175) (UDP-GalNac
DE transferase); N-acetylgalactosaminyl-proteoglycan 3-beta-
DE glucuronosyltransferase (EC 2.4.1.226) (UDP-GlcUA transferase)].
GN Name=kfoc;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RC NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND CHARACTERIZATION.
RP STRAIN=05_K4(L)H4 / ATCC 23502;
RX MEDLINE=22050655; PubMed=11943778; DOI=10.1074/jbc.M201719200;
RA Kinomiyu T., Sugiyama N., Tawada A., Sugimoto K., Watanabe H.,
RA Kimata K.;
RT "Molecular cloning and characterization of chondroitin polymerase from
RT Escherichia coli strain K4.";
```

```
RL J. Biol. Chem. 277:21567-21575(2002).
CC -I- FUNCTION: Catalyzes the polymerization of chondroitin, a
CC polysaccharide composed of a repeating disaccharide of N-
CC acetylgalactosamine (GalNAc) and glucuronic acid (GlcUA) units.
CC Each unit has the composition in beta-(1->4)-GlcUA-beta-(1->3)-
CC GalNAc.
CC -I- CATALYTIC ACTIVITY: UDP-alpha-D-glucuronate + N-acetyl-beta-D-
CC galactosaminyl-(1->4)-beta-D-glucuronosyl-proteoglycan = UDP +
CC beta-D-glucuronosyl-(1->3)-N-acetyl-beta-D-galactosaminyl-(1->4)-
CC beta-D-glucuronosyl-proteoglycan.
CC -I- CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + beta-D-
CC glucuronosyl-(1->3)-N-acetyl-beta-D-galactosaminyl-proteoglycan =
CC UDP + N-acetyl-beta-D-galactosaminyl-(1->4)-beta-D-glucuronosyl-
CC (1->3)-N-acetyl-beta-D-galactosaminyl-proteoglycan.
CC -I- COFACTOR: Manganese.
CC -I- BIOPHYSICOCHEMICAL PROPERTIES:
CC Kinetic parameters:
CC KM=3.44 uM for UDP-GlcUA;
CC KM=31.6 uM for UDP-GalNAc;
CC pH dependence:
CC Optimum pH is 7-7.5;
CC Temperature dependence:
CC Optimum temperature is 30 degrees Celsius for highest reaction
CC speed, and 25 degrees Celsius to obtain highest molecular weight
CC of product chondroitin;
CC -I- SIMILARITY: Belongs to the glycosyltransferase 2 family. CS/HAS
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB079602; BAC00523.1; -; Genomic_DNA.
CC InterPro; IPR001173; Glyco trans 2.
CC DR Pfam; PF00535; Glycos transf 2; 2.
CC KW Glycosyltransferase; Repeat; Transferase.
CC FT REGION 143 317 A2.
CC FT REGION 424 596 A1.
CC SQ SEQUENCE 686 AA; 79257 MW; 6FB941623D9EC9D4 CRC64;

Query Match 43.2%; Score 2209; DB 1; Length 686;
Best Local Similarity 59.6%; Pred. No. 7.1e-113;
Matches 412; Conservative 117; Mismatches 150; Indels 12; Gaps 4;

Qy 1 MNTLSQAIKAYNSNDYQALALFKESAETIYGRKIVFQITCKCKELSAHPSVNSAHLVN 60
Db 1 MSILNQAINLYKNYRQALSIFKVAEIVDVSWEANIKLCQTALNLSEVD- ---KLN 56
Qy 61 KEEKNVVCDSPLDIATQLLLSNVKLVLSDSSEKNTLKNWKLTEKKSSENAEVRVALVP 120
Db 57 RKAVIDI-----DAATKIMCSNAKAISLNEVEKNEIISKYREITAKKSRAELKVEPIP 111
Qy 121 KDFPKDLVLPDHDVNDFTWYKKRIGIKPEHOHV--GLSIVTTNRPAILSLITLA 178
Db 112 LDWPSDLTUPPESTNDIVWAGKRKE-LDDYPRKQLIDGLSIVITPTNRKAILAITLA 170
Qy 179 CLVNRKQTHYPPFVIVTDDGSQSDLSPIITRQYENKLDIRYVRQKNGFQASARNMGLRLA 238
Db 171 CLCNQKTIYDEIVVADDSKENIEIREFESLLNIKYVRQKDYGYQLCAVRNLGLRAA 230
Qy 239 KYDFIGLLDCDMAPNPLWVHSVVAELLEDDDITITIGPRKYIDTQHDIDPKDFLNASLLS 298
Db 231 KINYVAILDCDMAPNPLWVQSYMELAVDDNVALIGPRKYIDTSHKTYLDFLSQKSLINE 290
Qy 299 LPEETNNNSVAAKGCTVSLDWRLOPEKTNLRLSDSPFRFAAGNVAFAKWLKNSGF 358
Db 291 IFEIITNNQVAGKVEQNSVDWRIEHFKNDNLRLCNETFRFSGGNVAFAPAKKULFRAGW 350
Qy 359 FDEEFNHGGEDEVERGYLRFVSGSFKTDIGTMAYHQBPPEKNETDREAGKNTLIDIMR 418
Db 351 FDEEFTHMGGEDEVERGYLRFVSGCYFRSVEGAMAYHQBPPEKNETDREAGKNTITVOLLQ 410
```

```
Qy 419 EKVPYIRKLLPIEDSHINRPLVSIYIPAYNCANYIORCVDSALNOTVVDLEVCICNDG 478
Db 411 QKVPYFYRKEKESATLKRPLVSIYIPAYNCYSKIIVRCVESALNTGTTDLEVCICDDG 470
Qy 479 STDNTLVINKLYGNPRVRIMSPKNGIGIASAASNAVSAFAGYIYGQDSDDDVLEPAVE 538
Db 471 STDTLAILQEHYANHRVRFISQKNKGIGASNTAVRLCRGFFYIGQDSDDDVLEPAVE 530
Qy 539 LCLKEFKDKTKLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTMTAMIAHHFRMFTTAW 598
Db 531 LCLDEFRKDLSLACVYTTNRNIDREGLISNGYNWPIYSREKLTMSAMICHFRMFTTARAW 590
Qy 599 HLTDGPFNEKIENAVDYDMFLKSLVGKFKHLNKLKCYNRVLHGDNTSITKGLGIQKNHFPV 658
Db 591 NLTEGFNESISNAVYDYMFLKSLVGPFKHLNKLKCYNRVLHGTENTSITKGLDIQKNHFKV 650
Qy 659 VNQSLNRQGIYYNYNDFDDIDESRKYIFNK 689
Db 651 VNESLSRLGIKKYKYSPLTNLNECRKYTWK 681

RESULT 4
Q847L4_PASMU PRELIMINARY; PRT; 253 AA.
AC Q847L4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Kmt1 (Fragment).
GN Name=hyaD;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jabbari A.R., Emaeliazad M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225345; AA063009.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 253 AA; 29539 MW; A6BF4E189802367D CRC64;

Query Match 25.6%; Score 1306; DB 2; Length 253;
Best Local Similarity 98.4%; Pred. No. 7.1e-64;
Matches 248; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 721 NTLGLVKLNIIIEYNKNIFVILHVDKNHLTPDIKKEILAFYHKHQNILLNNDISYY 780
Db 2 SVLSLVKLNIIIEYNKNIFVILHVDKNHLTPDIKKEILAFYHKHQNILLNNDISYY 61
Qy 781 TSNRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGMPFSALTH 840
Db 62 TSNRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGMPFSALTH 121
Qy 841 DWIEKINAHPPPKLIKTYPFNDNLDKSMNVKASQGMFTYALAHELLTIKEVITSCOS 900
Db 122 DWIEKINAHPPPKLIKTYPFNDNLDKSMNVKASQGMFTYALAHELLTIKEVITSCOS 181
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLTQWNEQIESAKRGNI 960
Db 182 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLTQWNEQIESAKRGNI 241
Qy 961 PVNKEIINSITL 972
Db 242 PVNKEIINSITL 253

RESULT 5
Q847L2_PASMU PRELIMINARY; PRT; 253 AA.
AC Q847L2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
```

```
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Kmt1 (Fragment).
GN Name=hyaD;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jabbari A.R., Emaeliazad M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225347; AA063011.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 253 AA; 38946AAD8FCC178F CRC64;

Query Match 25.5%; Score 1303; DB 2; Length 253;
Best Local Similarity 98.4%; Pred. No. 1e-63;
Matches 246; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 723 LNLGLVKLNIIIEYNKNIFVILHVDKNHLTPDIKKEILAFYHKHQNILLNNDISYYTS 782
Db 4 LNLGLVKLNIIIEYNKNIFVILHVDKNHLTPDIKKEILAFYHKHQNILLNNDISYYTS 63
Qy 783 NRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGMPFSALTHDW 842
Db 64 NRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGMPFSALTHDW 123
Qy 843 IEKINAHPPPKLIKTYPFNDNLDKSMNVKASQGMFTYALAHELLTIKEVITSCQSID 902
Db 124 IEKINAHPPPKLIKTYPFNDNLDKSMNVKASQGMFTYALAHELLTIKEVITSCQSID 183
Qy 903 SVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLTQWNEQIESAKRGNI 962
Db 184 SVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLTQWNEQIESAKRGNI 243
Qy 963 NKFIINSITL 972
Db 244 NKFIINSITL 253

RESULT 6
Q847L3_PASMU PRELIMINARY; PRT; 220 AA.
AC Q847L3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Kmt1 (Fragment).
GN Name=hyaD;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jabbari A.R., Emaeliazad M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225346; AA063010.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 220 AA; 25709 MW; 4A04535EB0CE5C14 CRC64;

Query Match 22.5%; Score 1148.5; DB 2; Length 220;
Best Local Similarity 99.1%; Pred. No. 2.6e-55;
Matches 219; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 752 LTPDIKKEILAFYHKHQNILLNNDISYYTSNRLIKTEAHLNSINKLSQNLNCEYIIFD 811
Db 1 LTP-VKKEILAFYHKHQNILLNNDISYYTSNRLIKTEAHLNSINKLSQNLNCEYIIFD 59
Qy 812 NHDLSLFVKNDSYAYMKYDVGMPFSALTHDWIEKINAHPPPKLIKTYPFNDNLDKSMNVK 871
Db 60 NHDLSLFVKNDSYAYMKYDVGMPFSALTHDWIEKINAHPPPKLIKTYPFNDNLDKSMNVK 119
```





```

AC OTU8H3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative glycosyltransferase family 2 protein.
GN OrderedLocusNames=SYNW0645;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN NUCLEOTIDE SEQUENCE.
RA Malek J.A., Eremeeva M.E., Dasch G.A.;
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahambha B., Latimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569690; CAB07160.1; -; Genomic_DNA.
DR HSP; P39621; I170.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 2.
DR Complete proteome; Transferase.
KW SEQUENCE 804 AA; 92268 MW; FE49920809F9F22C CRC64;

Query Match 5.8%; Score 297; DB 2; Length 804;
Best Local Similarity 22.2%; Pred. No. 8.2e-08;
Matches 119; Conservative 103; Mismatches 210; Indels 104; Gaps 23;

QY 366 WGGDEVEFGYRL--FRYGSFPTKIDGIMAYHQBPQKNETDRAGNI-----TLDIMR 418
DB 176 WRTQI---YRLAQIRHQWPKT-----PSDKPTQ-ETDERYENYKEIBELPDHNE 224

QY 419 EKVPYIRKLLPIEDSHINRVPLSVIIPAYNC-ANVIQRCVDSALNQTVVDLEVCINC 477
DB 225 EQI-----REWLQNOD---APLISIIPTNTNSHLRECIESVCRQSYPNWELCI 276

QY 478 GSTDNTLEVINLY-GNNPRV-IMSKPNGIASNAASVAFKGYIGOLDSDYLEPD 535
DB 277 SSSAVSVKTLRSYQSDPRVKLIIFREKNGHICASNDALRMATGEVALLDHDIDILADN 336

QY 536 AVELCLKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPFSSREKLTAMIAHFRMTI 595
DB 337 ALYVARELQKQPAOILYSDKINDGWRACPHFK-PARNIDLLSYNFISHLGVYR 395

QY 596 RAWHLTDGFNEKIENAVDYDMFLK---SEVGKPKHLNKICYNRVLHGDNTS----- 644
DB 396 BILQIGGFRVFGSQDHDALATVLESPPQIHIIPRVLYHWRHSESTASNPDSKDY 455

QY 645 IKKLGIOKKNHFVVN-----QSLNRQGITVYNYDEFDLDESRYIFNKTA 692
DB 456 TTSGHKAVOHFLDEQHRGGRVATARIKAKNRFTQWHIPDKSPSVE-----LIIPTR 510

QY 693 YQEEIDILKD-----IKIQNDKIAVSIYPNTLNGLVKLN-----NII 736
DB 511 QAEVLNLAVDIIITTYNTITVDNQSEVATKLPK-----LKRHVGEKINIKY 565

QY 737 NKNHIFVILVHVDKNHLPDIKEILAFYKHQVHNLANDISYTSNRILIKTEAHLNIN 796
DB 566 NKKFNYSAIN--NVAVRKSTADIV-----VLVNDVEVISKKWLBIVSHTSRPD 613

QY 797 -----KLSQNLNCEY--IIFD-----NHDLSLFKNDISAYMKYDVGWNFSA 839
DB 614 VGCVGAKLYSNRTIQHGVGIGIQVAGHAHKYFPGDSPGVQVRLQIVQOMTAVT 669

RESULT 10
Q/PBI2_RICS1
ID Q7PBI2_RICS1 PRELIMINARY; PRT; 604 AA.
AC Q7PBI2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```

```

DE Putative two-domain glycosyltransferase.
GN Names:rib_orf.242;
OS Rickettsia sibirica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia; spotted fever group;
OC Rickettsia sibirica subgroup.
OX NCBI_TaxID=35793;
RN NUCLEOTIDE SEQUENCE.
RA Malek J.A., Eremeeva M.E., Dasch G.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABW01000001; EAA25501.1; -; Genomic DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 2.
DR Transferase.
KW SEQUENCE 604 AA; 69114 MW; AF2201951783E823 CRC64;

Query Match 5.8%; Score 295; DB 2; Length 604;
Best Local Similarity 24.6%; Pred. No. 7.2e-08;
Matches 123; Conservative 73; Mismatches 212; Indels 92; Gaps 19;

QY 426 RKLLPIEDSHINRVPLSVIIPAYNCANVIQRCVDSALNQTVVDLEVCINCDSGTDN-TL 484
DB 4 RKDKPLNIYH---TLVSIIPVYNGANYKKEINSALAQTYKNIETIIVVNDGSKNGET 59

QY 485 EVINKLYGNNPRVIRIISKPNKGIGIASNAASVAFKGYIGOLDSDYLEPDVAVS---LC 540
DB 60 ERVLSYGD--KIRYPHKENGCGSALNYGKMGQEFYFWLSHDDIYYPNKIEHQVDIL 117

QY 541 LKEFLKDKTLACVY-----TTNRNVNPDGSLIANGYNWPFSSREKLTAMIAHFRMF 593
DB 118 NKLDNKDTIYGGYELIDKGNLSRYIKPDSVLPINKLN---ISLLPLRLGLIHGCSILM 174

QY 594 TIRAWHLTDGFNEKIENAVDYDMFLKSEVGKPKHLNKICYNRVLHGDNTSIIKKLGIOKK 653
DB 175 PAKYFHEVGIFNEALPTQDYDLWFKIFRVAPIHFDESILIKSRFHSEQGS--KKISNHN 233

QY 654 N-----HFVVNQSILNRQGITVYNYDEFDLDESRYIFNKTAIEYGEIILDKIK 704
DB 234 ECNVLSFSLHETEEEMIKNMGSPYL-----FLTRTATFLSNNT-PYKACADLANTMA 286

QY 705 IIQNDKIAVSIYPNTLNGLVKLNLI-IEYNKNIFFVILH-----VDKNHLTPDIKKE 759
DB 287 KQVNDIKISVIIPVYNRINWAEIAESVLIQTHKFEILLIDGSTDIDSELTACKD 346

QY 760 -ILAFYKHQVHNLANDISYTSNRILIKTEAHLNINLSQNLNCEYIIFDNDHSLFV 818
DB 347 KRIKYPHK-----KNEGPAAARN-LGIKNAIGKYIAFLDSDDLFY 385

QY 819 KNDISAYMKYDVGWNFSAITHDWIEKINAHPPPKLKIYFNNDLKSMMVKGASQGMF 878
DB 386 K-DKIEIQLFMEENNF-IFSHTSYQKINE-----KGYIESVHSGILF 426

QY 879 MYALAHLELLTIKEVITSC 898
DB 427 SG-----NVFPQVIQTC 438

RESULT 11
Q92IF9_RICCN
ID Q92IF9_RICCN PRELIMINARY; PRT; 604 AA.
AC Q92IF9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative two-domain glycosyltransferase [EC:2.4.1.-].
GN OrderedLocusNames=RC0461;
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;

```

```
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxID=781;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; A5008609; AAL02999.1; -; Genomic_DNA.
DR PTR; E97757;
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 2.
DR Complete proteome; Transferase.
SQ SEQUENCE 604 AA; 69121 MW; 514CDD81DC3FB3AB CRC64;

Query Match 5.7%; Score 293; DB 2; Length 604;
Best Local Similarity 24.6%; Pred. No. 9.3e-08;
Matches 123; Conservative 72; Mismatches 213; Indels 92; Gaps 19;

QY 426 RKLPIEDSHINRPLVSIYPAYNCANYIQRQVDSALNQTVDLEVCINCDSSTON-TL 484
DB 4 RDKPLNIYH-----TLVSIIPVNGANYKKEINSALAQTYKNIIIVVNDGSKONGET 59
QY 485 EVINKLYGNPRVRIMSKPNGGIASNAVSPAKGYIIGQLSDDDYLEPDAVE-----LC 540
DB 60 ERVALSYGD--KIRYFVKENGCGSALNYGKMKQGEYFSLSHDDIYFNKIEHQVDIL 117
QY 541 LKEFLKDKTLACY-----TTRNVNPDGSLIANGYNWPEPSREKLTMTAMTAHFRMP 593
DB 118 NKLDNDKTIYGYGEIIDEKGNLSRYIKPDSVLPINKLN---ISLLPLRLGLHGCSSLM 174
QY 594 TTRAWHLTDGFKENIENAVDYMFLKLSVKGPKHLNKCYNRVLHGDNTSIKKLGIOKK 653
DB 175 PAKYFHEVGIFNEALPTQDYDLWFKIFRVAPTHFDESILIKRFSHEQGS--KKISNHNE 233
QY 654 N-----HFVVNQSLNRQGIYYNYVDEPDLDSESKYIFNKTAEQEIEDILKDIK 704
DB 234 ECNVLWSSFLHELTEEMIKMEGSPYL-----FLTRTATFLSNNT--PYKKACDLANTWA 286
QY 705 IQNKDAKTAVSIFYENTLNGLVKLLNI--IENKMFIVVLH-----VDKNHLTPDIKKE 759
DB 287 KOVLNDTKSIIVPVYNRINWAIEATKSVLIQTHKNFEIILIDGSTDIDSELTATCKKD 346
QY 760 -ILAFYKHQVNLNNDISYTSNRLIKTEAHLNINKLSQNLNCEYIIPDNHDSLFV 818
DB 347 KRIKYFKH-----KNEGPAARN-LGKNAIGKYIAFLDSDDLFF 385
QY 819 KNDSYAYMKYDVGMMFSAIETHDWIEKINAHPPFKLIKITYFNDNDLKMNVKASQGMF 878
DB 386 K-DKIEIQLKMBENN-IFSHTSYHKINE-----KGYIESVHSGLF 426
QY 879 MYALAHELLTIKEVITSC 898
DB 427 SG-----NVPPQVIQTC 438

RESULT 12
Q9CLR9_PASMU PRELIMINARY; PRT; 337 AA.
AC Q9CLR9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Pw1140.
GN OrderedLocusNames=Pw1140;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
```

```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; A5006155; AAK03224.1; -; Genomic_DNA.
DR InterPro; IPR001173; Glyco_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 337 AA; 39267 MW; 8639CBF5F700DB4 CRC64;

Query Match 5.7%; Score 289; DB 2; Length 337;
Best Local Similarity 26.5%; Pred. No. 7.1e-08;
Matches 95; Conservative 72; Mismatches 116; Indels 76; Gaps 17;

QY 440 PLVSIYPAYNCANYIQRQVDSALNQTVDLEVCINCDSSTNTLEVINKLYGNPRVRI 499
DB 7 PLVSVLICAYNADKYIEECIDAILNQTYKNIIIVVNDGSTDTTLKLYHFAGKDPRIKI 66
QY 500 M-SKPNGGIASNAVSPAKGYIIGQLSDDDYLEPDAVELCLKEFLKDKTLACV--YTT 556
DB 67 INNEENKGFIAISINIGIASINGDYLAARTDADITKPEWIEKILGYMLSHPHQIIAMGSYLT 126
QY 557 NRVNPDGSLIANGY-----NWPE-PSREKLTMTAMTAH-----PMFTIRAW 598
DB 127 ILSDGNGSLNANYEHGDEWRNPLSHREIVEAMLFRNPINHNMSIVKSTVPREHGLR-- 184
QY 599 HLTGDNKIEINAVDYMFLKLSVKGPK-KHLNKCYNRVLHGDNTSIKKLGIOKKNHV 657
DB 185 -----FDPAQHTEDYQFWLEVRUGELANYPESLVYR-LH--NTQTSLNHKNYQN--- 233
QY 658 VVQNQLNRQGIYYNYVDEPDLDSESKYIFNKTAEQEIEDI-LKDIKIQNKDAKIAV- 715
DB 234 LMAKKIRKAINY---LQDLG-----VIHRLGE-----DIFFHDITQELASLSLL 279
QY 716 -----SIYPNTLNGLVKLLNIENYKNVIFVLVDKNHLTPDIKKEILAFYKHQ 768
DB 280 DNCIIRILYDCYLSLVNDKLNILYFLR-----DKNN-----SYFNKKQ 319

RESULT 13
Q831L3_ENTFA PRELIMINARY; PRT; 836 AA.
AC Q831L3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycosyl transferase, group 2 family protein.
GN OrderedLocusNames=EF2491;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 293:2071-2074(2003).
DR EMBL; A5016954; AAO82207.1; -; Genomic_DNA.
DR TIGR; EF2491; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco_transf_2; 2.
DR Pfam; PF00535; Glycos_transf_2; 2.
```



KW	Complete proteome; Transferase.		
SQ	SEQUENCE	836 AA; 97409 MW; F62EAF321113083C2 CRC64;	
	Query Match	5.6%; Score 287.5; DB 2; Length 836;	
	Best Local Similarity	19.5%; Pred. No. 2.9e-07;	
	Matches	191, Conservative 147; Mismatches 315; Indels 327; Gaps 42;	
Qy	156 QHVLGIIVTFNRPAILSLTCLVQKTHYPEVIVTDGSGEDLSPIROVENKLDI	215	
Db	2 ENKVSIVPVYVETYLEEALMSLKNQ-TLKEIFLIINDGSDNSQKILIE-----	53	
Qy	216 RYVRKQNGFOASARNMGLRLAKYDFIGLLDCOMAPNPLMVHVSVAELLEDLDTIIGP	275	
Db	54 --IAQDDPRFVFNKGG--IGKAFNLGVSEAK-----GEYIAEFESDDIVALTHAY	101	
Qy	276 RKYIDT---QHIDPKDFLNASLLESPEVKTNNVAAKGGTVSLD--WRL--EQPKTE	329	
Db	102 ERLYNTAKSHAD-----VVRCNWVEFSSEEVERDILWQYDKYNQLI	145	
Qy	330 NLRSDSPFRFAAGNVAFAKWNKSGP-PDEFNHWGGEDVEFGYRLFRYGSFPK---	385	
Db	146 DLKTTDLIVQVY-PWNAIYKKSMEKENVTWDEIKSYGDT-----GULFWKINS	193	
Qy	386 -----TIDGIMAYHOBPPCKENETDREACKNITLDMREKVPYIVR-----	426	
Db	194 ASQNVIFIKOCLFYRQNP-----NSTVNVATKVFLPQOFKLIRSNLIEQ	241	
Qy	427 -----KLLPIED-----	433	
Db	242 NKPERYKGYFYKMPKIFYMAIEKLTHLRDESVYEVIOKVAVDFRQALETLQDLNDIDPEY	301	
Qy	434 -----SHINRPLVSIYIPAYCANYIQRVDSALNQTVVDLEVCICND	477	
Db	302 IKQFYQIANDPAAYYEDYLNLYKVSVMPPTHNASKYLRQLTLEVCGSLREIILVEN	361	
Qy	478 GSTNTLEVINLKGNNPRIMSPNGGSIASNAASVAFKYYVIGOLDSDDDYLE----	533	
Db	362 GSTNTMDIINEFAVKDPRITGISIGKSNPGHARVNGISMARGYQLQFLDADDDHEANLL	421	
Qy	534 -----PDAVELCKEFLDKDTLACVYTTNRNVPDGLSIANG--YVWPEFSREK	580	
Db	422 QDAYYRAYSATDILLFCMKEKLPNGEVHVH-----NP---LLTNGRMSGSEISLDE	472	
Qy	581 LTTAMIAHFRMFTIRAWHLTDGFNEKJENAVDYMFL---KLSEVGKFKHLNKICYNRV	637	
Db	473 VTPYLYDKLFLLEYIKENNLVN-----LEQFVGEDAYFTYALLGTEKIVALKYLLTRI	527	
Qy	638 LHGDNYSIKKLGIOKKNHFVVVNQSL-----NR-----OGITYNYDEFD--DLDE	681	
Db	528 VRQDGL--MSTYGMNVRDEFNLHDKMLEYLKHQAPNRIEAYRLKIINTLNWFIQDMNRYDQ	586	
Qy	682 SRKYIFNKTAEQEIDILDKITIQNKDAKIAVSIFYPNTLNGI--VKLLNNIIEYKNK	739	
Db	587 AFKERF-----YQE-----LKB-KYIQQLGLDLVKKEKYSNDEQVERITRIQNILQYNLE	636	
Qy	740 IFVIV---LHVDKNHLTPDIK-----KEILAPYHGHQVN-----ILLNNDISYTS	782	
Db	637 IYQNIYKDFGMMKFTIIPNVHTQERGKVIQGEKTOGNGTAIEMFSIIADND-----TS	692	
Qy	783 NPLIKTEAHLNKLSQLNCEVILIPDNHDSLKVNDYSAYMKYDVGMMFSAALTHDW	842	
Db	693 N-----ASGVIDFVYMGDNTKII-----HOSLIVS-----LLIKEGGTTLSIVLQAEW	736	
Qy	843 IEKINAHPPFKKLIKTYFNDNDLKMVMKVGASQGMFTYALAHALL--TIIKEVITSQOS	900	
Db	737 -----EKG-----YTLQENMYTFVDNVFT-----	757	
Qy	901 IDSVPEYNTEDTW-----FQFALLILEKKTGHVFNKTSITLYMPWERKLTQWNEQI	951	
Db	758 -----IWAGYTKYAAFDYNVIRILTSTREGE-----THFSVVRQNGQYIQT	798	
Qy	952 ESAKGENIPUNKFINSIT	971	
	1799 MTSIGNELTPINKIEGNEPT	818	
Db	799 MTSIGNELTPINKIEGNEPT	818	
RESULT 14			
Q9ALS8_CAMJE			
ID	Q9ALS8_CAMJE PRELIMINARY;	PRT;	350 AA.
AC	Q9ALS8;		
DT	01-JUN-2001 (T-EMBLrel. 17, Created)		
DT	01-JUN-2001 (T-EMBLrel. 17, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.		
OS	Campylobacter jejuni.		
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;		
OC	Campylobacteriaceae; Campylobacter.		
OX	NCBI_TaxID=197;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=NCTC 11828;		
RX	MEDLINE=21912296; PubMed=11914340;		
RX	DOI=10.1128/JB.184.8.2100-2107.2002;		
PA	Oldfield N.J., Moran A.P., Millar L.A., Prendergast M.M., Ketley J.M.;		
RT	"Characterization of the Campylobacter jejuni heptosyltransferase II		
RT	gene, waar, provides genetic evidence that extracellular		
RT	polysaccharide is lipid A core independent."		
RL	J. Bacteriol. 184:2100-2107(2002).		
DR	EMBL; AF343914; AAK12955.1; -; Genomic_DNA.		
DR	InterPro; IPR001173; Glyco_trans_2.		
DR	Pfam; PF00535; Glycos_transf_2; 1.		
KW	Hypothetical protein.		
SQ	SEQUENCE 350 AA; 41616 MW; FB19017F89326E9E CRC64;		
	Query Match	5.5%; Score 282.5; DB 2; Length 350;	
	Best Local Similarity	26.2%; Pred. No. 1.7e-07;	
	Matches	106; Conservative 66; Mismatches 134; Indels 99; Gaps 17;	
Qy	440 PLVSIYIPAYCANYIQRVDSALNQTVVDLEVCICNDGSTDNTLEVINLKGNNPRVI	499	
Db	5 PLVSIIPCYNAENFIENCSIINQTYINVEIICVDDGSTDNTLKLKMLSNNSRLKA	64	
Qy	500 MSKNGGIAS-ASNAVSFAKYYVIGOLDSDDDYLEPDAVELCKEFLDKTLCVYT---	555	
Db	65 YSINHGTGPSVVKYNGYGLAKGEFLILSDSDMTIEVLEKGIKIFQDNPDVILYPIKF	124	
Qy	556 ~-TVNRNVDPDGLIANGVNWPEFSREKLTAMIAHFRMFTIRAWHLTDGFNEKIEAVD	613	
Db	125 MFSNNYKIGGIYNNSLNISDVNLGATNKIISGR-----DAFRNIYNKLI	172	
Qy	614 YDMFLKLSVEGKFKHLANKICYNRVLHGDNTSIKKLGIOKK-----NHFVVVNQSLNRQ	667	
Db	173 GFPPVK-KTIKIIINFNEESFN---GDEVSFRHLLQAKKIAFTDTEFYVYN--FNQES	225	
Qy	668 IT-----YVWPEFDDLESRKVIEN--KTAE-YQEEIDILKDIKIQNKDAKIAVSIFVP	720	
Db	226 ITKKIGVHHWDW-----KTWFNLEKLAQKNYEKKLIKKIN-----KIRYSIYI-	270	
Qy	721 NTNLGLVKLNNIIEYKNKIFVILVHVDKNHLTPDIKKEILAFYHKKHGVNILLNNDISY	780	
Db	271 -----ELCKIFNKTEYL-----FSQNEKNIL-----	292	
Qy	781 TSNRLIKTEAHLNKLSQLNLCN-----EYIFDNHDSLFVK	819	
Db	293 --NKILEKNHLSRINSIFDFLFCCKDEKGYIKINKYTFYK	335	
RESULT 15			
Q7BG51_BACST			
ID	Q7BG51_BACST PRELIMINARY;	PRT;	1127 AA.
AC	Q7BG51-		
DT	05-JUL-2004 (T-EMBLrel. 27, Created)		
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.		
OS	Bacillus stearothermophilus.		



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 15:48:30 ; Search time 139 seconds  
(without alignments)  
3072.490 Million cell updates/sec

Title: US-10-642-248-2

Perfect score: 5108

Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAKGENIPVKNKFIINSITL 972

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5104	99.9	972	2	AAY06212 Pasteurel
2	5104	99.9	972	3	AAY43099 P. multoc
3	5104	99.9	972	7	ABJ72189 Pasteurel
4	5104	99.9	972	7	ADC77479 Pasteurel
5	5104	99.9	972	7	ADD93926 Pasteurel
6	4502.5	88.1	965	5	AAM47336 Pasteurel
7	4502.5	88.1	965	7	ADP75651 Pasteurel
8	4502.5	88.1	965	9	AEA04965 Chondroit
9	4490.5	87.9	965	3	AAY96213 P. multoc
10	4490.5	87.9	965	5	AAM47335 Pasteurel
11	4490.5	87.9	965	7	ADP75649 Pasteurel
12	4475.5	87.6	965	8	ADN40555 Glycosami
13	3697	72.4	703	9	AEA04963 Hyaluron
14	3693	72.3	703	7	ADP75656 Pasteurel
15	3690	72.2	703	7	ADP75758 Pasteurel
16	3690	72.2	703	7	ADP75759 Pasteurel
17	3689	72.2	703	7	ADP75742 Pasteurel
18	3689	72.2	703	7	ADP75761 Pasteurel
19	3689	72.2	703	7	ADP75749 Pasteurel
20	3689	72.2	703	7	ADP75746 Pasteurel
21	3689	72.2	703	7	ADP75755 Pasteurel
22	3689	72.2	703	7	ADP75753 Pasteurel
23	3689	72.2	703	7	ADP75762 Pasteurel
24	3689	72.2	703	7	ADP75744 Pasteurel

25	3688	72.2	703	7	ADP75747	Adp75747 Pasteurel
26	3688	72.2	703	7	ADP75760	Adp75760 Pasteurel
27	3688	72.2	703	7	ADP75756	Adp75756 Pasteurel
28	3688	72.2	703	7	ADP75752	Adp75752 Pasteurel
29	3688	72.2	703	7	ADP75740	Adp75740 Pasteurel
30	3688	72.2	703	7	ADP75750	Adp75750 Pasteurel
31	3688	72.2	703	7	ADP75741	Adp75741 Pasteurel
32	3686	72.2	703	7	ADP75751	Adp75751 Pasteurel
33	3686	72.2	703	7	ADP75754	Adp75754 Pasteurel
34	3686	72.2	703	7	ADP75743	Adp75743 Pasteurel
35	3686	72.2	703	7	ADP75745	Adp75745 Pasteurel
36	3686	72.2	703	7	ADP75748	Adp75748 Pasteurel
37	3686	72.2	703	7	ADP75757	Adp75757 Pasteurel
38	3686	72.2	703	7	ADP75763	Adp75763 Pasteurel
39	3673.5	71.9	702	3	AAY96212	Asy96212 P. multoc
40	2209	43.2	686	6	ABR42041	ABr42041 Escherich
41	2209	43.2	686	9	ADY52710	Ady52710 Escherich
42	2202	43.1	686	9	ADY52720	Ady52720 Escherich
43	2202	43.1	686	9	ADY52716	Ady52716 Escherich
44	556	10.9	107	8	ADN40570	Adn40570 Glycosami
45	537.5	10.5	104	8	ADN40571	Adn40571 Glycosami

ALIGNMENTS

RESULT 1

AD	AAY06212	standard; protein; 972 AA.
XX	AC	AAY06212;
XX	XX	
DT	16-AUG-1999	(first entry)
XX	XX	
DE	Pasteurella multocida hyaluronate synthase pmHAS.	
XX	XX	
KW	Hyaluronate synthase; pmHAS; hyaluronic acid; hyaluronan.	
OS	Pasteurella multocida.	
XX	XX	
PN	WO9923227-A2.	
XX	XX	
PD	14-MAY-1999.	
XX	XX	
PF	30-OCT-1998; 98WO-US023153.	
XX	XX	
PR	31-OCT-1997; 97US-0064435P.	
PR	26-OCT-1998; 98US-00178851.	
XX	XX	
PA	(OKLA ) UNIV OKLAHOMA STATE.	
XX	XX	
PI	Weigel PH, Kumari K, Deangelis P;	
XX	XX	
DR	WPI; 1999-337486/28.	
XX	XX	
DR	N-PSDB; AAX58857.	
PT	Nucleic acid encoding hyaluronate synthase for production of hyaluronic acid with controlled molecular weight and targeting specificity.	
XX	XX	
PS	Disclosure; Page 123-125; 125pp; English.	
XX	XX	
CC	CC	This present sequence represents the hyaluronate synthase (pmHAS) of Pasteurella multocida Carter Type A. The pmHAS enzyme has different kinetic optima with respect to pH and metal ion dependence, and different Km values compared with the HAS enzymes of Streptococcus equisimilis (see AAY06206) and Streptococcus pyogenes. Km values are about 2- to 3-fold lower for UDP sugars, and Vmax values are about 2- to 3-fold higher. The invention provides recombinant vectors containing hyaluronate synthase DNA, especially S. equisimilis hyaluronate synthase DNA (see AAX58841), and prokaryotic or eukaryotic host cells which produce the enzyme and its hyaluronic acid product, particularly a product with modified structure or molecular size. The hyaluronic acid produced this way is purer than that produced by conventional methods

XX SQ Sequence 972 AA; Query Match 99.9%; Score 5104; DB 2; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQLALKEFKSAEYIGRKIVFQITCKECKLSAHPVSNSAHLVSN 60  
Db 1 MNTLSQAIKAYNSNDYQLALKEFKSAEYIGRKIVFQITCKECKLSAHPVSNSAHLVSN 60

Qy 61 KEEKVNVCSPDLDIATQALLSNVKLVSDSEKNTLKNWKLLTEKKSENAEVRAVALVP 120  
Db 61 KEEKVNVCSPDLDIATQALLSNVKLVSDSEKNTLKNWKLLTEKKSENAEVRAVALVP 120

Qy 121 KDFFKDLVLAPDPHVDNFTWYKRKRGLGIKEPHOHVGLSIIVTFNRPAILSTTLACL 180  
Db 121 KDFFKDLVLAPDPHVDNFTWYKRKRGLGIKEPHOHVGLSIIVTFNRPAILSTTLACL 180

Qy 181 VNQKTHYPFEVITVDGQSDELSPIIQVENKLDIRYVRQKONGFQASARNMGLRLAKY 240  
Db 181 VNQKTHYPFEVITVDGQSDELSPIIQVENKLDIRYVRQKONGFQASARNMGLRLAKY 240

Qy 241 DFTGLDCDMPNLWHSVAELLEDDELTIIGPRKYDTQHIDPKDFLNNASLESIP 300  
Db 241 DFTGLDCDMPNLWHSVAELLEDDELTIIGPRKYDTQHIDPKDFLNNASLESIP 300

Qy 301 EVKTNNVAAGTGVSLDWRLQFQETENLRDSPPRFFAAGNVAFACKWLKSGFPD 360  
Db 301 EVKTNNVAAGTGVSLDWRLQFQETENLRDSPPRFFAAGNVAFACKWLKSGFPD 360

Qy 361 EEFNHMGEDVEFGYRLFYGSFFKTDIGIMAYHQEPGPKENETDREACKNITLDMREK 420  
Db 361 EEFNHMGEDVEFGYRLFYGSFFKTDIGIMAYHQEPGPKENETDREACKNITLDMREK 420

Qy 421 VPVIYRKLPIEDSHINRPLVSIYIIPANCANYIORCVDSALNQTVLDVICNDGST 480  
Db 421 VPVIYRKLPIEDSHINRPLVSIYIIPANCANYIORCVDSALNQTVLDVICNDGST 480

Qy 481 DNTLEVINLKYGNNPRVIRMSKNGGIASNAASFAGYYIGQLSDDDYLEPDAVELC 540  
Db 481 DNTLEVINLKYGNNPRVIRMSKNGGIASNAASFAGYYIGQLSDDDYLEPDAVELC 540

Qy 541 LKEFLDKDTLACVYTNRNPNPGSLIANGYNWPFSREKLTTAMIAHFMRFTIRAWHL 600  
Db 541 LKEFLDKDTLACVYTNRNPNPGSLIANGYNWPFSREKLTTAMIAHFMRFTIRAWHL 600

Qy 601 TDGENEKIENAVDYDMLKLSYGVKGKHLNKICYNRVLHGDNITSIKLGIIQKHNFVVVN 660  
Db 601 TDGENEKIENAVDYDMLKLSYGVKGKHLNKICYNRVLHGDNITSIKLGIIQKHNFVVVN 660

Qy 661 QSLNRQGITYNYNDEPDLDSESRYIFNKTAEQEBIDILKDIIQNKDIAVISFYFP 720  
Db 661 QSLNRQGITYNYNDEPDLDSESRYIFNKTAEQEBIDILKDIIQNKDIAVISFYFP 720

Qy 721 NTLNGLVKLLNIIEYNNKINFVLHVDRKHLTPDIKKKILAFYHKHQVNILLNNDISY 780  
Db 721 NTLNGLVKLLNIIEYNNKINFVLHVDRKHLTPDIKKKILAFYHKHQVNILLNNDISY 780

Qy 781 TSNRLIKTEAHLNINKLSQNLNCBYIIPDNHDSL FVNDSYAYMKYDVGMNFSALT H 840  
Db 781 TSNRLIKTEAHLNINKLSQNLNCBYIIPDNHDSL FVNDSYAYMKYDVGMNFSALT H 840

Qy 841 DWTEKINAHPPFKKLKITFDNDNDLSMNKVGASQGMFWTYALAHELLTIIKEVITSCQS 900  
Db 841 DWTEKINAHPPFKKLKITFDNDNDLSMNKVGASQGMFWTYALAHELLTIIKEVITSCQS 900

Qy 901 IDSVPEYNTEDIWFQFALLILEKTKGHVFNKTSITLYMPWERKLQWTNEQIESAKRGNI 960  
Db 901 IDSVPEYNTEDIWFQFALLILEKTKGHVFNKTSITLYMPWERKLQWTNEQIESAKRGNI 960

Qy 961 PVNKFINSITL 972  
XXXXXXXXXXXXX

Db 961 PVNKFINSITL 972  
XXXXXXXXXXXXX

RESULT 2  
AAY43099  
ID AAY43099 standard; protein; 972 AA.  
XX AAY43099;  
AC AC  
XX XX  
DT 06-AUG-2003 (revised)  
DT 01-FEB-2000 (first entry)  
XX P. multocida hyaluronate synthase (PmHAS) amino acid sequence.  
DE Hyaluronate synthase; PmHAS; hyaluronan; hyaluronic acid; HA; cosmetic;  
KW drug delivery; angiogenesis; wound healing; capsule synthesis;  
KW fowl cholera; shipping fever.  
XX Pasteurella multocida.  
OS WO9951265-A1.  
XX XX  
FN 14-OCT-1999.  
XX PD  
XX 01-APR-1999; 99WO-US007289.  
PF 02-APR-1998; 98US-0080414P.  
XX PR 26-OCT-1998; 98US-00178851.  
XX PA (OKLA ) UNIV OKLAHOMA.  
XX PT Deangelis P;  
PT WPI; 2000-013032/01.  
XX DR N-PSDB; AA235589.  
XX CC This is the Pasteurella multocida hyaluronate synthase (PmHAS) amino acid  
CC sequence. Hyaluronic acid (HA) or hyaluronan, is a polysaccharide that  
CC serves both structural and recognition roles in higher animals. Bacteria  
CC produce extracellular capsules of HA which mimic their host HA and aid  
CC escape from a host immune response. The invention includes a vector  
CC containing the PmHAS nucleotide sequence which can be used to express  
CC PmHAS in a foreign host. The HS nucleic acids can be used for the  
CC production of HA. Also, specific changes to the HS coding sequence can  
CC result in the production of HA having a modified size distribution or  
CC structural configuration and functional properties. The HA products can  
CC be used in e.g. drug delivery, angiogenesis and wound healing.  
CC stabilisation of recombinant proteins and in cosmetics. The HS nucleic  
CC acids can also be used to develop agents to block capsule synthesis by  
CC pathogens and act as antibiotics. The avirulent P. multocida strains can  
CC be used as vaccines for fowl cholera or shipping fever. (Updated on 06-  
CC AUG-2003 to correct OS field.)  
XX SQ Sequence 972 AA;  
Query Match 99.9%; Score 5104; DB 3; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQLALKEFKSAEYIGRKIVFQITCKECKLSAHPVSNSAHLVSN 60  
Db 1 MNTLSQAIKAYNSNDYQLALKEFKSAEYIGRKIVFQITCKECKLSAHPVSNSAHLVSN 60

Qy 61 KEEKVNVCSPDLDIATQALLSNVKLVSDSEKNTLKNWKLLTEKKSENAEVRAVALVP 120  
Db 61 KEEKVNVCSPDLDIATQALLSNVKLVSDSEKNTLKNWKLLTEKKSENAEVRAVALVP 120

Qy 121 KDFFKDLVLAPDPHVDNFTWYKRKRGLGIKEPHOHVGLSIIVTFNRPAILSTTLACL 180  
Db 121 KDFFKDLVLAPDPHVDNFTWYKRKRGLGIKEPHOHVGLSIIVTFNRPAILSTTLACL 180

Qy 181 VNQKTHYPFEVITVDGQSDELSPIIQVENKLDIRYVRQKONGFQASARNMGLRLAKY 240  
Db 181 VNQKTHYPFEVITVDGQSDELSPIIQVENKLDIRYVRQKONGFQASARNMGLRLAKY 240

Qy 241 DFTGLDCDMPNLWHSVAELLEDDELTIIGPRKYDTQHIDPKDFLNNASLESIP 300  
Db 241 DFTGLDCDMPNLWHSVAELLEDDELTIIGPRKYDTQHIDPKDFLNNASLESIP 300

Qy 301 EVKTNNVAAGTGVSLDWRLQFQETENLRDSPPRFFAAGNVAFACKWLKSGFPD 360  
Db 301 EVKTNNVAAGTGVSLDWRLQFQETENLRDSPPRFFAAGNVAFACKWLKSGFPD 360

Qy 361 EEFNHMGEDVEFGYRLFYGSFFKTDIGIMAYHQEPGPKENETDREACKNITLDMREK 420  
Db 361 EEFNHMGEDVEFGYRLFYGSFFKTDIGIMAYHQEPGPKENETDREACKNITLDMREK 420

Qy 421 VPVIYRKLPIEDSHINRPLVSIYIIPANCANYIORCVDSALNQTVLDVICNDGST 480  
Db 421 VPVIYRKLPIEDSHINRPLVSIYIIPANCANYIORCVDSALNQTVLDVICNDGST 480

Qy 481 DNTLEVINLKYGNNPRVIRMSKNGGIASNAASFAGYYIGQLSDDDYLEPDAVELC 540  
Db 481 DNTLEVINLKYGNNPRVIRMSKNGGIASNAASFAGYYIGQLSDDDYLEPDAVELC 540

Qy 541 LKEFLDKDTLACVYTNRNPNPGSLIANGYNWPFSREKLTTAMIAHFMRFTIRAWHL 600  
Db 541 LKEFLDKDTLACVYTNRNPNPGSLIANGYNWPFSREKLTTAMIAHFMRFTIRAWHL 600

Qy 601 TDGENEKIENAVDYDMLKLSYGVKGKHLNKICYNRVLHGDNITSIKLGIIQKHNFVVVN 660  
Db 601 TDGENEKIENAVDYDMLKLSYGVKGKHLNKICYNRVLHGDNITSIKLGIIQKHNFVVVN 660

Qy 661 QSLNRQGITYNYNDEPDLDSESRYIFNKTAEQEBIDILKDIIQNKDIAVISFYFP 720  
Db 661 QSLNRQGITYNYNDEPDLDSESRYIFNKTAEQEBIDILKDIIQNKDIAVISFYFP 720

Qy 721 NTLNGLVKLLNIIEYNNKINFVLHVDRKHLTPDIKKKILAFYHKHQVNILLNNDISY 780  
Db 721 NTLNGLVKLLNIIEYNNKINFVLHVDRKHLTPDIKKKILAFYHKHQVNILLNNDISY 780

Qy 781 TSNRLIKTEAHLNINKLSQNLNCBYIIPDNHDSL FVNDSYAYMKYDVGMNFSALT H 840  
Db 781 TSNRLIKTEAHLNINKLSQNLNCBYIIPDNHDSL FVNDSYAYMKYDVGMNFSALT H 840

Qy 841 DWTEKINAHPPFKKLKITFDNDNDLSMNKVGASQGMFWTYALAHELLTIIKEVITSCQS 900  
Db 841 DWTEKINAHPPFKKLKITFDNDNDLSMNKVGASQGMFWTYALAHELLTIIKEVITSCQS 900

Qy 901 IDSVPEYNTEDIWFQFALLILEKTKGHVFNKTSITLYMPWERKLQWTNEQIESAKRGNI 960  
Db 901 IDSVPEYNTEDIWFQFALLILEKTKGHVFNKTSITLYMPWERKLQWTNEQIESAKRGNI 960

Qy 961 PVNKFINSITL 972  
XXXXXXXXXXXXX

QY 121 KDPKDLVLAPLPHVNDFTWYKRRKRLGKPEHQHVGSLSIIVTTNRPAILSLTACL 180  
 DB 121 KDPKDLVLAPLPHVNDFTWYKRRKRLGKPEHQHVGSLSIIVTTNRPAILSLTACL 180  
 QY 181 VNQKTHYPFEVITDDSGQEDLSPIIRQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240  
 DB 181 VNQKTHYPFEVITDDSGQEDLSPIIRQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240  
 QY 241 DFIGLLDCMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDIDPKDFLNNASLESPL 300  
 DB 241 DFIGLLDCMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDIDPKDFLNNASLESPL 300  
 QY 301 EVKTNNSVAAKGEVTSIDWRLEOFKTEENLRSDSPRFFAAGNVAFAKKWLNKSGFFD 360  
 DB 301 EVKTNNSVAAKGEVTSIDWRLEOFKTEENLRSDSPRFFAAGNVAFAKKWLNKSGFFD 360  
 QY 361 EEFNHWGGEVFGYRLFRYSGPFTIDGIMAYHQEPGKNETDREAGKNITLIDIMREK 420  
 DB 361 EEFNHWGGEVFGYRLFRYSGPFTIDGIMAYHQEPGKNETDREAGKNITLIDIMREK 420  
 QY 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRVDSALNQTVDLEVCICNDGST 480  
 DB 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRVDSALNQTVDLEVCICNDGST 480  
 QY 481 DNTLEVINKLGNNPRVRIMSPKNGGIASANAASVAFKGYIIGQLSDDDVLEPDAVELC 540  
 DB 481 DNTLEVINKLGNNPRVRIMSPKNGGIASANAASVAFKGYIIGQLSDDDVLEPDAVELC 540  
 QY 541 LKEFLKOKTLACVTTNNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFFRMFTIRAWHL 600  
 DB 541 LKEFLKOKTLACVTTNNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFFRMFTIRAWHL 600  
 QY 601 TDGNEKIENAVDYMFLKSEVGFKILNKICYNRVLHGDNSTIKKLGIOKKNHFVVVN 660  
 DB 601 TDGNEKIENAVDYMFLKSEVGFKILNKICYNRVLHGDNSTIKKLGIOKKNHFVVVN 660  
 QY 661 QSLNRQGITVYNYDEFDLDSRKYIFNKTAEYOEIDILDKIIONKDAKIAVSIFYP 720  
 DB 661 QSLNRQGITVYNYDEFDLDSRKYIFNKTAEYOEIDILDKIIONKDAKIAVSIFYP 720  
 QY 721 NTNLGLVKLNNIIEYNKNIIFVILVHVDKNHLTPDIKKEILAFYHKKHQVNILLNNDISYY 780  
 DB 721 NTNLGLVKLNNIIEYNKNIIFVILVHVDKNHLTPDIKKEILAFYHKKHQVNILLNNDISYY 780  
 QY 781 TSNRLIKTEAHLNSINKLSQNLNCEYIIFONHDSLFVNDSYAYMKKYDVGMPFSALTH 840  
 DB 781 TSNRLIKTEAHLNSINKLSQNLNCEYIIFONHDSLFVNDSYAYMKKYDVGMPFSALTH 840  
 QY 841 DWIEKINAHPPKLIKTYFNDDNLSKMNKVGASQGMFTVALAHELLTIKEVITSQOS 900  
 DB 841 DWIEKINAHPPKLIKTYFNDDNLSKMNKVGASQGMFTVALAHELLTIKEVITSQOS 900  
 QY 901 IDSVPEYNTEDWIFALLILEKTKGHVFNKSTLTITYPWERKLTQWNTNEQIESAKRGNI 960  
 DB 901 IDSVPEYNTEDWIFALLILEKTKGHVFNKSTLTITYPWERKLTQWNTNEQIESAKRGNI 960  
 QY 961 PVNKFIINSITL 972  
 DB 961 PVNKFIINSITL 972

RESULT 3

ABJ72189  
 ID ABJ72189 standard; protein; 972 AA.  
 XX  
 AC ABJ72189;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Pasteurella multocida hyaluronan synthase protein.  
 XX  
 KW Hyaluronic acid; glycosaminoglycan; hyaluronan synthase; antirheumatic;  
 KW UDP-glucose 6-dehydrogenase; UDP-glucose pyrophosphorylase; orthopaedic;

KW UDP-N-acetylglucosamine; ophthalmological; dermatological; joint surgery;  
 KW eye; rheumatology; dermatology; adhesion; development; cell motility;  
 KW cancer; angiogenesis; wound healing; enzyme.  
 XX Pasteurella multocida.  
 XX WO2003054163-A2.  
 XX 03-JUL-2003.  
 XX 20-DEC-2002; 2002WO-US041067.  
 XX 21-DEC-2001; 2001US-0342644P.  
 XX (NOVO ) NOVOZYMES BIOTECH INC.  
 XX Sloma A, Behr R, Widner W, Tang M, Sternberg D, Brown S;  
 DR WPI; 2003-559139/52.  
 DR N-PSDB; ABT44090.  
 XX Producing a hyaluronic acid (e.g. for use in eye and joint surgery,  
 PT orthopedics, rheumatology or dermatology) comprises cultivating a  
 PT Bacillus host cell and recovering the hyaluronic acid from the  
 PT cultivation medium.  
 XX Claim 10; Page 190-194; 218pp; English.  
 XX The invention relates to a novel method which comprises producing a  
 CC hyaluronic acid via cultivating a Bacillus host cell under conditions  
 CC suitable for production of the hyaluronic acid and subsequently  
 CC recovering the hyaluronic acid from the cultivation medium. The most  
 CC abundant heteropolysaccharides of the body are the glycosaminoglycans, of  
 CC which hyaluronic acid is an example. A number of enzymes are involved in  
 CC the biosynthesis of hyaluronic acid including hyaluronan synthase, UDP-N-  
 CC glucose 6-dehydrogenase, UDP-glucose pyrophosphorylase and UDP-N-  
 CC acetylglucosamine. The molecules of the invention demonstrate  
 CC ophthalmological, antirheumatic and dermatological activities, whilst the  
 CC method itself may be useful for producing a hyaluronan in a recombinant  
 CC host cell. The hyaluronan generated may be used in eye and joint surgery,  
 CC orthopaedics, rheumatology, or dermatology and may exhibit further uses  
 CC within the fields of adhesion, development, cell motility, cancer,  
 CC angiogenesis and wound healing. The current sequence is that of the  
 CC protein of the invention which plays a role in the synthesis of  
 CC hyaluronic acid  
 XX Sequence 972 AA;  
 SQ  
 Query Match 99.9%; Score 5104; DB 7; Length 972;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNTLSQAIKAYNSNDYQIALKLFKSAIEYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 60  
 DB 1 MNTLSQAIKAYNSNDYQIALKLFKSAIEYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 60  
 QY 61 KEEKVNVCDSPLDIATQLLNSNVKLVLSDESKNTLKNKWLLEKKSSENAEVRVALVP 120  
 DB 61 KEEKVNVCDSPLDIATQLLNSNVKLVLSDESKNTLKNKWLLEKKSSENAEVRVALVP 120  
 QY 121 KDFPKDLVLAPLPHVNDFTWYKRRKRLGKPEHQHVGSLSIIVTTNRPAILSLTACL 180  
 DB 121 KDFPKDLVLAPLPHVNDFTWYKRRKRLGKPEHQHVGSLSIIVTTNRPAILSLTACL 180  
 QY 181 VNQKTHYPFEVITDDSGQEDLSPIIRQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240  
 DB 181 VNQKTHYPFEVITDDSGQEDLSPIIRQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240  
 QY 241 DFIGLLDCMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDIDPKDFLNNASLESPL 300  
 DB 241 DFIGLLDCMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHDIDPKDFLNNASLESPL 300  
 QY 301 EVKTNNSVAAKGEVTSIDWRLEOFKTEENLRSDSPRFFAAGNVAFAKKWLNKSGFFD 360

Db 301 EVKTNNSVAAKGEGTSLDWRLEQFEKTEKRLSDSPFRFAAGNVAFAKKWLNKSGFFD 360  
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFPTIDGIMAYHQEPGKENETDREAGKNITLIDINREK 420  
Db 361 EEFNHWGGEDVEFGYRLFRYGSFPTIDGIMAYHQEPGKENETDREAGKNITLIDINREK 420  
Qy 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRCDVSALNQTVDLVCICNDGST 480  
Db 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRCDVSALNQTVDLVCICNDGST 480  
Qy 481 DNTLEVINLKYGNPNRVRIMSKPNGGIASNAASPAKGYIIGOLSDDDYDLBPDAVELC 540  
Db 481 DNTLEVINLKYGNPNRVRIMSKPNGGIASNAASPAKGYIIGOLSDDDYDLBPDAVELC 540  
Qy 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
Db 541 LKEFLKDKTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
Qy 601 TDGFNEKIEANVDYDMFLKSEVGKFGHLNKICNVRVLHGDNTSIKKLGIOKKQHFVVVN 660  
Db 601 TDGFNEKIEANVDYDMFLKSEVGKFGHLNKICNVRVLHGDNTSIKKLGIOKKQHFVVVN 660  
Qy 661 QSLNRQGITTYNYDEPDLDDESRYIFNKTAEOEEDILDKIKIIONKDAKIAVSIFFP 720  
Db 661 QSLNRQGITTYNYDEPDLDDESRYIFNKTAEOEEDILDKIKIIONKDAKIAVSIFFP 720  
Qy 721 NTNLGLVKLNNIIEYKNKIFVIVLHVDKNHLPDIDKEILAFYHKHQVNILLNNDISYY 780  
Db 721 NTNLGLVKLNNIIEYKNKIFVIVLHVDKNHLPDIDKEILAFYHKHQVNILLNNDISYY 780  
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKQDSYAYMKKYDVGMNFSALTH 840  
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKQDSYAYMKKYDVGMNFSALTH 840  
Qy 841 DWIEKINAHPEPKLIKITYFNNDLKSNNVKGASQGMFMTYALAHELLTIIKEVITSCQS 900  
Db 841 DWIEKINAHPEPKLIKITYFNNDLKSNNVKGASQGMFMTYALAHELLTIIKEVITSCQS 900  
Qy 901 IDSVPYNTEDIWQFALLILEKKTGHVFNKTSLTLYMPWERKLOWTNEQIESAKRGENI 960  
Db 901 IDSVPYNTEDIWQFALLILEKKTGHVFNKTSLTLYMPWERKLOWTNEQIESAKRGENI 960  
Qy 961 PVNKFINSITL 972  
Db 961 PVNKFINSITL 972  
RESULT 4  
ADC77479  
ID ADC77479 standard; protein; 972 AA.  
XX  
AC ADC77479;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Pasteurella multocida hyaluronate synthase (HAS) amino acid sequence.  
XX  
KW hyaluronate synthase; HAS; streptococcal infection;  
KW streptococcal bacteria; phagocytic cell; foreign microorganism;  
KW polysaccharide capsule; hyaluronic acid capsule; HA capsule;  
KW antibacterial compound; bacterial infection; enzyme.  
XX  
OS Pasteurella multocida.  
XX  
PN US2003092118-A1.  
XX  
PD 15-MAY-2003.  
XX  
PF 13-JUN-2002; 2002US-00172527.  
XX  
PR 31-OCT-1997; 97US-0064435P.  
PR 26-OCT-1998; 98US-00178851.

PR 21-DEC-1999; 99US-00469200.  
PR 13-JUN-2001; 2001US-0297744P.  
PR 13-JUN-2001; 2001US-0297788P.  
XX  
PA (DEAN/) DEANGELIS P L.  
PA (WEIG/) WEIGEL P H.  
PA (KUMA/) KUMARI K.  
XX  
PI Deangelis PL, Weigel PH, Kumari K;  
XX  
DR WPI; 2003-755179/71.  
XX N-PSDB; ADC77478.  
DR  
XX  
PT Recombinant host cell is a Bacillus cell comprising a recombinant vector  
PT having purified nucleic acid segment with a coding region encoding  
PT enzymatically active hyaluronan synthase.  
XX  
PS Claim 104; SEQ ID NO 10; 79pp; English.  
XX  
CC This invention relates to a recombinant Bacillus host cell containing a  
CC recombinant vector including a nucleic acid segment with a coding region  
CC encoding enzymatically active hyaluronate synthase (HAS), where the  
CC coding region is under control of a promoter. The incidence of  
CC streptococcal infections is a major health and economic problem  
CC worldwide. Streptococcal bacteria can grow undetected by the body's  
CC phagocytic cells which are responsible for recognising and engulfing  
CC foreign microorganisms. One way the bacteria evades these cells is by  
CC coating themselves with polysaccharide capsules, such as a hyaluronic  
CC acid (HA) capsule. As HA is non-immunogenic, the encapsulated bacteria do  
CC not illicit an immune response. The present invention provides a means of  
CC preparing HA which may prove useful for the identification of novel  
CC antibacterial compounds for the treatment of bacterial infection. The  
CC present sequence is the amino acid sequence of the hyaluronate synthase  
CC (HAS) of Pasteurella multocida, used in the method of the invention.  
XX  
SQ Sequence 972 AA;  
Query Match 99.9%; Score 5104; DB 7; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNTLSQAIKAYNSNDYQLALALKEKSAEYIGRKIVFQITKCKEKLSAHPSVNSAHLNVN 60  
Db 1 MNTLSQAIKAYNSNDYQLALALKEKSAEYIGRKIVFQITKCKEKLSAHPSVNSAHLNVN 60  
Qy 61 KEEKVNVCDSPDLATQLLLSNVKLVLSDSSEKNTLKNWKLLTEKKSENAEYRAVALVP 120  
Db 61 KEEKVNVCDSPDLATQLLLSNVKLVLSDSSEKNTLKNWKLLTEKKSENAEYRAVALVP 120  
Qy 121 KDFPKDLVLAPLDPHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTFNRPAILISITLACL 180  
Db 121 KDFPKDLVLAPLDPHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTFNRPAILISITLACL 180  
Qy 181 VNOKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVRQKNGFQASARNNGRLAKY 240  
Db 181 VNOKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVRQKNGFQASARNNGRLAKY 240  
Qy 241 DFIGLLDCMAPNPLWVHSYVAELLEDLDTIIGPRKYIDTQHDIDPKDFLNNSALESPL 300  
Db 241 DFIGLLDCMAPNPLWVHSYVAELLEDLDTIIGPRKYIDTQHDIDPKDFLNNSALESPL 300  
Qy 301 EVKTNNSVAAKGEGTSLDWRLEQFEKTEKRLSDSPFRFAAGNVAFAKKWLNKSGFFD 360  
Db 301 EVKTNNSVAAKGEGTSLDWRLEQFEKTEKRLSDSPFRFAAGNVAFAKKWLNKSGFFD 360  
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFPTIDGIMAYHQEPGKENETDREAGKNITLIDINREK 420  
Db 361 EEFNHWGGEDVEFGYRLFRYGSFPTIDGIMAYHQEPGKENETDREAGKNITLIDINREK 420  
Qy 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRCDVSALNQTVDLVCICNDGST 480  
Db 421 VPYIYRKLPIEDSHINRPLVSIYIIPAYNCANYIQRCDVSALNQTVDLVCICNDGST 480

QY 481 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 540  
DB 481 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 540  
QY 541 LKEFLKDKTACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
DB 541 LKEFLKDKTACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
QY 601 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKKIYNRVLHGDNTSIKKGIGKQKHFFVNVN 660  
DB 601 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKKIYNRVLHGDNTSIKKGIGKQKHFFVNVN 660  
QY 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEYQSEIDILKDIKIQNDKAKIAVSIFYP 720  
DB 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEYQSEIDILKDIKIQNDKAKIAVSIFYP 720  
QY 721 NTNLGLVKLNIIIEYNKNIIFVILVHDKNHLTPDIKKEILAFYHKGQVNLNNDISYY 780  
DB 721 NTNLGLVKLNIIIEYNKNIIFVILVHDKNHLTPDIKKEILAFYHKGQVNLNNDISYY 780  
QY 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHSLFVNDSYAYMKYDVGWNFSAETH 840  
DB 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHSLFVNDSYAYMKYDVGWNFSAETH 840  
QY 841 DWIEKINAHPPFKLIKTYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCOS 900  
DB 841 DWIEKINAHPPFKLIKTYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCOS 900  
QY 901 IDSPEYNTEDIWFOFALLIIEKKTGHVFNKTSITLTYPWPKLQWNTNEQIESAKRGNI 960  
DB 901 IDSPEYNTEDIWFOFALLIIEKKTGHVFNKTSITLTYPWPKLQWNTNEQIESAKRGNI 960  
QY 961 PVNKFINSITL 972  
DB 961 PVNKFINSITL 972

RESULT 5  
ADD93926  
ID ADD93926 standard; protein; 972 AA.  
XX  
AC ADD93926;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Pasteurella multocida hyaluronan synthase protein.  
XX  
KW hyaluronan synthase; HAS; Streptococcal infection;  
KW Streptococcal bacterium; phagocytic cell; macrophage;  
KW polymorphonuclear cell; PMN; polysaccharide capsule; hyaluronic acid;  
KW HA capsule; vaccine; enzyme.  
XX  
OS Pasteurella multocida.  
XX  
XX WO2003048330-A2.  
PN  
XX  
PD 12-JUN-2003.  
XX  
XX 03-DEC-2002; 2002WO-US038596.  
PF  
XX  
PR 03-DEC-2001; 2001US-0336105P.  
PR 11-DEC-2001; 2001US-00011771.  
XX  
XX (WEIG/) WEIGEL P H.  
PA (KUMARI/) KUMARI K.  
XX  
PI Weigel PH, Kumari K;  
XX  
DR WPI; 2003-482708/45.  
DR N-PSDB; ADD93925.  
XX  
XX Novel functionally active hyaluronan synthase having at least one  
PT modified amino acid residue in it as compared to a corresponding

functionally active native hyaluronan synthase, useful for producing  
hyaluronic acid.  
Claim 22; SEQ ID NO 8; 362pp; English.  
XX This invention relates to a novel functionally active hyaluronan synthase  
CC (HAS) having at least one modified amino acid residue in it or having  
CC altered enzymatic activity as compared to a corresponding functionally  
CC active native hyaluronan synthase. Streptococcal infection is a major  
CC health and economic problem worldwide, particularly in developing  
CC countries. Streptococcal bacteria can grow undetected by the body's  
CC phagocytic cells (macrophages and polymorphonuclear cells; PMNs). The  
CC bacteria can evade detection by coating itself with polysaccharide  
CC capsules, such as a hyaluronic acid (HA) capsule. The invention is useful  
CC for producing hyaluronic acid and may aid the production of therapeutics  
CC and vaccines against Streptococcal infection. The present sequence is  
CC that of the Pasteurella multocida HAS protein which is related to the  
CC invention.  
XX  
SQ Sequence 972 AA;  
Query Match 99.9%; Score 5104; DB 7; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNTLSQAIKAYNSNDYQALAKLFEKSABEIIYGRKIVEFQITCKEKL SAHPSVNSAHSVN 60  
DB 1 MNTLSQAIKAYNSNDYQALAKLFEKSABEIIYGRKIVEFQITCKEKL SAHPSVNSAHSVN 60  
QY 61 KEEKVNVCDSPDLIATQLLLSNVKVLSDSEKVTLNKNWKLTEKKSSEAEVRAVALVP 120  
DB 61 KEEKVNVCDSPDLIATQLLLSNVKVLSDSEKVTLNKNWKLTEKKSSEAEVRAVALVP 120  
QY 121 KDFPKDLVLAFLPDHVNDFTHYKGRKLGITKPEHQHVGLSIIIVTTFNRPAILSTILACL 180  
DB 121 KDFPKDLVLAFLPDHVNDFTHYKGRKLGITKPEHQHVGLSIIIVTTFNRPAILSTILACL 180  
QY 181 VNQKTHYPFEVITDDGSQEDLSPIIROYENKLDIYRVQKDNQFQASAAARMGLRLAKY 240  
DB 181 VNQKTHYPFEVITDDGSQEDLSPIIROYENKLDIYRVQKDNQFQASAAARMGLRLAKY 240  
QY 241 DFILGLDCDMAPNPLWVHSYVAELLEDLTIIGPRKYIDTQHDIDPKDFLNNASLESUP 300  
DB 241 DFILGLDCDMAPNPLWVHSYVAELLEDLTIIGPRKYIDTQHDIDPKDFLNNASLESUP 300  
QY 301 EVKTNNSVAAKGEFTVSLDWLEQFEKTENRLSDSPERFPAAGNVAFKWLKSGPFD 360  
DB 301 EVKTNNSVAAKGEFTVSLDWLEQFEKTENRLSDSPERFPAAGNVAFKWLKSGPFD 360  
QY 361 EEFNHWGGEDEVFGYRLFRYGSFPKTIIDGIMAYHQEPGKNETDREAGKNITLDMREK 420  
DB 361 EEFNHWGGEDEVFGYRLFRYGSFPKTIIDGIMAYHQEPGKNETDREAGKNITLDMREK 420  
QY 421 VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRVDSALNQTVDVLEVCINDGST 480  
DB 421 VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRVDSALNQTVDVLEVCINDGST 480  
QY 481 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 540  
DB 481 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 540  
QY 541 LKEFLKDKTACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
DB 541 LKEFLKDKTACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
QY 601 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKKIYNRVLHGDNTSIKKGIGKQKHFFVNVN 660  
DB 601 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKKIYNRVLHGDNTSIKKGIGKQKHFFVNVN 660  
QY 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEYQSEIDILKDIKIQNDKAKIAVSIFYP 720  
DB 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEYQSEIDILKDIKIQNDKAKIAVSIFYP 720



QY 721 NTNLGLVKLNIIIEYNKNI FVILVHVDKXHLTPDIKKEILAFYHKHVNILLNNDISYY 780  
 DB |||||  
 QY 721 NTNLGLVKLNIIIEYNKNI FVILVHVDKXHLTPDIKKEILAFYHKHVNILLNNDISYY 780  
 DB |||||  
 QY 781 TSNRLIKTEAHLNINKLSQLNLNCEYIIFDNHDSLFVKNDISYAYMKKYDVGMNFSALTH 840  
 DB |||||  
 QY 781 TSNRLIKTEAHLNINKLSQLNLNCEYIIFDNHDSLFVKNDISYAYMKKYDVGMNFSALTH 840  
 DB |||||  
 QY 841 DWIEKINAHPPPKLIKTIFYNDNDLKSMMVKGASQGMFTYALAHELLTIIKEVITSCQS 900  
 DB |||||  
 QY 841 DWIEKINAHPPPKLIKTIFYNDNDLKSMMVKGASQGMFTYALAHELLTIIKEVITSCQS 900  
 DB |||||  
 QY 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKGENI 960  
 DB |||||  
 QY 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKGENI 960  
 DB |||||  
 QY 961 PVNKFIIINSITL 972  
 DB |||||  
 QY 961 PVNKFIIINSITL 972  
 DB |||||

RESULT 6  
 AAM47336  
 ID AAM47336 standard; protein; 965 AA.  
 XX  
 AC AAM47336;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Pasteurella multocida chondroitin synthase #2.  
 XX  
 KW Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer;  
 KW eye application; joint application; moisturiser; drug delivery;  
 KW wound dressing; biocompatible film.  
 XX  
 OS Pasteurella multocida.  
 XX  
 PN WO200180810-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 25-APR-2001; 2001WO-US013395.  
 XX  
 PR 25-APR-2000; 2000US-0199538P.  
 XX  
 PA (DANG/) DE ANGELIS P L.  
 XX  
 PI De Angelis PL;  
 XX  
 DR WPI; 2002-049237/06.  
 DR N-PSDB; ABA05098.  
 XX

PT New chondroitin synthase gene obtained from Pasteurella multocida, useful  
 PT as hyaluronan polysaccharide substitute in medial or cosmetic  
 PT applications, e.g. for eye or joint applications, for moisturizer or  
 PT wound dressings.  
 XX

PS Claim 3; Page 122; 125pp; English.  
 XX

CC The present invention relates to the coding sequence of the Pasteurella  
 CC multocida chondroitin synthase. A chondroitin polysaccharide may be used  
 CC as a hyaluronan polysaccharide substitute in medial or cosmetic  
 CC applications, for example in eye or joint applications, for moisturiser  
 CC or wound dressings. The enzyme may be used in covalently coupling  
 CC specific drugs, proteins or toxins to the structurally modified  
 CC chondroitin for general or targeted drug delivery or radiological  
 CC procedures, covalently cross linking the hyaluronan acid itself or to  
 CC other supports to achieve a gel or other three dimensional biomaterial  
 CC with stronger physical properties, and covalently linking hyaluronan acid  
 CC to a surface to create a biocompatible film or monolayer. The present  
 CC sequence is one version of the protein of the invention  
 XX  
 XX Sequence 965 AA;

Query Match 88.1%; Score 4502.5; DB 5; Length 965;  
 Best Local Similarity 86.9%; Pred. No. 0;  
 Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;  
 QY 1 MNTLSQAIKAYNSNDYQALAKLFEKSAEYIGRIKVEFQITKCKEKLKSAHSAHVSNAHLSVN 60  
 DB |||||  
 QY 1 MNTLSQAIKAYNSNDYQALAKLFEKSAEYIGRIKVEFQITKCKEKLKSAHSAHVSNAHLSVN 60  
 DB |||||  
 QY 61 KEKVNVCOSPLDIATOLLNSNVKLVLSDESKTKLNKWKLLTEKKSNAEYAVRALVP 120  
 DB |||||  
 QY 54 EDKNSVCDSSLDIATOLLNSNVKLVLSDESKTKLNKWKLLTEKKSNAEYAVRALVP 113  
 DB |||||  
 QY 121 KDFPKDLVLAPLDHNDFTWYKRRKRLIGIKPEHGHVGLSIIIVTFNRPALISITLACL 180  
 DB |||||  
 QY 114 KDFPKDLVLAPLDHNDFTWYKRRKRLIGIKPEHGHVGLSIIIVTFNRPALISITLACL 173  
 DB |||||  
 QY 181 VNOKTHYPEVIVTDDGSOEDLSPIIROYENKLDIRYRQKNGPFOASARNMGLRLAKY 240  
 DB |||||  
 QY 174 VNOKTHYPEVIVVADGSKENLLTIVQYEQKLDIYVYRQKDYQYQLCAVRNLGLRTAKY 233  
 DB |||||  
 QY 241 DPTGLDCCMAPNPLVHVSVAELLEDLTIIGPRKYIDTOHIDPKDFLNNASLESPL 300  
 DB |||||  
 QY 234 DFVSILDCDMPQOQLVVHVSYLELLEDNDIVLIGPRKYVDTHNITAEQFLNDPVLIESLP 293  
 DB |||||  
 QY 301 EVKTNNSVAAKGEVTSVLDWRLEQPEKTENLRSDSPFFFAAGNVAFAKWLKNGSFPD 360  
 DB |||||  
 QY 294 ETATNNPSTISKGNISLDWRLEHFKKTDNLRCDSPFFRYFCGNVAFKSEWLNKVGWFD 353  
 DB |||||  
 QY 361 EEPNHWGGEDVEFGYRLFRYGGFFKTDIGIMAYHQBPFGKENETDREAGNITLDMIREK 420  
 DB |||||  
 QY 354 EEPNHWGGEDVEFGYRLFAKGCFFRVIDGIMAYHQBPFGKENETDREAGNITLDMIREK 413  
 DB |||||  
 QY 421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVVLEVCINCNGST 480  
 DB |||||  
 QY 414 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVVLEVCINCNGST 473  
 DB |||||  
 QY 481 DNTLEVINKLYGNPRVRIMSKPNGGASASNAVSFAKGYIIGQLDSDDDYLEPDAVELC 540  
 DB |||||  
 QY 474 DNTLEVINKLYGNPRVRIMSKPNGGASASNAVSFAKGYIIGQLDSDDDYLEPDAVELC 533  
 DB |||||  
 QY 541 LKEFLKDKTLACVYTTNRNVPDGLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
 DB |||||  
 QY 534 LKEFLKDKTLACVYTTNRNVPDGLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 593  
 DB |||||  
 QY 601 TDGFNEKIENAVDYMFLKLSVGVKPKHLNKICYNRVLHGDNTSIKKGIGQKQHFVVVN 660  
 DB |||||  
 QY 594 TDGFNEKIENAVDYMFLKLSVGVKPKHLNKICYNRVLHGDNTSIKKGIGQKQHFVVVN 653  
 DB |||||  
 QY 661 QSLNRQGITYYNYDEPDLDDESKYIFNKTAEYQEBIDILKDIKTONKDAKIAVSIFYP 720  
 DB |||||  
 QY 654 QSLNRQGITYYNYDEPDLDDESKYIFNKTAEYQEBIDILKDIKTONKDAKIAVSIFYP 713  
 DB |||||  
 QY 721 NTNLGLVKLNIIIEYNKNI FVILVHVDKXHLTPDIKKEILAFYHKHVNILLNNDISYY 780  
 DB |||||  
 QY 714 NTNLGLVKLNIIIEYNKNI FVILVHVDKXHLTPDIKKEILAFYHKHVNILLNNDISYY 773  
 DB |||||  
 QY 781 TSNRLIKTEAHLNINKLSQLNLNCEYIIFDNHDSLFVKNDISYAYMKKYDVGMNFSALTH 840  
 DB |||||  
 QY 774 TSNRLIKTEAHLNINKLSQLNLNCEYIIFDNHDSLFVKNDISYAYMKKYDVGMNFSALTH 833  
 DB |||||  
 QY 841 DWIEKINAHPPPKLIKTIFYNDNDLKSMMVKGASQGMFTYALAHELLTIIKEVITSCQS 900  
 DB |||||  
 QY 834 DWIEKINAHPPPKLIKTIFYNDNDLKSMMVKGASQGMFTYALAHELLTIIKEVITSCQS 893  
 DB |||||  
 QY 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKGENI 960  
 DB |||||  
 QY 894 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKGENI 953  
 DB |||||  
 QY 961 PVNKFIIINSITL 972  
 DB |||||  
 QY 954 PVNKFIIINSITL 965



```
RESULT 7
ADP75651
ID ADP75651 standard; protein; 965 AA.
XX AC
XX ADP75651;
XX
DT 12-AUG-2004 (first entry)
XX DE
XX Pasteurella multocida chondroitin synthase #1.
XX polymer production; hyaluronic acid polymer; chondroitin polymer;
XX chondroitin synthase; enzyme.
XX Pasteurella multocida.
XX WO2003029261-A2.
XX PN
XX 10-APR-2003.
XX PD
XX 12-JUL-2002; 2002WO-US022386.
XX PF
XX 13-JUL-2001; 2001US-0305263P.
XX PR 22-JAN-2002; 2002US-0350642P.
XX PR 08-MAY-2002; 2002US-00142143.
XX
XX (DEAN/) DEANGELIS P L.
XX PA
XX Deangelis PL;
XX PI
XX WPI; 2003-532558/50.
XX DR N-PSDB; ADP75650.
XX
XX Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by
XX providing a functional acceptor, a synthase capable of elongating the
XX acceptor and sugars such that synthase elongates the acceptor to provide
XX polymer.
XX
XX Claim 95; SEQ ID NO 4; 538pp; English.
XX
XX The invention comprises a method for producing a polymer, especially a
XX hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than
XX 150 sugars. The method involves providing a functional acceptor,
XX providing a synthase capable of elongating the functional acceptor, and
XX providing sugars such that the synthase elongates the functional acceptor
XX to provide the polymer. The method of the invention is useful for
XX producing a hyaluronic acid or chondroitin polymer composed of 1-150
XX sugars. The present amino acid sequence represents a Pasteurella
XX multocida chondroitin synthase of the invention.
XX
XX Sequence 965 AA;
XX
Query Match 88.1%; Score 4502.5; DB 7; Length 965;
Best Local Similarity 86.9%; Pred. No. 0;
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;
XX
QY 1 MNTLSQAIKAYNSNDYQALALFEKSAEYGRKIVEFQITCKEKLKLSAHPVSNSAHLVSN 60
DB 1 MNTLSQAIAKAYNSNDYELALFEKSAEYGRKIVEFQIKCKEKL----STNS---YVS 53
XX
QY 61 KEEKVNCVDSPIADIATOLLISNVKLVLSDSSEKNTLKNKWKLLTEKKSSENAEVRVALVLP 120
DB 54 EDKQNSVCSSSDIATQLLSNVKLVLTJUSESEKNSLKNKWKSIITGKKSSENAEIRKVELVP 113
XX
QY 121 KDFPKDLVLAPLDHVDNFTWYKGRKLGKPEHQHVGLSIIVTFNRPAILSLITLACL 180
DB 114 KDFPKDLVLAPLDHVDNFTWYKGRKSLGKIPVKNIGLSIIPTFNRSRILDTLACL 173
XX
QY 181 VNQKTHYPEVITDQSGQEDLSPIROYENKLDIRYVRQKNGQFQASARNNGRLAKY 240
DB 174 VNQKTHYPEVIVADDGSKENLLTIYQKYEQLDIIKYVRQKDYGYQLCAVRNLGLRTAKY 233
XX
QY 241 DFGLGLDCDMAFNPLVWHSYVAELLEDDDTLTIIGPRKYDTQHDIPKDFLNNASLLESPL 300
XX
```

```
Db 234 DFVSIILDCDMAFQQLVWHSYLTLELLENDNDVLIGPRKYVDTHNITABQFNDPVLIESLP 293
QY 301 EVKTNNSVAAKGCTGVSLDWRLEQFTEKTNLRSLSDSPFRFFAAGNVAFAKKWLNKSGFFD 360
Db 294 ETATNNPSITSGNISLSDWRLEHFHFKTDNRLCDSFRYFPCGNVAFSKWLNKVGWFD 353
QY 361 EEFNHWGGEDVEFGYRLFRYGSFPTIDGIMAYHQEPGPKENETDRAGKNITLIDIMREK 420
Db 354 EEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAYHQEPGPKENETDRBAGKSITLKVKEK 413
QY 421 VPYIYRKLPIEDSHINRPLVSIYIPAYCANYIOECVDSALNQTVDLEVCICNDGST 480
Db 414 VPYIYRKLPIEDSHIHRIPLVSIYIPAYCANYIOECVDSALNQTVDLEVCICNDGST 473
QY 481 DNTLEVINKLYGNPRVRIRMSKPGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 540
Db 474 DNTLEVINKLYGNPRVRIRMSKPGGIASASNAVSPAKGYIIGQLSDDDYLEPDAVELC 533
QY 541 LKEFLDKDTLACVYTTNRNVPDGLIANGYVWPEFSREKLTAMIAHHPMFRTIRAWHL 600
Db 534 LKEFLDKDTLACVYTTNRNVPDGLIANGYVWPEFSREKLTAMIAHHPMFRTIRAWHL 593
QY 601 TDGFNEKIENAVDYDMFLKLSEVCKFKHLNKICYNRVLHGDNSTIKKLGIOKKHFFVVVN 660
Db 594 TDGFNEKIENAVDYDMFLKLSEVCKFKHLNKICYNRVLHGDNSTIKKLGIOKKHFFVVVN 653
QY 661 QSLNRQGITVYNYDEFDLDESRYIFNKTAEYOEEDILKDIKIONKDAKIAVSIFYP 720
Db 654 QSLNRQGITVYNYDKFDLDESRYIFNKTAEYOEEMDILKDLKIQNKDAKIAVSIFYP 713
QY 721 NTNLGLVKLNNIIEYNKNIFVILHVDKXHLTPDIKKEILAFYHKGQVNNLLNNDISYY 780
Db 714 NTNLGLVKLNNIIEYNKNIFVILHVDKXHLTPDIKKEILAFYHKGQVNNLLNNDISYY 773
QY 781 TSNRLIKTEAHLNINKLSQLNLNCEYIIFNHDLSLVKNDISYAYMKKYDVGWNPFSALTH 840
Db 774 TSNRLIKTEAHLNINKLSQLNLNCEYIIFNHDLSLVKNDISYAYMKKYDVGWNPFSALTH 833
QY 841 DWIEKINAHPPFKKLIKTYFNNDNLKSNMNVKASQGMFTYALAHELLTIKEVITSCQS 900
Db 834 DWIEKINAHPPFKKLIKTYFNNDNLKSNMNVKASQGMFTYALAHELLTIKEVITSCQS 893
QY 901 IDSYPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKQWLTNEQIESAKRGNI 960
Db 894 IDSYPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKQWLTNEQIESAKRGNI 953
QY 961 PVNKPFIINSITL 972
Db 954 PVNKPFIINSITL 965
XX
RESULT 8
AEA04965
ID AEA04965 standard; protein; 965 AA.
XX AC
XX AEA04965;
XX
DT 11-AUG-2005 (first entry)
XX
DE Chondroitin synthase, PmCS, SEQ ID 3.
XX
KW Chondroitin synthase; polysaccharide; enzyme.
XX
OS Pasteurella multocida.
XX
PN US2005124046-A1.
XX
XX 09-JUN-2005.
XX
PF 16-JUL-2002; 2002US-00197153.
XX
XX 10-NOV-1999; 99US-00437277.
XX
```

```
XX (DEAN/) DEANGELIS P L.
PA Deangelis PL;
XX WPI; 2005-417007/42.
XX N-PSDB; AEA04966.
XX
PT Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin),
PT useful in polysaccharide polymer grafting, comprises providing hyaluronic
PT acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the
PT functional acceptor.
XX
PS Disclosure; SEQ ID NO 3; 41pp; English.
XX
CC The present invention relates to a method for elongating a functional
CC acceptor. The method comprises providing a hyaluronic acid (HA) synthase
CC (PmHAS; AEA04963) capable of elongating the functional acceptor and
CC providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid
CC synthase elongates the functional acceptor. PmHAS adds sugars to the
CC nonreducing end of a growing polymer chain. The PmHAS sequence is
CC significantly different from the other known HA synthases: there appears
CC to be only two short potential sequence motifs (AEA04967 and AEA04968) in
CC common between PmHAS and the other HA synthases. The method is useful in
CC polysaccharide polymer grafting, which may be utilized in the development
CC of biotechnological medical improvements. These may be used for producing
CC hybrid polysaccharides or for forming polysaccharide coatings. Also
CC disclosed is chondroitin synthase (PmCS; AEA04965) and its coding
CC sequence (AEA04966) from Pasteurella multocida. Type A P. multocida
CC produces a HA capsule [GlcUA-GlcNAc repeats] and possesses the PmHAS
CC enzyme. On the other hand, Type P P. multocida produce a chondroitin or
CC chondroitin-like polymer capsule [GlcUA-GalNAc repeats] using PmCS. both
CC Either HA or chondroitin chains can serve as acceptors for PmCS as both
CC acceptors serve well for PmHAS.
XX
SQ Sequence 965 AA;

Query Match      88.18; Score 4502.5; DB 9; Length 965;
Best Local Similarity 86.94; Pred. No. 0;
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

QY 1 MNTLSQAIKAYNSNDYQALALFEKSAEYGRKIVEFQITKCKEKLSAHPVSNSAHSVN 60
DB 1 MNTLSQAIKAYNSNDYELALFEKSAEYGRKIVEFQIICKCKEKL----STNS---YVS 53

QY 61 KEKKNVCDSPDLATOLLISNVKKVLSDSEKNTLKNKKLLETKKSENAEVRVALVP 120
DB 54 EDKNSVCDSSLATOLLISNVKKVLTLSSEKNSLKNKWSITGKKSSENAEIRKVELVP 113

QY 121 KDFPKDLVLAPLPDHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTTENRPAILSITLACL 180
DB 114 KDFPKDLVLAPLPDHVNDFTWYKNRKKSLGKPKVKNKGISLIITPFRSRILDIITLACL 173

QY 181 VNQKTHYFVEVIVTDDGSQBDLSPRIQYENKLDIRYVRQKMGFQASAAARNMGLRLAKY 240
DB 174 VNQKTHYFVEVIVVADDSKENLLTIVQYEQGLDKYVRQKDYGYQLCAVRNLGLRTAKY 233

QY 241 DFTGLDCMAPNPLVHVSVAELLEDLDDTTITIGPKRYIDTOHIDPKDFLNNASLESPL 300
DB 234 DFTGLDCMAPQQLVAHVSYLTELLEDNDIVLIGPKRYVTDHITAITAQFLNDPYLEISLP 293

QY 301 EVKTNNSVAAKGSTVSLDRLEQFEXTENLRISDSFRFFAAGNVAPAKWLNKSGFFD 360
DB 294 ETATNNNPSITSKNSLDRLEHFKKTDNRLCDSFRFYFCGNVAFSKEWLNKGVWFD 353

QY 361 EEFNHMGGEVFGYRLFRYGSFKTTIDIGIMAYHQEPGPKENETDREAGKNITLIDIMREK 420
DB 354 EEFNHMGGEVFGYRLFANGCFRVIDGGWAYHQEPGPKENETDREAGKSITLKIYKEK 413

QY 421 VPIYRKLLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVICNDGST 480
DB 414 VPIYRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVICNDGST 473

QY 481 DNTLEVINKLYGNPRVRIMSKPENGIGIASASNAAVSFAKGYIIGOLDSDDDYLPDAVELC 540
DB 474 DNTLEVINKLYGNPRVRIMSKPENGIGIASASNAAVSFAKGYIIGOLDSDDDYLPDAVELC 533

QY 541 LKEFLKDKTCLACVYTTNRNVNPDGSLIANGYNNPFSREKLTTAMIAHFRMFTIRAWHL 600
DB 534 LKEFLKDKTCLACVYTTNRNVNPDGSLIANGYNNPFSREKLTTAMIAHFRMFTIRAWHL 593

QY 601 TDGFNEKIEANVDYDMFLKSEVGKPKHLNKCYNRVLHGDNTSIKKLGIOKQKHFFVNVN 660
DB 594 TDGFNEKIEANVDYDMFLKSEVGKPKHLNKCYNRVLHGDNTSIKKLGIOKQKHFFVNVN 653

QY 661 QSLNRGIIYVNYDEFDLDESRSKYIFNKTAEYQBEIDILKOIKIQNKDAKIAVSIFYP 720
DB 654 QSLNRGIIYVNYDKFDLDESRSKYIFNKTAEYQBEWDILKDKLQNKDAKIAVSIFYP 713

QY 721 NTNLGLVKKLNIIIEYNKNIIFVILVHVDKNHLPDIKKEILAFYHKGHVNNILLNNDISYY 780
DB 714 NTNLGLVKKLNIIIEYNKNIIFVILVHVDKNHLPDIKKEILAFYHKGHVNNILLNNDISYY 773

QY 781 TSNRLIKTEAHLNINIKLSQNLNCEYIIFDNHDSLFVKNDISYAYMKYDVGWNFSAETH 840
DB 774 TSNRLIKTEAHLNINIKLSQNLNCEYIIFDNHDSLFVKNDISYAYMKYDVGWNFSAETH 833

QY 841 DWIEKINAHPPPKKLTKTYFNDNDLKSMMVKGASQGMFMTYALAHELLTTIIEKIVITSCQS 900
DB 834 DWIEKINAHPPPKKLTKTYFNDNDLKSMMVKGASQGMFMTYALAHELLTTIIEKIVITSCQS 893

QY 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSLTLYMPWERKLTQWNTNEQIESAKRGNI 960
DB 894 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSLTLYMPWERKLTQWNTNEQIQSAKKGENI 953

QY 961 PVNKFPIINSITL 972
DB 954 PVNKFPIINSITL 965

RESULT 9
AAAY96213
ID AAY96213 standard; protein; 965 AA.
XX
AC AAY96213;
XX
DT 17-AUG-2000 (first entry)
XX
DE P. multocida chondroitin synthase.
XX
KW Chondroitin synthase; CS; enzyme; hyaluronic acid; ulcer;
KW tissue abrasion; viscoelastic replacement; bioadhesive.
XX
OS Pasteurella multocida.
XX
PN WO200027437-A2.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US026501.
XX
PR 11-NOV-1998; 98US-0107929P.
XX
PR 01-APR-1999; 99US-00283402.
XX
PA (OKLA ) UNIV OKLAHOMA STATE.
XX
PI Deangelis PL;
XX
DR WPI; 2000-376319/32.
DR N-PSDB; AAA27449.
XX
PT Novel method for the enzymatic transfer of sugar molecules to an
PT acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or
PT drug delivery systems, including hybrid molecules.
XX
PS Claim 15; Page 85; 86pp; English.
```

XX The present sequence is the Pasteurella multocida chondroitin synthase  
CC PmCS. PmCS catalyses glycosaminoglycan polymerisation to produce  
CC chondroitin: a linear polysaccharide which has viscoelastic properties  
CC which makes it useful for a number of applications. Chondroitin can be  
CC used with hyaluronic acid (HA) to coat medical devices e.g. catheters and  
CC sensors to reduce tissue abrasion. In addition, they can be used as  
CC broadsides for haemostatic sealing and healing of wounds and surgical  
CC incisions; and as biomaterials that provide sustained delivery of  
CC encapsulated drugs, to wounds, ulcers, injuries or surgical sites  
XX  
SQ Sequence 965 AA;

Query Match 87.9%; Score 4490.5; DB 3; Length 965;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 843; Conservative 62; Mismatches 60; Indels 7; Gaps 2;

Qy 1 MNTLSQAIKAYNSNDYQALALFKPKSAEYGRKIVEFQITCKEKLKSAHPNSVNSAHLNVN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFKPKSAEYGRKIVEFQITCKEKLKSAHPNSVNSAHLNVN 53  
Qy 61 KEEKVNVCSDPLDIATQLLSNVKLVLSSEKNTLKNKWLTKKSENAEVRVALVP 120  
Db 54 EDKNSVCSSLDIATQLLSNVKLVLSSEKNTLKNKWLTKKSENAEVRVALVP 113  
Qy 121 KDFPKDLVLAFLPDHVDFTYKRRKGLGKPEHQVGLSIIVTNRPAILSITLACL 180  
Db 114 KDFPKDLVLAFLPDHVDFTYKRRKGLGKPEHQVGLSIIVTNRPAILSITLACL 173  
Qy 181 VNQKTHVPFVIVTDDSGOEDLSPIROYENKLDIRYVROKNGFQASAAARMGLRLAKY 240  
Db 174 VNQKTHVPFVIVTDDSGOEDLSPIROYENKLDIRYVROKNGFQASAAARMGLRLAKY 233  
Qy 241 DFIGLLDCMAPLWVHSYVAELLEDLLTIIGPKYIDTOHIDPKDFLNNASLESPL 300  
Db 234 DFVSLDCMAPLWVHSYVAELLEDLLTIIGPKYIDTOHIDPKDFLNNASLESPL 293  
Qy 301 EVKTNNSVAAGBGTSLDWLEQPEKTENIRLSDSPRFPFAAGNVAFAKKWLKNSGFPD 360  
Db 294 ETATNNPSSITSGNISLDMLEHFKPTDNLRLCDSPPRYFVAGNVAFAKKWLKNSGFPD 353  
Qy 361 EEFNHGGEDEFGVRLFRYGFPTIDIGIMAYHQEPGKNETDREAGKNITLIDIREK 420  
Db 354 EEFNHGGEDEFGVRLFRYGFPTIDIGIMAYHQEPGKNETDREAGKNITLIDIREK 413  
Qy 421 VPYIYKLLPIEDSHINRPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGST 480  
Db 414 VPYIYKLLPIEDSHINRPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGST 473  
Qy 481 DNTLEVINKLYGNPRVRIMSKPNGGIIASASNAAVSPAKGYIYGQDSDDDYLEDPAVELC 540  
Db 474 DNTLEVINKLYGNPRVRIMSKPNGGIIASASNAAVSPAKGYIYGQDSDDDYLEDPAVELC 533  
Qy 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMAHFRMFTIRAWHL 600  
Db 534 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMAHFRMFTIRAWHL 593  
Qy 601 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKCYNRVLHGDNSTSIKLGIOKKNHFVVVN 660  
Db 594 TDGFNEKIENAVDYDMFLKSEVGKFKHLNKCYNRVLHGDNSTSIKLGIOKKNHFVVVN 653  
Qy 661 QSLNRQGITVYNYDFDLDDESKYIFNKTAQYQBEIDLKDIKIQNDKAKIAYSIFYP 720  
Db 654 QSLNRQGITVYNYDFDLDDESKYIFNKTAQYQBEIDLKDIKIQNDKAKIAYSIFYP 713  
Qy 721 NTGLGVKKLNNIIEYNKNIIVILVHDKNHLTPDKKEILAFYHKHVNILLNDISY 780  
Db 714 NTGLGVKKLNNIIEYNKNIIVILVHDKNHLTPDKKEILAFYHKHVNILLNDISY 773  
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDISYAYMKKYDVGMMFSALTH 840  
Db 774 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDISYAYMKKYDVGMMFSALTH 833

Qy 841 DWIEKINAHPPFKKLIKTYFENDNLDKSMNVKGASQGMFTYALAHELLTTIKKEVITSQCS 900  
Db 834 DWIEKINAHPPFKKLIKTYFENDNLDKSMNVKGASQGMFTYALAHELLTTIKKEVITSQCS 893  
Qy 901 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGNI 960  
Db 894 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGNI 953  
Qy 961 PVNKFIIINSITL 972  
Db 954 PVNKFIIINSITL 965

RESULT 10  
AAM47335  
ID AAM47335 standard; protein; 965 AA.  
XX  
AC AAM47335;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Pasteurella multocida chondroitin synthase #1.  
XX  
XX Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer;  
KW eye application; joint application; moisturiser; drug delivery;  
KW wound dressing; biocompatible film.  
XX  
OS Pasteurella multocida.  
XX  
PN WO200180810-A2.  
XX  
PD 01-NOV-2001.  
XX  
PF 25-APR-2001; 2001WO-US013395.  
XX  
PR 25-APR-2000; 2000US-0199538P.  
XX  
XX (DANG/) DE ANGELIS P L.  
XX  
XX De Angelis PL;  
XX  
XX WPI; 2002-049237/06.  
DR N-PSDB; ABA05097.  
XX  
PT New chondroitin synthase gene obtained from Pasteurella multocida, useful  
PT as hyaluronan polysaccharide substitute in medial or cosmetic  
PT applications, e.g. for eye or joint applications, for moisturizer or  
PT wound dressings.  
XX  
PS Claim 3; Page 119; 125pp; English.  
XX  
CC The present invention relates to the coding sequence of the Pasteurella  
CC multocida chondroitin synthase. A chondroitin polysaccharide may be used  
CC as a hyaluronan polysaccharide substitute in medial or cosmetic  
CC applications, for example in eye or joint applications, for moisturiser  
CC or wound dressings. The enzyme may be used in covalently coupling  
CC specific drugs, proteins or toxins to the structurally modified  
CC chondroitin for general or targeted drug delivery or radiological  
CC procedures, covalently cross linking the hyaluronic acid itself or to  
CC other supports to achieve a gel or other three dimensional biomaterial  
CC with stronger physical properties, and covalently linking hyaluronic acid  
CC to a surface to create a biocompatible film or monolayer. The present  
CC sequence is one version of the protein of the invention  
XX  
SQ Sequence 965 AA;

Query Match 87.9%; Score 4490.5; DB 5; Length 965;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 843; Conservative 62; Mismatches 60; Indels 7; Gaps 2;

Qy 1 MNTLSQAIKAYNSNDYQALALFKPKSAEYGRKIVEFQITCKEKLKSAHPNSVNSAHLNVN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFKPKSAEYGRKIVEFQITCKEKLKSAHPNSVNSAHLNVN 53



```
Db 354 EEFNHWGGEVEFCYRLFAKGCPRVDDGMAHQEPGKENETEREAGKSITLKI VKEK 413
Qy 421 VPIYIRKLLPTEDSHINRPLVSIYIPAYNCANIYIQRVDSALNQTVVDLEVCINDGST 480
Db 414 VPIYIRKLLPTEDSHIHRIPLVSIYIPAYNCANIYIQRVDSALNQTVVDLEVCINDGST 473
Qy 481 DNTLEVINLKLYGNPRVIRMSKPNGGTASASNAVSPAKGYIIGQLSDDDYLEDAVELC 540
Db 474 DNTLEVINLKLYGNPRVIRMSKPNGGTASASNAVSPAKGYIIGQLSDDDYLEDAVELC 533
Qy 541 LKEFLDKDTLACVYTTNRNPNPDGSLIANGYNNPEFSREKLTAMIAHHFRMFTIRAWHL 600
Db 534 LKEFLDKDTLACVYTTNRNPNPDGSLIANGYNNPEFSREKLTAMIAHHFRMFTIRAWHL 593
Qy 601 TDGNEKIENAVYDMFLKSEVCKFHLNKKICYNRVLHGDNTSIKLGICQKHQHFVVVN 660
Db 594 TDGFENIENAVYDMFLKSEVCKFHLNKKICYNRVLHGDNTSIKLGICQKHQHFVVVN 653
Qy 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEOEEIDILKDIKIQNKDAKIAVSIFYP 720
Db 654 QSLNRQGINYYNDFDLDDESRYIFNKTAEOEEIDILKDIKIQNKDAKIAVSIFYP 713
Qy 721 NTLNGLVKLNIIIEYKNKIFVILVHVDKNHLPDIKKEILAFYKHQVNIILLNNDISYY 780
Db 714 NTLNGLVKLNIIIEYKNKIFVILVHVDKNHLPDIKKEILAFYKHQVNIILLNNDISYY 773
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHSLFVNDSYAYMKKYDVGWNFSAETH 840
Db 774 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHSLFVNDSYAYMKKYDVGWNFSAETH 833
Qy 841 DWIEKINAHPPKLIKTYFNNDLKSNNVKGASQGMFTYALAEHLITIKIVITSCQS 900
Db 834 DWIEKINAHPPKLIKTYFNNDLKSNNVKGASQGMFTYALAEHLITIKIVITSCQS 893
Qy 901 IDSVPENYNTDIWFQFALLILEKKTGHVFNKTSITLTYMPWKRKLQWNTNEQISAKRGNI 960
Db 894 IDSVPENYNTDIWFQFALLILEKKTGHVFNKTSITLTYMPWKRKLQWNTNEQISAKRGNI 953
Qy 961 PVNKFPIINSITL 972
Db 954 PVNKFPIINSITL 965

RESULT 12
ADN40555
ID ADN40555 standard; protein; 965 AA.
XX
AC ADN40555;
XX
DT 15-JUL-2004 (first entry)
XX
DE Glycosaminoglycan (GAG) polymer production-related pmcS protein #1.
XX
KW enzymatic production; glycosaminoglycan; GAG; functional acceptor;
KW uronic acid; hexosamine; GAG transferase; UDP-sugar; cytosolic;
KW anticoagulant; immunosuppressive; antiallergic; cell growth;
KW behaviour modulator; blood vessel formation; dendritic cell maturation;
KW polysaccharide biomaterial; bioadhesive sealant; tissue engineering aid;
KW cell matrix mimetic; cell behaviour; growth modulator;
KW drug delivery agent; wound; ulcer; injury; surgical site; cytokine;
KW angiogenic; bFGF; heparin-binding growth factor; blood coagulation;
KW cancer metastasis; cell growth; infection; allograft reaction; allergy;
KW cancer; autoimmune disease.
XX
OS Pasteurella multocida.
XX
PN WO2004032830-A2.
XX
PD 22-APR-2004.
XX
PF 14-AUG-2003; 2003WO-US025750.
XX
```

```
PR 16-AUG-2002; 2002US-0404356P.
PR 18-JUN-2003; 2003US-0479432P.
PR 31-JUL-2003; 2003US-00479432.
XX
PA (DEAN/) DEANGELIS P L.
XX
PI Deangelis PL, Jing W;
XX
XX WPI; 2004-375496/35.
XX
PT Enzymatically producing defined glycosaminoglycan (GAG) polymers, by
PT providing functional acceptor, recombinant GAG transferase and UDP-sugar
PT to elongate functional acceptor to provide GAG polymers having desired
PT size distribution.
XX
PS Disclosure; SEQ ID NO 4; 163pp; English.
XX
CC This invention relates to a novel method of enzymatically producing
CC defined glycosaminoglycan (GAG) polymers, by providing functional
CC acceptor chosen from uronic acid and hexosamine, providing recombinant
CC GAG transferase capable of elongating functional acceptor in controlled
CC or repetitive fashion to form extended GAG, providing UDP-sugar to
CC functional acceptor such that GAG transferase elongates functional
CC acceptor to provide GAG polymers having desired size distribution. The
CC method may be useful for the production of compounds with a cytosolic,
CC anticoagulant, immunosuppressive or antiallergic activity acting as cell
CC growth and/or behaviour modulators or blood vessel formation and
CC dendritic cell maturation stimulators. The invention is useful for
CC enzymatically producing defined glycosaminoglycan polymers or for
CC producing a polysaccharide biomaterial. The polysaccharide biomaterial
CC produced is useful as a bioadhesive sealant, a tissue engineering aid a
CC cell matrix mimetic, a cell behaviour or growth modulator, a drug
CC delivery agent. The invention is also useful for producing a
CC polysaccharide biomaterial containing a medicament delivery assembly for
CC administration at a wound, ulcer, injury or surgical site. The
CC glycosaminoglycan polymers produced by the method of the invention are
CC capable of interacting, triggering or binding a variety of molecules
CC including cytokines, receptors and growth factors and hence useful for
CC modulating cell behaviour and/or growth through numerous natural pathways
CC in mammals. The glycosaminoglycan polymers are useful for promoting
CC growth and angiogenic activities of bFGF and other heparin-binding growth
CC factors. The glycosaminoglycan polymers are also useful as potential non-
CC toxic to therapeutic agents to modulate blood coagulation, cancer
CC metastasis or cell growth and stimulating blood vessel formation and
CC stimulating dendritic cell maturation and hence for prophylaxis and/or
CC treatment of infections, allograft reaction, allergy, cancer and
CC autoimmune disease. The method enables efficient production of
CC glycosaminoglycan polymers with very narrow, substantially monodisperse
CC size distributions. The present sequence is that of a protein which is
XX related to the invention.
XX
SQ Sequence 965 AA;
```

```
Query Match 87.6%; Score 4475.5; DB 8; Length 965;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 841; Conservative 62; Mismatches 62; Indels 7; Gaps 2;
Qy 1 MNTLSQAIKAYNSNDYQALALFKESARIYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 60
Db 1 MNTLSQAIKAYNSNDYQALALFKESARIYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 53
Qy 61 KEEKNVNCDSPLDIATQILLNSNVKLVLSDESKNTLKNKWLTKKSKSENAEVRVALVLP 120
Db 54 EDKKNVNCDSPLDIATQILLNSNVKLVLSDESKNTLKNKWLTKKSKSENAEVRVALVLP 113
Qy 121 KDFPKDLVLAFLPDHVNDFTWYKRRKGLGKPBHQHVGSLIIVTFRPAILSLITLACL 180
Db 114 KDFPKDLVLAFLPDHVNDFTWYKRRKGLGKPBHQHVGSLIIVTFRPAILSLITLACL 173
Qy 181 VNQKTHYFEVITVDDGSOEDLSPIROYENKLDIRYVRQKDNFGQFASARNMGLRLAKY 240
Db 174 VNQKTHYFEVITVDDGSOEDLSPIROYENKLDIRYVRQKDNFGQFASARNMGLRLAKY 233
```

Qy	241	DFIGLLDCD	MAPNPLW	HSYVAE	LBDEDD	LTTIG	PRKYID	TOHID	PKOP	FNNA	SLL	ESLP	300																																														
Db	234	DI	SILDCD	MAPQ	OLWHSY	LTELEED	NDILV	IGPRKY	VDTHN	ITAEQ	FLND	PYLITESLP	293																																														
Qy	301	EVT	TNNSVAA	KGEGT	VSJDM	RL	EQEKT	ENLFL	SDSP	FFAAG	NVAF	AKKWL	INSGFPD	360																																													
Db	294	ETA	TNNP	SI	TSGN	ISJDM	RL	EHFK	KTDL	CLDS	PPFY	FVAG	NVAF	SKEWL	IN	KVGWFD	353																																										
Qy	361	EEF	NHGWG	EDVE	FGYRL	FRYGS	FFKTID	IGIMAY	HQB	PGKEN	ETDRE	AGKNT	ITL	DMRK	420																																												
Db	354	EEF	NHGWG	EDVE	FGYRL	FAK	CGFFAV	DG	MAHQ	B	PGKEN	ETDRE	AGKNT	ITL	DMRK	413																																											
Qy	421	VPIY	RKLLP	IEDSH	INRV	PLV	SIYI	PAY	CANYI	QRCV	DSAL	NTQ	VDLE	VCI	CNDGST	480																																											
Db	414	VPIY	RKLLP	IEDSH	INRV	PLV	SIYI	PAY	CANYI	QRCV	DSAL	NTQ	VDLE	VCI	CNDGST	473																																											
Qy	481	DNTL	EV	IN	KLV	GNN	PRV	IMSK	PNG	G	IASA	NA	VSFA	KYI	IGOL	DSDD	YLE	DA	VELC	540																																							
Db	474	DNTL	EV	IN	KLV	GNN	PRV	IMSK	PNG	G	IASA	NA	VSFA	KYI	IGOL	DSDD	YLE	DA	VELC	533																																							
Qy	541	LKEFL	KOKT	LACV	YTTNR	NVNP	DG	SLI	ANG	YNW	PEFS	REKLT	TAM	IAH	FRM	FTI	PA	WHL	600																																								
Db	534	LKEFL	KOKT	LACV	YTTNR	NVNP	DG	SLI	ANG	YNW	PEFS	REKLT	TAM	IAH	FRM	FTI	PA	WHL	593																																								
Qy	601	T	DG	NEK	T	ENAV	DYDM	F	LK	SEV	G	P	K	HLN	KI	CYN	R	V	L	H	G	D	N	T	S	I	K	K	L	G	I	G	I	K	K	N	H	P	V	V	N	660																	
Db	594	T	DG	NEK	T	ENAV	DYDM	F	LK	SEV	G	P	K	HLN	KI	CYN	R	V	L	H	G	D	N	T	S	I	K	K	L	G	I	G	I	K	K	N	H	P	V	V	N	653																	
Qy	661	QSLNR	QGI	TY	NY	DE	F	DL	DS	R	KYI	F	N	K	T	A	B	Y	Q	E	I	D	L	K	D	I	K	I	O	N	K	D	A	K	I	A	S	I	F	Y	720																		
Db	654	QSLNR	QGI	TY	NY	DE	F	DL	DS	R	KYI	F	N	K	T	A	B	Y	Q	E	I	D	L	K	D	I	K	I	O	N	K	D	A	K	I	A	S	I	F	Y	713																		
Qy	721	N	T	L	N	G	L	V	K	L	N	N	I	E	Y	N	K	N	I	F	V	I	L	H	V	D	K	Q	H	L	T	P	D	I	K	E	I	L	A	F	Y	H	K	Q	N	I	L	N	D	I	S	Y	780						
Db	714	N	T	L	N	G	L	V	K	L	N	N	I	E	Y	N	K	N	I	F	V	I	L	H	V	D	K	Q	H	L	T	P	D	I	K	E	I	L	A	F	Y	H	K	Q	N	I	L	N	D	I	S	Y	773						
Qy	781	T	S	N	R	L	I	K	T	E	A	H	L	S	N	I	K	L	S	Q	L	N	L	N	C	E	Y	I	F	D	N	H	S	L	F	V	K	N	D	S	I	A	Y	M	K	K	Y	D	V	G	N	F	S	A	L	P	H	840	
Db	774	T	S	N	R	L	I	K	T	E	A	H	L	S	N	I	K	L	S	Q	L	N	L	N	C	E	Y	I	F	D	N	H	S	L	F	V	K	N	D	S	I	A	Y	M	K	K	Y	D	V	G	N	F	S	A	L	P	H	833	
Qy	841	D	W	I	E	K	I	N	A	H	P	P	F	K	L	I	K	T	Y	E	N	D	N	D	L	S	K	N	V	N	G	A	S	O	G	M	E	N	T	A	L	A	H	E	L	L	T	I	I	K	E	V	I	T	S	C	O	S	900
Db	834	D	W	I	E	K	I	N	A	H	P	P	F	K	L																																												

RESULT 13  
AEA04963

AEA04963  
ID AEA04963 standard; protein; 703 AA.

XX

AC  
XX  
AEA04963;

DT 11-AUG-2005 (first entry)

XX DE Hyaluronic acid synthase PMHAS SEQ ID 1

[illegible]KW Hyaluronic acid syntha  
XX

OS Pasteurella mult

XX  
PN 1152005124046

XX  
XX  
14-060471C000700

yy  
pd

PR	10-NOV-1999;	99US-00437277.
XX	(DEAN/) DEANGELIS P L.	
PA		
XX	Deangelis PL;	
PI		
XX	WPI; 2005-417007/42.	
XX	N-PSDB; AEA04964.	
DR		
DR		
XX		
PT	Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin),	
PT	useful in polysaccharide polymer grafting, comprises providing hyaluronic	
PT	acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the	
PT	functional acceptor.	
XX		
XX	Claim 1; SEQ ID NO 1; 41pp; English.	
PS		
CC	The present invention relates to a method for elongating a functional	
CC	acceptor. The method comprises providing a hyaluronic acid (HA) synthase	
CC	(PmHAS; AEA04963) capable of elongating the functional acceptor and	
CC	providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid	
CC	synthase elongates the functional acceptor. PmHAS adds sugars to the	
CC	nonreducing end of a growing polymer chain. The PmHAS sequence is	
CC	significantly different from the other known HA synthases: there appears	
CC	to be only two short potential sequence motifs (AEA04967 and AEA04968) in	
CC	common between PmHAS and the other HA synthases. The method is useful in	
CC	polysaccharide polymer grafting, which may be utilized in the development	
CC	of biotechnological medical improvements. These may be used for producing	
CC	hybrid polysaccharides or for forming polysaccharide coatings.	
XX		
XX	Sequence 703 AA;	
SQ		

ଅଦ



```
Db 541 LKEFLDKTKLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHHFRMFTIRAWHL 600
Qy 601 TDGFNEKIENAVDYDMFLKJSEVCKFKHLNKKICYNRVLHGDNTSIKKLGIOKKHFFVVVN 660
Db 601 TDGFNEKIENAVDYDMFLKJSEVCKFKHLNKKICYNRVLHGDNTSIKKLGIOKKHFFVVVN 660
Qy 661 QSLNRQGITTYNNDYDFDDLDSESKYIFNKTAAYQEEIDILKDI 703
Db 661 QSLNRQGITTYNNDYDFDDLDSESKYIFNKTAAYQEEIDILKDI 703

RESULT 14
ADP75656
ID ADP75656 standard; protein; 703 AA.
XX AC
XX ADP75656;
XX DT
XX 12-AUG-2004 (first entry)
XX DE
XX Pasteurella multocida hyaluronid acid synthase #2.
XX KW
XX polymer production; hyaluronid acid polymer; chondroitin polymer;
XX KW hyaluronid acid synthase; enzyme.
XX OS
XX Pasteurella multocida.
XX PN
XX WO2003029261-A2.
XX PD
XX 10-APR-2003.
XX PF
XX 12-JUL-2002; 2002WO-US022386.
XX PR
XX 13-JUL-2001; 2001US-0305263P.
XX PR 22-JAN-2002; 2002US-0350642P.
XX PR 08-MAY-2002; 2002US-00142143.
XX XX
XX (DEAN/) DEANGELIS P L.
XX PA
XX Deangelis PL;
XX PI
XX WPI; 2003-532558/50.
XX XX

Producing polymer, e.g. hyaluronid acid or chondroitin polymer, by
providing a functional acceptor, a synthase capable of elongating the
acceptor and sugars such that the synthase elongates the acceptor to provide
polymer.
Disclosure; SEQ ID NO 9; 538pp; English.
The invention comprises a method for producing a polymer, especially a
hyaluronid acid (HA) or chondroitin (CD) polymer composed of less than
150 sugars. The method involves providing a functional acceptor,
providing a synthase capable of elongating the functional acceptor, and
providing sugars such that the synthase elongates the functional acceptor
to provide the polymer. The method of the invention is useful for
producing a hyaluronid acid or chondroitin polymer composed of 1-150
sugars. The present amino acid sequence represents a Pasteurella
multocida hyaluronid acid synthase of the invention.
Sequence 703 AA;
Query Match 72.3%; Score 3693; DB 7; Length 703;
Best Local Similarity 99.9%; Pred. No. 1.9e-287;
Matches 702; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNTLSQAIKAYNSNDYQLALFKESAIEYGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Db 1 MNTLSQAIKAYNSNDYQLALFKESAIEYGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Qy 61 KEEKNVCDSPDIATQALLSNVKKLVLSDESKNTLKNKKWLLTEKKSNAEVRVALVP 120
Db 61 KEEKNVCDSPDIATQALLSNVKKLVLSDESKNTLKNKKWLLTEKKSNAEVRVALVP 120
```

```
Qy 121 KDFPKDLVLAPLDPHVDFTWYKKRKKRLGIKPEHQHVGLSIIIVTTNRRPAILISITLACL 180
Db 121 KDFPKDLVLAPLDPHVDFTWYKKRKKRLGIKPEHQHVGLSIIIVTTNRRPAILISITLACL 180
Qy 181 VNOKTHYPFVIVTDDGSQEDLSPIITROYENKLDIRVYROKDNQFOASAARNMGLRLAKY 240
Db 181 VNOKTHYPFVIVTDDGSQEDLSPIITROYENKLDIRVYROKDNQFOASAARNMGLRLAKY 240
Qy 241 DFTGLLDCDMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHIDPDKFLNNALESLSLP 300
Db 241 DFTGLLDCDMAPNPLVHVSVAELLEDLTIIGPRKYIDTQHIDPDKFLNNALESLSLP 300
Qy 301 EVKTNNSVAAKGEFTVSLDWRLRLEQFEKTEMLRLSDSPFRFAAGNAVFAKWLKNSGFFD 360
Db 301 EVKTNNSVAAKGEFTVSLDWRLRLEQFEKTEMLRLSDSPFRFAAGNAVFAKWLKNSGFFD 360
Qy 361 BEFNHWGGEDEVFGYRLFRYGSFPKTTIDGIMAYHQEPGKENETDREAGKNITLIDIMREK 420
Db 361 BEFNHWGGEDEVFGYRLFRYGSFPKTTIDGIMAYHQEPGKENETDREAGKNITLIDIMREK 420
Qy 421 VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRVDSALNQTVVDLEVCIKNDGST 480
Db 421 VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRVDSALNQTVVDLEVCIKNDGST 480
Qy 481 DNTLEVINKLYGNPNRVRIMSKPNGGIASASNAASPAKGYIIGQLSDDDYLEPDAVELC 540
Db 481 DNTLEVINKLYGNPNRVRIMSKPNGGIASASNAASPAKGYIIGQLSDDDYLEPDAVELC 540
Qy 541 LKEFLDKTKLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHHFRMFTIRAWHL 600
Db 541 LKEFLDKTKLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHHFRMFTIRAWHL 600
Qy 601 TDGFNEKIENAVDYDMFLKJSEVCKFKHLNKKICYNRVLHGDNTSIKKLGIOKKHFFVVVN 660
Db 601 TDGFNEKIENAVDYDMFLKJSEVCKFKHLNKKICYNRVLHGDNTSIKKLGIOKKHFFVVVN 660
Qy 661 QSLNRQGITTYNNDYDFDDLDSESKYIFNKTAAYQEEIDILKDI 703
Db 661 QSLNRQGITTYNNDYDFDDLDSESKYIFNKTAAYQEEIDILKDI 703

RESULT 15
ADP75758
ID ADP75758 standard; protein; 703 AA.
XX AC
XX ADP75758;
XX DT
XX 12-AUG-2004 (first entry)
XX DE
XX Pasteurella multocida mutant hyaluronid acid synthase.
XX KW
XX polymer production; hyaluronid acid polymer; chondroitin polymer;
XX KW hyaluronid acid synthase; enzyme; mutant; muten.
XX OS
XX Pasteurella multocida.
XX OS Synthetic.
XX XX
XX WO2003029261-A2.
XX PN
XX 10-APR-2003.
XX PD
XX 12-JUL-2002; 2002WO-US022386.
XX PF
XX 13-JUL-2001; 2001US-0305263P.
XX PR 22-JAN-2002; 2002US-0350642P.
XX PR 08-MAY-2002; 2002US-00142143.
XX XX
XX (DEAN/) DEANGELIS P L.
XX DE
XX Deangelis PL;
XX PI
XX WPI; 2003-532558/50.
XX XX
```

PT Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by  
PT providing a functional acceptor, a synthase capable of elongating the  
PT acceptor and sugars such that synthase elongates the acceptor to provide  
PT polymer.

XX Disclosure; SEQ ID NO 111; 538pp; English.

XX  
CC The invention comprises a method for producing a polymer, especially a  
CC hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than  
CC 150 sugars. The method involves providing a functional acceptor,  
CC providing a synthase capable of elongating the functional acceptor, and  
CC providing sugars such that the synthase elongates the functional acceptor  
CC to provide the polymer. The method of the invention is useful for  
CC producing a hyaluronic acid or chondroitin polymer composed of 1-150  
CC sugars. The present amino acid sequence represents a mutant Pasteurella  
CC multocida hyaluronic acid synthase of the invention.

XX Sequence 703 AA;

Query Match		72.2%	Score 3690;	DB 7;	Length 703;	
Best Local Similarity		99.7%;	Pred. No. 3.4e-287;			
Matches 701;		Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MNTLSQAIKAYNSNDYQALALKEKSAEIIYGRKIVEFOITKCKEKL	SAHPSVNSAHL	SVN	60	
Db	1	MNTLSQAIKAYNSNDYQALALKEKSAEIIYGRKIVEFOITKCKEKL	SAHPSVNSAHL	SVN	60	
Qy	61	KEEKVNCDSPLDIATQALLSNVKKLVLSDSEKNTLKNWKLLTEK	KSENAEVR	VALVP	120	
Db	61	KEEKVNCDSPLDIATQALLSNVKKLVLSDSEKNTLKNWKLLTEK	KSENAEVR	VALVP	120	
Qy	121	KDFPKDLVLAPLDHVNDFTWYKKRKRGLIKPEHQHVGLSII	VTTNRPAIL	SITLACL	180	
Db	121	KDFPKDLVLAPLDHVNDFTWYKKRKRGLIKPEHQHVGLSII	VTTNRPAIL	SITLACL	180	
Qy	181	VNQKTHYPFEVIVTDGQSQEDLSPIIROYENKLDIRYVROKNG	FOASAARN	MGLRLAKY	240	
Db	181	VNQKTHYPFEVIVTDGQSQEDLSPIIROYENKLDIRYVROKNG	FOASAARN	MGLRLAKY	240	
Qy	241	DFIGLLDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTOHID	PKDFLNNAS	LLESPL	300	
Db	241	DFIGLLDCMAPNPLVHVSVAELLEDDDLTIIGPRKYIDTOHID	PKDFLNNAS	LLESPL	300	
Qy	301	EVTNNSVAAKSGTYSLDWRLRQFEKTEENLRISDSPFRFAAG	NAVAFACKWL	NKSGFFD	360	
Db	301	EVTNNSVAAKSGTYSLDWRLRQFEKTEENLRISDSPFRFAAG	NAVAFACKWL	NKSGFFD	360	
Qy	361	EEFNHWGGEDVEFGYRLFYRGSFPKTDGIMAYHQEP	PGKENETD	REAGKNITL	420	
Db	361	EEFNHWGGEDVEFGYRLFYRGSFPKTDGIMAYHQEP	PGKENETD	REAGKNITL	420	
Qy	421	VPYIYRKLPIEDSHINRVLPSIYIPAYNCANYIQR	CVDSALN	QTVVDLEVC	480	
Db	421	VPYIYRKLPIEDSHINRVLPSIYIPAYNCANYIQR	CVDSALN	QTVVDLEVC	480	
Qy	481	DNTLEVINKLYGNPNRINMSKNGGIASASNAAVS	FAKGYIIG	OLDSDDY	540	
Db	481	DNTLEVINKLYGNPNRINMSKNGGIASASNAAVS	FAKGYIIG	OLDSDDY	540	
Qy	541	LKEFLDKDTLACVYTTNRNVPDGSIIANGYNWPF	SREKLT	TAMIAHFR	600	
Db	541	LKEFLDKDTLACVYTTNRNVPDGSIIANGYNWPF	SREKLT	TAMIAHFR	600	
Qy	601	TGDFNEKIENAVDYMFLKLSVKGKFKHLNKI	CYNRLHGD	NTSIKKLGI	QKKNHFVYN	660
Db	601	TGDFNEKIENAVDYMFLKLSVKGKFKHLNKI	CYNRLHGD	NTSIKKLGI	QKKNHFVYN	660
Qy	661	QSLNRQGITYYNYDEFDDLDES	SKYIFNKT	AEYQEE	IDILKDI	703
Db	661	QSLNRQGITYYNYDEFDDLDES	SKYIFNKT	AEYQEE	IDILKDI	703



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 15:56:36 ; Search time 40 Seconds  
(without alignments)  
2338.067 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAKRGENIPVKFIINSITL 972

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No... is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5104	99.9	972	2 T09595	Glucuronosyltransf
2	298.5	5.8	327	2 A31211	Glycosyltransferas
3	293	5.7	604	2 E97757	hypothetical prote
4	276.5	5.4	696	2 D95206	hypothetical prote
5	263.5	5.2	323	2 A02189	hypothetical prote
6	260.5	5.1	324	2 A82190	hypothetical prote
7	259.5	5.1	303	2 A84114	Glycosyltransferas
8	257	5.0	298	2 B75096	Glycosyl transfera
9	251	4.9	321	2 AG2188	hypothetical prote
10	248.5	4.9	333	2 B97168	Glycosyltransferas
11	247	4.8	333	2 H97167	Glycosyltransferas
12	242	4.7	318	2 E71690	minor teichoic aci
13	238.5	4.7	333	2 AH2026	hypothetical prote
14	238	4.7	306	2 T50038	beta-1,3-N-acetyl
15	238	4.7	318	2 AH2189	hypothetical prote
16	236.5	4.6	257	2 E84107	teichuronic acid b
17	236.5	4.6	336	2 A97168	Glycosyltransferas
18	235	4.6	344	2 A70037	capsular polysacch
19	234.5	4.6	1013	2 AE1876	hypothetical prote
20	232.5	4.6	776	2 F81289	probable sugar tra
21	231.5	4.5	322	2 T44647	Glycosyl transfera
22	231.5	4.5	323	1 H64130	Glycosyl transfera
23	230	4.5	316	2 AE2189	hypothetical prote
24	229	4.5	318	2 T50039	beta-1,4-galactosy
25	229	4.5	389	2 E81318	probable galactosy
26	227	4.4	334	1 G71153	hypothetical prote
27	227	4.4	340	2 T44330	Glycosyl transfera
28	226.5	4.4	445	2 B81289	probable sugar tra
29	225	4.4	349	2 D81027	lacto-N-neotetraos

ALIGNMENTS

RESULT 1

T09595

Glucuronosyltransferase (EC 2.4.1.17) - Pasteurella multocida

N;Alternate names: hyaluronan synthase

C;Species: Pasteurella multocida

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: T09595

R;DeAngelis, P.L.; Jing, W.; Drake, R.R.; Achyuthan, A.M.

J. Biol. Chem. 273, 8454-8458, 1998

A;Title: Identification and molecular cloning of a unique hyaluronan synthase from Paste

A;Reference number: 216757; MUID:98192645; PMID:9525958

A;Accession: T09595

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-972 <DEA>

A;Cross-references: UNIPROT:O68389; UNIPARC:UPI000000B47B2; EMBL:AF036004; NID:G3043922;

A;Experimental source: strain P-1059; ATCC 15742

C;Genetics:

A;Gene: HAS

C;Function:

A;Description: polymerizes hyaluronan (HA, hyaluronate, hyaluronic acid) polysaccharide

C;Keywords: capsule synthesis; glycosyltransferase; hexosyltransferase; hyaluronan acid

Query Match 99.9%; Score 5104; DB 2; Length 972;  
Best Local Similarity 99.9%; Pred. No. 1.3e-268;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNTLSQAIKAYNSNDYQLALFKESABIIYGRKIVEFOITKCKEKLSSHPSVNSAHLNVN	60
DB	1	MNTLSQAIKAYNSNDYQLALFKESABIIYGRKIVEFOITKCKEKLSSHPSVNSAHLNVN	60
QY	61	KEEKVNCDSPLDITATQLLSNVKKLVLSDEKNTLKNKKLLTEKKSENAEVRVALVP	120
DB	61	KEEKVNCDSPLDITATQLLSNVKKLVLSDEKNTLKNKKLLTEKKSENAEVRVALVP	120
QY	121	KDFPKDLVLAPLPHVNDFTWYKKRKGKLGKPEHQHVGLSIIIVTFNRPAILSLITLACL	180
DB	121	KDFPKDLVLAPLPHVNDFTWYKKRKGKLGKPEHQHVGLSIIIVTFNRPAILSLITLACL	180
QY	181	VNQKTHYPFEIVITDDGSQEDLSPIIROYENKLDIRYVRQKNGFQASAAARNMGLRLAKY	240
DB	181	VNQKTHYPFEIVITDDGSQEDLSPIIROYENKLDIRYVRQKNGFQASAAARNMGLRLAKY	240
QY	241	DFIGLLDCDMAPNLVHSHYVAELLEDDDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL	300
DB	241	DFIGLLDCDMAPNLVHSHYVAELLEDDDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL	300
QY	301	EVKTTNSVAAKGGEGTVSLDWLEQPEKTENLRSLSPRFFFAAGNVAFKKWLKNSGGPFD	360
DB	301	EVKTTNSVAAKGGEGTVSLDWLEQPEKTENLRSLSPRFFFAAGNVAFKKWLKNSGGPFD	360
QY	361	EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGKENETDREAGNITLIDIMREK	420

```
Db 361 EEFNHWGGEDEVEGYLFRYGSFVKIDIGMAHQEPGKENTDREAGNKIITLDMREK 420
QY 421 VPYIYRKLLPIEDSHINRVLPSIYIIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHINRVLPSIYIIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
QY 481 DNTLEVINKLYGNPRVIRMSKNGGSIASASNAAVSFAKGYIYGOLDSDDDYLEPDAVELC 540
Db 481 DNTLEVINKLYGNPRVIRMSKNGGSIASASNAAVSFAKGYIYGOLDSDDDYLEPDAVELC 540
QY 541 LKEFLDKDKTLACVYITNRNPNVPGSLIANGYNWPFERSREKLTMTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLDKDKTLACVYITNRNPNVPGSLIANGYNWPFERSREKLTMTAMIAHFRMFTIRAWHL 600
QY 601 TDGFNEKIEENAVDYMFLKLSEVGKFKHLNKKIYNRVLHGDNTSIKKLGIGQKKNHFWVNV 660
Db 601 TDGFNEKIEENAVDYMFLKLSEVGKFKHLNKKIYNRVLHGDNTSIKKLGIGQKKNHFWVNV 660
QY 661 QSLNRQGITVYNNDEFDLDESRYIFNKTAEQEIEDILKDIKIIONKDAKIAVSIFYP 720
Db 661 QSLNRQGITVYNNDEFDLDESRYIFNKTAEQEIEDILKDIKIIONKDAKIAVSIFYP 720
QY 721 NTNLGLVKKLNNIIEYNKNIIFVLVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
Db 721 NTNLGLVKKLNNIIEYNKNIIFVLVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
QY 781 TSNRLIKTEAHLNINKLSQLNLNCEYIIFDNHDSLFVNKDSYAYMKKYDVGWNFSAETH 840
Db 781 TSNRLIKTEAHLNINKLSQLNLNCEYIIFDNHDSLFVNKDSYAYMKKYDVGWNFSAETH 840
QY 841 DWIEKINAHPPPKLLIKTFVNDNLDKSMNVKGASQGMFTYALAHELLTIIEKEVITSQOS 900
Db 841 DWIEKINAHPPPKLLIKTFVNDNLDKSMNVKGASQGMFTYALAHELLTIIEKEVITSQOS 900
QY 901 IDSVPPYNTEDIWFQFALLILEKKTGHVFNKTKTTLTVMPEWKQWNTNEOIESAKRGENI 960
Db 901 IDSVPPYNTEDIWFQFALLILEKKTGHVFNKTKTTLTVMPEWKQWNTNEOIESAKRGENI 960
QY 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972

RESULT 2
AB1211
glycosyltransferases homolog lmo1090 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB1211
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tlierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679699
A:Accession: AB1211
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <GLA>
A:Cross-references: UNIPROT:Q8Y828; UNIPARC:UPI000000CF134; GB:NC_003210; PIDN:CAC99168.1
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1090
C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 5.8%; Score 298.5; DB 2; Length 327;
Best Local Similarity 28.0%; Pred. No. 4.3e-09;
Matches 99; Conservative 49; Mismatches 130; Indels 75; Gaps 11;

QY 440 PLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNPRVRI 499
```

```
Db 3 PLVSVIIPYVNEKVKRCLEDSVLGTYHNLEVVNDGATDNSAKVIKISDN--RIRY 60
QY 500 MSKPGNGSIASASNAAVSFAKGYIYGOLDSDDDYLEPDAVELCKEFLDKDKTLACVYITNRN 559
Db 61 FEKENGQATARNFGLDVATGDYIVMWVSDDDYISKVLVETCL-DTVQKTNADLVLFSTYN 119
QY 560 VNPDSG-----LIANGYNWPFERSREKLTMTAMIAHFRMFTIRAWHLTDGF--- 604
Db 120 VQEGKMQYIKRKDKGKIVLDAGFTPMNKFYQADLMKG-----SRPPVGVYEDLGIIPV 173
QY 605 -----NEKIEENAVDYMFLKLSEVGKFKHLNKKIYNRVLHGDNTSIKKLGIGQKKN 654
Db 174 VTLKAKNPVKIQDALYYITDRADSQSNIQQVDHFLDVVI--MLENVETELKKLGI---- 227
QY 655 HFVWVQSLNRQGITVYNNDEFDLDESRYIFNKTAEQEIEDILKDIKIIONKDAKIA 714
Db 228 -----YEESKD--QLAYLVIEHLIYRL--VLRKAIYITNKQER-- 261
QY 715 VSIFVPNTNLGLVKKLNNIIEYNKNIIFVLVHVDKNHLPDIKKEILAFYKH 767
Db 262 -----KKLIKTIISTIIQKFFPNWGSYPYQAGGKLATATLKKKALWLYLHH 305

RESULT 3
E97757
hypothetical protein RC0461 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: E97757
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: E97757
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-604 <R>
A:Cross-references: UNIPROT:Q921F9; UNIPARC:UPI000000CBDC1; GB:AE006914; PIDN:AAL02999.1;
C:Genetics:
A:Gene: RC0461

Query Match 5.7%; Score 293; DB 2; Length 604;
Best Local Similarity 24.6%; Pred. No. 2e-06;
Matches 123; Conservative 72; Mismatches 213; Indels 92; Gaps 19;

QY 426 RKLLPIEDSHINRVLPSIYIIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST-DTL 484
Db 4 RKDKPLNIYH----TLVSIIPVYNGANYMKEAINSALAAQTYKNIHIIIVNDGSKDNGET 59
QY 485 EVINKLYGNPRVIRMSKPNKGSIASASNAAVSFAKGYIYGOLDSDDDYLEPDAVE-----LC 540
Db 60 ERVALSYGD--KIRVYFENGGSGSALNYGKNNMQGEYFSLSHDDIYYYPNKIEHQVDIL 117
QY 541 LKEFLDKDKTLACVY-----TTNRNVPDGLSIANGYNWPFERSREKLTMTAMIAHFRMF 593
Db 118 NKLDNKDTIYGGYELIDKGNLSRYIKPDSVLPINKLN---ISLLPLLRGIHGSLSLM 174
QY 594 TIRAWHLTDGFNEKTEENAVDYMFLKLSEVGKFKHLNKKIYNRVLHGDNTSIKKLGIGQK 653
Db 175 PAKYFHEVGIFNEALPTTDYDLWFKIFRVAIPHEDESILIKSRPHSEQGS-KKISNHN 233
QY 654 N-----HFVWVQSLNRQGITVYNNDEFDLDESRYIFNKTAEQEIEDILKDIKI 704
Db 234 ECVNLWSSFLHETBEEMIKMEGSPYL-----FLTRTATFLSNNT-PYKACDLANTWA 286
QY 705 IIONKDAKIAVSI FYPNTNLGLVKKLNNI-IEYNKNI FVLH-----VDKNHLPDIKKE 759
Db 287 KOVLNDTKISVLIIPVYNNIRINWAIEAKSVLIQTHKNFEILIIDDGDSTDDISELTAICCKD 346
QY 760 -ILAFYKHQVNNILNNDISYYTSNRLIKTEAHLNINKLSQLNLNCEYIIFDNHDSLFV 818
Db 347 KRIFYHK-----KNEGPAAARN-LGINKAIGKVI AFLDSDDLFY 385
```

QY 819 KNDISYAMKKYDVGMFNSALTDWIEKINAHPPFKKLITKYFNDNDLKSMNVKASQCMF 878  
Db 386 K-DRIETQLKFMENNF-IFSHTSYHKINE-----KGKYIESVHSGLF 426  
QY 879 MTYALAHELLTIKEVITSC 898  
Db 427 SG-----NVFPQVQTC 438

RESULT 4  
D95206  
hypothetical protein SPI771 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C/Accession: D95206  
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
neon, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; UID:21357209; PMID:11463916  
A:Accession: D95206  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-696 <KUR>  
A:Cross-references: UNIPROT:Q97P72; UNIPARC:UPI00000519A1; GB:AE005672; PIDN:AAK75845.1;  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SPI771

Query Match 5.4%; Score 276.5; DB 2; Length 696;  
Best Local Similarity 21.3%; Pred. No. 1.9e-07;  
Matches 107; Conservative 86; Mismatches 175; Indels 135; Gaps 17;  
QY 442 VSIYIPAYNCANYIQCVCDSALNQTVDLEVCICNDGSDTNTLEVINKLYGNPRVRIMS 501  
Db 7 ITVIVPVYVNYLRKCLDSITQYKRIEIVVNDGSDTASGEICKREFSEMDHRIILYIE 66  
QY 502 KPNGGIAASNAASNAVYIGQLSDSDYILEPAVELCLK---EFLKDKTLACVYTNR 558  
Db 67 QENAGLSAARTGLNMSGNVTFVDSDDWIEQDYVELYKKIVEYQADIAVGNYSFNE 126  
QY 559 N-----VNPDSLIANGYNWPEFSREKLTAMIAHFRMTIRAWHL-- 600  
Db 127 SEGMPYFHLGDSYVEKVDNVSIPENLYE---TQEMKSFALISAWGLYKARLFEQLR 182  
QY 601 -----TDGF-NEKIENAVDYMFLKLSEVCKPKHLANKICY-NRVLHGD----- 641  
Db 183 FDIGKLGEDGYLNQV-----YLLSE--KVYLNKSLYAVRIKGSLSRVVTEKWM 231  
QY 642 -----NTSIKKLGIQKNHFVWVQNQL-----NRQ-----ITYNYD----- 674  
Db 232 HALVDAMSERITLLANMGVPLEKHLAVYRQMLEVSLANGQASGLSDTATYKEFEMKQRL 291  
QY 675 -EFDLDRSRKYIFNKTAYEQSEIDILKDIKIQNKDAKIAVISIYPNTLNGLVKLLNI 733  
Db 292 NQLSRQSESEKKAIVLAANYGVVDQVLTIKSICVHNRSIRFYLIHSDFFNEWIKQLNKR 351  
QY 734 IRYNKNIFIVLVHVDKNHLTPDKKEILAFYHKHQVNNLLNNDISYTTNRLIKTEAHL 793  
Db 352 LE-----KFDSEIINCRVTSEQISCY-----KSDISYTVFLRYFIADF--- 389  
QY 794 NINKLSQLNLNCEYIIFDNHDSLFVKN-DSY-----A 824  
Db 390 -VQEDKALYLDCLVLTQKLDLDPATDLDQDYPLAAVRDGGRAYFGQEIFNAGVLLVNA 448  
QY 825 YMKKYDVGMFNSALTDWIEKIN 847  
Db 449 FWKKENWTKLDVINEWHDKVD 471

## RESULT 5

AD2189  
hypothetical protein alr3067 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C/Accession: AD2189  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; UID:21595285; PMID:11759840  
A:Accession: AD2189  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-323 <KUR>  
A:Cross-references: UNIPROT:Q8YSL7; UNIPARC:UPI000000CE669; GB:BA000019; PIDN:BAW74766.1;  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr3067  
C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 5.2%; Score 263.5; DB 2; Length 323;  
Best Local Similarity 25.0%; Pred. No. 3.4e-07;  
Matches 90; Conservative 67; Mismatches 114; Indels 89; Gaps 16;  
QY 436 INRVPLSVIIPAYNCANYIQCVCDSALNQTVDLEVCICNDGSDTNTLEVINKLYGNRP 495  
Db 7 LNFVPLISVLPVNGEKTIETIASVQHTFLDIEIIVNDGSDTNTFELVRNIQDN-- 64  
QY 496 RVRIMSPKNGGIAASNAASNAVYIGQLSDSDYILEPAVEL---CLKEFLKDKTLAC 552  
Db 65 RLKIFSYENGGLPVARNRGITHAVGQFIAPTDADLWTDTKLEQFAALOQY-PEAGLAY 123  
QY 553 VYTNRNVPDGS-----LIANGYNWPEFSREKLTAMIAHFRM 592  
Db 124 SWTYKPFANEADSYADESNFAGDVYAEILLIKNFLQNSN-PLIRRAIDSVGL----- 176  
QY 593 PTIRAWHLTDGFNEKIENAVDYMFLKLSEVCKPKHLNK--ICYNRVLHGDNTSIKKLGI 650  
Db 177 -----FDPTLKSCEWDYFLRLAAKQWQALVKQAIIYRQ---SPTMTSKLDV 222  
QY 651 QKQNHFFVVN-----QSLNRQGITV--YNYDEFDDLDESRYIFNKTAYEQSEIDI 699  
Db 223 MEKYSSIVIERAFNAAPPQLHLKKQSLAWYKE---TAQCCLKYNSHK----- 268  
QY 700 LKDIKIQNKDAKIAVISIYPNTL-----NGLVKLLNIIEYNKIFIVLVH--DKNH 751  
Db 269 LADIKLAA-KRLKMAITLYPKNLLEDYTHGLIRKL-----IKSWILLQFHMVYIPKSH 321

## RESULT 6

AB2190  
hypothetical protein alr3073 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C/Accession: AB2190  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; UID:21595285; PMID:11759840  
A:Accession: AB2190  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-324 <KUR>  
A:Cross-references: UNIPROT:Q8YSL1; UNIPARC:UPI000000CE66F; GB:BA000019; PIDN:BAW74772.1;  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr3073  
C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match	5.1%;	Score 260.5;	DB 2;	Length 324;
Best Local Similarity	25.9%;	Pred. No. 4.9e-07;		
Matches	101;	Conservative	63;	Mismatches 123; Indels 103; Gaps 16;
Qy	439	VPLVSIYPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTNTLTLEVINKLYGNPRVR	498	
Db	1	MPKISVIIPAYNAERTILETINSVLNQTFSDLIIVINDSGTDRTVEVLQNV--DDARLK	58	
Qy	499	IMSKPNGGIASASNAAVSFAGYYIGOLDSDDYLEPDAVELCLKFEUKDTLACVYTTNR	558	
Db	59	VYSYENSRASGARNHGISHAVGDFISFLDADDLWTPDKLEQLSALNHPPEAGVAYSWTY	118	
Qy	559	NVNPDGSLIANGYNWPEFSREKLTMTAMIAHFRMFTIRAMHLLTDGENEKIENAVDYMFL	618	
Db	119	TIDDKGELLKPF--PUEGNAVYTDLLAN-----FLTNGSNPLIRKAA-----	160	
Qy	619	KLSEVGKFKHLNKICYNRVLHGDNSTSIKK-----IGIQKNHFVVV--NQSLNRQGIT	669	
Db	161	-IASIGEF-----DITLRSGEDWDYMLRAYKWPFFVVVKHQHILYRSVT	204	
Qy	670	YNYDFDLDLSEKRYIFNKTAEQBEIDILDKIKI-IQNKDAKIAVSIFYPNTLNLGVK	728	
Db	205	SKSF-----KLQIIRASLAILDKAMKV-----LPLELQYLKK	237	
Qy	729	KLNNIIEYNKNIFVILVHYD--KNHLTPDIK-----KEILAFYKHQ	768	
Db	238	HSLSNIYRYN-----VELYLDSSNNSTVDIKVIGNLLSYIRSRPOTLKEI--YTYKLI	290	
Qy	769	VNILLNNDISYYTSNRL---IKTEAHLNSI	795	
Db	291	IKILLVIVLSPKLSRLQLQFIKSKQMKNL	320	
RESULT 7				
A84114	Glycosyltransferase BH3713 [imported] - Bacillus halodurans (strain C-125)			
C;Species:	Bacillus halodurans			
C;Date:	01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004			
C;Accession:	A84114			
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira	Nucleic Acids Res. 28, 4317-4331, 2000			
A;Title:	Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and			
A;Reference number:	A83650; PMID:20512582; PMID:11058132			
A;Accession:	A84114			
A;Status:	preliminary			
A;Molecule type:	DNA			
A;Residues:	1-303 <STO>			
A;Cross-references:	UNIPROT:Q9K6L6; UNIPARC:UPI00000C429F; GB:AP001519; GB:BA000004; NID			
A;Experimental source:	strain C-125			
C;Genetics:				
A;Gene:	BH3713			
C;Superfamily:	Neisseria meningitidis glycosyl transferase A			
Query Match	5.1%;	Score 259.5;	DB 2;	Length 303;
Best Local Similarity	26.2%;	Pred. No. 5.1e-07;		
Matches	89;	Conservative	60;	Mismatches 96; Indels 95; Gaps 14;
Qy	442	VSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTNTLTLEVINKLYGNPRVRIMS	501	
Db	3	VSIITPHNRAKLLKRALESTLNTQYKNIEVIVVSDGSTNT-DIVMDEVKDRSRVNFIS	61	
Qy	502	KPENGGIASASNAAVSFAGYYIGOLDSDDYLEPDAVELCLKFEUKDTLACVYT-----	555	
Db	62	YHPAKGGYARNRTGIKNAKGFTAFLLDDDDWMPDKLELQIKFENQNAVNGLVYGVETI	121	
Qy	556	---TNRNVNPDGSLIANGYNWPE---FSREKL-----TTAMIAHFRMFTIRAMHLLTD	602	
Db	122	YNFNKNI-----KYSLPKTKTGNLSKEILVANCIGTSSV-----WVRKLIITE	166	
Qy	603	--GFNEKIENAVDYMFLKLSEVGKFKHLNKICYNRVLHGDNSTSIKKLGICQKQHFVVVN	660	
Db	167	CGMFDEKLKARQDYDLWI-----RVC-----QKTLGVVN	196	

Qy	661	QSLNRQGITVYNY-----DEPDLDLSEKRYIFNKTAE-----YQEEIDILK	701	
Db	197	KPL-----VRYNYTNNKQISDDIKKYESAIEYIDNKYVDLYSKVSEIRKRRHRSMTMLI	252	
Qy	702	DIKIIQNKDAKIA-----VSIPYPTNLGLVKKLNIIIEY	736	
Db	253	VNKALRNQSPKVARAVLKNKSFLLKRPFLTAIIMVMLSFLKY	292	
RESULT 8				
B75096	glycosyl transferase PAB0772 - Pyrococcus abyssi (strain Orsay)			
C;Species:	Pyrococcus abyssi			
C;Date:	20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004			
C;Accession:	B75096			
R;anonymous, Genoscope	submitted to the EMBL Data Library, July 1999			
A;Description:	Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc			
A;Reference number:	A75001			
A;Accession:	B75096			
A;Status:	preliminary			
A;Molecule type:	DNA			
A;Residues:	1-298 <KAW>			
A;Cross-references:	UNIPROT:Q9UZI6; UNIPARC:UPI0000034510; GB:AJ248286; GB:AL096836; NID			
A;Experimental source:	strain Orsay			
C;Genetics:				
A;Gene:	PAB0772			
C;Superfamily:	Neisseria meningitidis glycosyl transferase A			
Query Match	5.0%;	Score 257;	DB 2;	Length 298;
Best Local Similarity	24.9%;	Pred. No. 6.7e-07;		
Matches	83;	Conservative	65;	Mismatches 135; Indels 50; Gaps 8;
Qy	440	PLVSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTNTLTLEVINKLYGNPRVR-	498	
Db	4	PIVSVIIPYNRANLLRRALIASVLNQKPKDFELIVVDASTDNTPEVVESI--EDGRIRY	61	
Qy	499	IMSKPNGGIASASNAAVSFAGYYIGOLDSDDYLEPDAVELCLKFEFLK-DKTLACVYTTN	557	
Db	62	IRLKNKSGGPIARNIGIKKAKGFIALDDDDDEWLPHRLEQVQRKFENLGEFGVYGGF	121	
Qy	558	RNVNPDGSLIANGYNWPEFSREKLTMTAMIAHF-----RMFTIRAMHLLTDGFNEKIENAV	612	
Db	122	YVVSQDGRIL--GKRLPK-HRGDIYSHLKENFISGPTLLIRRECCKAGLFDPRLSQQ	178	
Qy	613	DYDMFLKLSEVGKFKHLNKICYNRVLHGDNSTSIKKLGICQKQHFVVVNQSLNRQGITYYN	672	
Db	179	DWDMLRIARYKFDVDEIIAKYYVHGKQISF-----	211	
Qy	673	YDFDLDLSEKRYIFNKTAEQBEIDILDKIKIQNKDAKIAVSIFYPNTLNLGVKKLN-	731	
Db	212	-----NMKKYIFGRERLIRKHLDIWKNPKILSIHLQMGMLLLLSNNTGKGLKYLTY	263	
Qy	732	--NIEYNKNIFVILVHDKNHLLTPDIKKEILA	762	
Db	264	STAIAPLNLENWILLKALDSRTVEYIKRILS	296	
RESULT 9				
AG2188	hypothetical protein alr3062 [imported] - Nostoc sp. (strain PCC 7120)			
C;Species:	Nostoc sp. PCC 7120			
A;Title:	Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120			
C;Date:	14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004			
C;Accession:	AG2188			
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,	Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.			
DNA Res. 8, 205-213, 2001				
A;Title:	Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab			
A;Reference number:	AB1807; PMID:21595285; PMID:11759840			
A;Accession:	AG2188			
A;Status:	preliminary			
A;Molecule type:	DNA			

A;Residues: 1-321 <KUR>  
A;Cross-references: UNIPROT:Q8YSM2; UNIPARC:UPI000000CB564; GB:BA000019; PIDN:BA074761.1;  
A;Experimental source: strain FCC 7120  
C;Genetics:  
C;Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 4.9%; Score 248.5; DB 2; Length 321;  
Best Local Similarity 26.1%; Pred. No. 2.3e-06;  
Matches 80; Conservative 54; Mismatches 126; Indels 47; Gaps 11;

Qy 441 LWSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTNTLEVINKLKYNPNRVRIM 500  
Db 1 MISVMPVNCCKYLEESIESILKQTYRDFEIIVNDGSDNKSIDIINKYANDNDNRIVV 60

Qy 501 KSPNG-GLASASNAVSPAKYIIGQLSDDDYLEPDAVELCLKEFLKDK---TLACVVT 556  
Db 61 SRDNNMGVSYLNEGIDRAKGSYVARMDDADIALPERFERQIYLNKNKDVLDLACKVEA 120

Qy 557 NRVNPDGSL-IANGVNWPEFSREK-----LTTAMIAHFRMFTIRAWHLTDGFNEKIE 610  
Db 121 FGDVREQLKREHYNVDLNNSESIESLFLNCYIAHPSVNMKSVLKGALGYNLNKR 180

Qy 611 AYDIDMFLKSEVG-KFHLNKCYNRVLHGDNTSIKLGIOKKHNFVVVNSLNROGIT 669  
Db 181 TEDYNLWRAIAKGYKIAMLEKMKIRLHNS-----KIHRA-- 219

Qy 670 YNYDEFDLDESRYKIFNKTAIEQIEDILDKIL-----QNKDAKIA---VSIFYPNT- 722

Query Match 4.9%; Score 248.5; DB 2; Length 333;  
Best Local Similarity 26.1%; Pred. No. 2.3e-06;  
Matches 80; Conservative 54; Mismatches 126; Indels 47; Gaps 11;

Qy 441 LWSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTNTLEVINKLKYNPNRVRIM 500  
Db 1 MISVMPVNCCKYLEESIESILKQTYRDFEIIVNDGSDNKSIDIINKYANDNDNRIVV 60

Qy 501 KSPNG-GLASASNAVSPAKYIIGQLSDDDYLEPDAVELCLKEFLKDK---TLACVVT 556  
Db 61 SRDNNMGVSYLNEGIDRAKGSYVARMDDADIALPERFERQIYLNKNKDVLDLACKVEA 120

Qy 557 NRVNPDGSL-IANGVNWPEFSREK-----LTTAMIAHFRMFTIRAWHLTDGFNEKIE 610  
Db 121 FGDVREQLKREHYNVDLNNSESIESLFLNCYIAHPSVNMKSVLKGALGYNLNKR 180

Qy 611 AYDIDMFLKSEVG-KFHLNKCYNRVLHGDNTSIKLGIOKKHNFVVVNSLNROGIT 669  
Db 181 TEDYNLWRAIAKGYKIAMLEKMKIRLHNS-----KIHRA-- 219

Qy 670 YNYDEFDLDESRYKIFNKTAIEQIEDILDKIL-----QNKDAKIA---VSIFYPNT- 722

A;Residues: 1-321 <KUR>  
A;Cross-references: UNIPROT:Q8YSM2; UNIPARC:UPI000000CB564; GB:BA000019; PIDN:BA074761.1;  
A;Experimental source: strain FCC 7120  
C;Genetics:  
C;Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 4.9%; Score 251; DB 2; Length 321;  
Best Local Similarity 27.7%; Pred. No. 1.6e-06;  
Matches 78; Conservative 48; Mismatches 122; Indels 34; Gaps 10;

Qy 439 VPLSVIIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTNTLEVINKLKYNPNRVR 498  
Db 1 MPKVSVIPAYNAMPYLPETLESVLRQTYHDFEVVVNDGSSDNTTEWVSQIL--DPLK 58

Qy 499 IMSPNGGIIASASNAVSPAKYIIGQLSDDDYLEPDAVELCLKEFLKDKTKLACVYTNR 558  
Db 59 LISQANQGLAGARTGTGIVNASGEYIAFLDADDIWEPTKLAKQVSLVDENPTVGLVYTW 118

Qy 559 NVNPDGSLI-----ANGVNWPEFSREKLTAMIAHFRMFTIRAWHLTDGFNEKIE 611  
Db 119 YIDBQGSSTGKIFKNQVEGYWPQLTEHNIVEGSGVALRRVCPEKGL---FDNLGSY 175

Qy 612 V-DVDMFLKSEVGKFKHLNKCYNRVLHGDNTSIK-----KLGIQKKHNFVVVNS 662  
Db 176 VEDWMDLRIATSYDFKVKVEALVYR--QRSNASKNWEAMHSPALVIEKAFATASQD 233

Qy 663 L-----NRQITYY-----NYDEFD-DLDESRYKIFNKTAIEY 693  
Db 234 LQVLKNKSYGFTYLCLAWKPLQSQDYKQKYSREFCQQA VAY 275

RESULT 10  
B97168  
glycosyltransferase [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: B97168  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: B97168  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-333 <KUR>  
A;Cross-references: UNIPROT:Q97H40; UNIPARC:UPI000000CA434; GB:AE001437; PIDN:AAK80131.1;  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC2173

Query Match 4.8%; Score 247; DB 2; Length 333;  
Best Local Similarity 29.3%; Pred. No. 2.7e-06;  
Matches 91; Conservative 54; Mismatches 106; Indels 60; Gaps 14;

Qy 442 VSIVIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTNTLEVINKLKYNPNRVRIM 501  
Db 4 VSVVMPVNCCKYLEESIESILNQSYSDFEIIINDGSTNSFKIKEYAKLDRINVIS 63

Qy 502 KPNNGGIIASASNAVSPAKYIIGQLSDDDYLEPDAVELCLKEFLKDKTKLACVYTNRNV 561  
Db 64 RENKGIYVSLNEALFLAKGEYIARMDDADDISAPKRIEKQI-SFLK-----SHRID 113

Qy 562 PDGSLI-----ANGVNWPEF-----SREKLT--AMIAHFRMFTIRAWHL 600  
Db 114 ILGTQVKKVGNISNDIKENKLN-IEFDYDNNREKILNRYWYCLAHPVNFKDIURE 172

Qy 601 TDGFNE-KIENAVDYDMFLKSEVG--KFHLNKCYNRVLHGDNTSIK-----KLGI 650  
Db 173 LKGYNDFKSE---DLDLWLAIESGFKIYKLEELIYFRMHEESKTRVDNQNYEGLKGI 229

Qy 651 Q-----KKNHFFVNVNQSILNRQGITVYNYDEFDLDESRYKIFN-KTAEYQBEID 698  
Db 230 KIKLIDVPKREFKDKFYIVWGSNGGKITKEVLDEFFEKSQCIAFVDKFTGEP-EKIR 288

Qy 699 IL--KDIKI 707  
Db 289 ILHPKIDINHIK 299

RESULT 12  
E71690  
minor teichoic acids biosynthesis protein ggab (ggab) RP339 - Rickettsia prowazekii  
C;Species: Rickettsia prowazekii  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: E71690  
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.; Nature 396, 133-140, 1998  
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
A;Reference number: A71630; MUID:99039499; PMID:9823893  
A;Accession: E71690  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-318 <AND>  
A;Cross-references: UNIPROT:Q9ZDI9; UNIPARC:UPI000000D37A5; GB:AJ235271; GB:AJ235269; NID  
A;Experimental source: strain Madrid E

```
C;Genetics:
A;Gene: gsaB; RP339
C;Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match      4.7%; Score 242; DB 1; Length 318;
Best Local Similarity 24.8%; Pred. No. 4.9e-06;
Matches 86; Conservative 47; Mismatches 122; Indels 92; Gaps 12;

QY 440 PLVSIIPAYNCANYIQRVCDSALNQTVVDLEVCICNDGSTDNTLEVINLKLYGNPRVRI 499
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8 PLVSIIPVNGYNGYREAIQYKIEIIVVNDGSKDET-ETIALSYGD--KICY 64
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 500 MSPXNGGIASNAASVAFKGYIIGQLSDSDYLEPDAVE-----LCLKE 543
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 LYKXGCGGALNGCKMKGKFTSWLSDHVVYPNKIEHQIINLKNLKNQKOVIVGYE 124
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 544 FL--KQTLACVYVYTRNNVNPDSGLIANGYNWPEFSREKLTITAM-----IAHFHFMFTI 595
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125 LIDQKSHSLYC-----VKPD-----QRYSEKLDISLFLPLLSLHGCTLLIP 167
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 596 RAWHLTDG-FNEKIENAVDYDMFLKSEVGFKHLNKKICYNRVLHGNTSIKLGIOQKN 654
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 168 SILFQKIGLDESILKYTHDYDFKFPVRSIYFDEHLIKSRIHAAQT-----217
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 HFVVVNSLRQGITYYNYDEPDLL-----DESRKYIFNKTAQYQEEIDI-----699
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 -----NTALNQ-----LBEYEDLWSGFLKLTKEEMIMIKGSTHOFLSDI AFLKNG 265
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 700 -----LKDIIKIQNDKAIKVSIFYENTLNGLVKLNIIYE 736
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 266 YIKSYQLALAMTQKIIGFYTSIITEIISLRHGHNTTITKIYK 312
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
AH2026
hypothetical protein all1766 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2026
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <KUR>
A;Cross-references: UNIPROT:Q8YWS0; UNIPARC:UPI000000CE1D8; GB:BA0000019; PIDN:BAB73465.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1766
C;Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match      4.7%; Score 238.5; DB 2; Length 333;
Best Local Similarity 27.4%; Pred. No. 7.9e-06;
Matches 64; Conservative 50; Mismatches 83; Indels 37; Gaps 6;

QY 439 PLVLSVIPAYNCANYIQRVCDSALNQTVVDLEVCICNDGSTDNTLEVINLKLYGNPRVR 498
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8 LPIISVIPAYNCEKTIKTTIDSVDLQSFDFELIVNDGSDQATLDIVSQI--EDSRIK 65
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 499 IMSKXNGGIASNAASVAFKGYIIGQLSDSDYLEPDAVELCFKFKDKTKLACVYVYTR 558
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 IFSFENAGGNVSRNGLNLAVGKFIPLDADDITWNTKLESQLEALHNNPGFHVAYSWTD 125
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 559 NVNPDGSLANG-----YNPWPSREKL--TTAMIAHFHFMFTIRAWHLT 601
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 YIDEDGNFLISGRVTLNGDVYKKLFINNPLENGSNPLCKEALIA-----L 172
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 602 DGFNEKIENAVDYDMFLKSEVGFKHLNKKICYNRVLH--GDNTSIKLGIOQKK 653
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

C;Genetics:
A;Gene: gsaB; RP339
C;Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match      4.7%; Score 238; DB 2; Length 306;
Best Local Similarity 25.2%; Pred. No. 7.5e-06;
Matches 83; Conservative 53; Mismatches 97; Indels 96; Gaps 14;

QY 442 VSIYIPAYNCANYIQRVCDSALNQTVVDLEVCICNDGSTDNTLEVINLKLYGNPRVIMS 501
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 VSIYIPIYNAEKTICNVCDSALKQNLESLEVILVNDGSDNSTSKILEQ-YGDNPQVMIFH 62
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 502 KPNGGIASNAASVAFKGYIIGQLSDSDYLEPDAVELCFKFKDKK---TLACVY---554
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 QVNWGVSARNVGLSVASGEYVFFLSDDLIDEGMLSK-MYQPAKSNKDKLLSCWKEPS 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 555 TT--NRNVNPDGSLIANGYNWPEFSREKLTITAMIAHF-----RMFTIRAWHLT 602
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 TTYQGGNDSSASFAR-----TKEIGHNFVDIFPRSCAKLFLRRRIE---166
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 603 GFNEKIENAVDYDMFLKSEVGFKHLNKKICYNRVLHGNTSIKLGIOQKHFFVVVNQS 662
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 167 -----ENNIAFSTENSLGEMDSF-----VC-----QYLMVSR 194
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 663 LNRQGITYYNYDEFDLDESRYIFNKTAQYQEEIDILDKIKIONK---DAKIAVSIFYP 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 IAVIDGLYTIQNVNPOSLSKRYVSN-----IENSLLMQNLWDQLLEV---YP 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 721 NTLNGLVKK-----LNNIIEYN 737
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 KTEENYKQHMDFRFYLASLYVNNLPKFD 269
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
AH2189
hypothetical protein alr3071 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2189
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <KUR>
A;Cross-references: UNIPROT:Q8YSL3; UNIPARC:UPI000000CE66D; GB:BA0000019; PIDN:BAB74770.1;
```

[illegible]

**THIS PAGE BLANK (USPS#)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 15:58:46 ; Search time 46 Seconds  
(without alignments)

1746.973 Million cell updates/sec

Title: US-10-642-248-2

Perfect score: 5108

Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAKGENIPVKNKFIINSITL 972

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	972	2	US-09-469-200E-9
2	5104	99.9	972	2	US-10-172-527A-10
3	4490.5	87.9	965	2	US-09-437-277-3
4	3673.5	71.9	702	2	US-09-437-277-1
5	301.5	5.9	721	2	US-09-107-532A-6889
6	300	5.9	331	2	US-09-634-238-247
7	287.5	5.6	842	2	US-09-134-000C-5749
8	264.5	5.2	333	2	US-09-107-532A-5123
9	250.5	4.9	534	2	US-09-134-000C-5087
10	244.5	4.8	327	2	US-09-107-532A-6181
11	241.5	4.7	330	2	US-09-134-000C-6392
12	238.5	4.7	324	1	US-08-597-236-10
13	238.5	4.7	324	1	US-08-746-682A-10
14	236.5	4.6	1056	2	US-09-134-000C-5086
15	231.5	4.5	674	2	US-08-961-083-200
16	231.5	4.5	674	2	US-09-536-784-200
17	231.5	4.5	674	2	US-09-765-272A-200
18	231.5	4.5	674	2	US-09-765-272A-200
19	228.5	4.5	727	2	US-09-134-001C-4067
20	212	4.2	270	2	US-09-495-406-25
21	212	4.2	270	2	US-09-816-028A-39
22	212	4.2	270	2	US-10-303-162-39
23	212	4.2	270	2	US-10-303-134-39
24	212	4.2	270	2	US-10-303-118-39
25	212	4.2	270	2	US-10-303-128-39
26	210	4.1	301	2	US-09-495-406-15
27	210	4.1	301	2	US-09-816-028A-27

ALIGNMENTS

RESULT 1

US-09-469-200E-9  
; Sequence 9, Application US/09469200E  
; Patent No. 6833264  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kshama  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/09/469,200E  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pastuerella Multocida  
US-09-469-200E-9

Query Match	100.0%	Score 5108;	DB 2;	Length 972;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 972;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNTLSQAIKAYNSNDYQLALFKESAEIYGRKIVEFOITKCKEKL	SAHPSVNSAHL	SVN 60
DB	1	MNTLSQAIKAYNSNDYQLALFKESAEIYGRKIVEFOITKCKEKL	SAHPSVNSAHL	SVN 60
QY	61	KEEKVNVCDSPDLTATQLLSNVKKLVLSDEKNTLKNKWL	TEKKSNAEVR	ALVLP 120
DB	61	KEEKVNVCDSPDLTATQLLSNVKKLVLSDEKNTLKNKWL	TEKKSNAEVR	ALVLP 120
QY	121	KDFPKDLVLAFLPDHVNDFTWYKKRKGRLGKPEHQHVG	LSIIVTTFNRP	PAILLSITLACL 180
DB	121	KDFPKDLVLAFLPDHVNDFTWYKKRKGRLGKPEHQHVG	LSIIVTTFNRP	PAILLSITLACL 180
QY	181	VNQKTHYFEVIVTDDGSOEDLSPIROYENKLDIRYVR	KDNGFQASARN	MGURLAKY 240
DB	181	VNQKTHYFEVIVTDDGSOEDLSPIROYENKLDIRYVR	KDNGFQASARN	MGURLAKY 240
QY	241	DFIGLLDCDMPNPLVHSHYVAELLEDLDTIIGPRKY	IDTQHDIDPK	FLNNASLESUP 300
DB	241	DFIGLLDCDMPNPLVHSHYVAELLEDLDTIIGPRKY	IDTQHDIDPK	FLNNASLESUP 300
QY	301	EYKTNNSVAAKGEGTVSLDWRLEQTEKNTENLRLSD	SPRFFPAAG	NVAFKKWLKSGFPD 360

Db 301 EVKTNNSVAAKGBGTSLDWRLEQPEKTEENLRSLSDSPFRFFAAGNVAFAKWLKNSGFFD 360  
Qy 361 EEFNHWGGEDVFGYRLFRYGSFKTTIDGIMAYHQBPCKENETDREAGNITLDMREK 420  
Db 361 EEFNHWGGEDVFGYRLFRYGSFKTTIDGIMAYHQBPCKENETDREAGNITLDMREK 420  
Qy 421 VPIYKRLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480  
Db 421 VPIYKRLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480  
Qy 481 DNTLEVINKLYGNPNRVRIMSKPNGGIIASASNAVSAFAKGYIIGOLDSDDDYLPDAVELC 540  
Db 481 DNTLEVINKLYGNPNRVRIMSKPNGGIIASASNAVSAFAKGYIIGOLDSDDDYLPDAVELC 540  
Qy 541 LKEFLKDKTKLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
Db 541 LKEFLKDKTKLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
Qy 601 TDGFNEKIENAVDYDMFLKLSVKGPKHLNKI CYNRVLHGDNTSIKKGIGQKKNHFVVVN 660  
Db 601 TDGFNEKIENAVDYDMFLKLSVKGPKHLNKI CYNRVLHGDNTSIKKGIGQKKNHFVVVN 660  
Qy 661 QSLNRQGITYYNYDEFDLDESRYKIFNKTAEYQEEIDILKDIKIIQNKDAKIAVSIFYP 720  
Db 661 QSLNRQGITYYNYDEFDLDESRYKIFNKTAEYQEEIDILKDIKIIQNKDAKIAVSIFYP 720  
Qy 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKXHLTPDKKEILAFYHKHQVNILLNNDISYY 780  
Db 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKXHLTPDKKEILAFYHKHQVNILLNNDISYY 780  
Qy 781 TSNRLIKTEAHLNINKLSQLNCEYII FDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840  
Db 781 TSNRLIKTEAHLNINKLSQLNCEYII FDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840  
Qy 841 DWIEKINAHPPPKKLI KTYFNDNDLKS MNVKGASQGMFTYALAHELLITIIKEVITSCQS 900  
Db 841 DWIEKINAHPPPKKLI KTYFNDNDLKS MNVKGASQGMFTYALAHELLITIIKEVITSCQS 900  
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKLOWTNEQIESAKRGENI 960  
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKLOWTNEQIESAKRGENI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972

RESULT 2  
US-10-172-527A-10  
; Sequence 10, Application US/10172527A  
; Patent No. 6951743  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Kshama  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: HYALURONAN SYNTHASE GENES AND EXPRESSION THEREOF IN BACILLUS HOST  
; FILE REFERENCE: 3554,048  
; CURRENT APPLICATION NUMBER: US/10/172,527A  
; CURRENT FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: 60/297,788  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 60/297,744  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 09/469,200  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: pasteurella multocida

US-10-172-527A-10  
Query Match 99.9%; Score 5104; DB 2; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNTLSQAIKAYNSNDYQALALKEKSAEYIGRKIVVEFOITKCKEKL SAHPSVNSAHL SVN 60  
Db 1 MNTLSQAIKAYNSNDYQALALKEKSAEYIGRKIVVEFOITKCKEKL SAHPSVNSAHL SVN 60  
Qy 61 KEEKVNVCSPDLIATQLLLSNVKLVLSDSSEKNTLKNWKLLTEKKSENAERAVALVP 120  
Db 61 KEEKVNVCSPDLIATQLLLSNVKLVLSDSSEKNTLKNWKLLTEKKSENAERAVALVP 120  
Qy 121 KOPPKDLVLAPLDHVNDFTWYKKRKRIGIKPEHOHVGLSII VTFNRPAILSI LACL 180  
Db 121 KOPPKDLVLAPLDHVNDFTWYKKRKRIGIKPEHOHVGLSII VTFNRPAILSI LACL 180  
Qy 181 VNOKTHYPPEVITVDDGSOEDLSPIIROYENKLDIRYVRQKONGFOASAARNMGLRLAKY 240  
Db 181 VNOKTHYPPEVITVDDGSOEDLSPIIROYENKLDIRYVRQKONGFOASAARNMGLRLAKY 240  
Qy 241 DFITGLDDCMAPNPLMVHSYVAELLEDDDLTIIGPRKYIDTQHI DPKDFLNNASLLES LP 300  
Db 241 DFITGLDDCMAPNPLMVHSYVAELLEDDDLTIIGPRKYIDTQHI DPKDFLNNASLLES LP 300  
Qy 301 EVKTNNSVAAKGBGTSLDWRLEQPEKTEENLRSLSDSPFRFFAAGNVAFAKWLKNSGFFD 360  
Db 301 EVKTNNSVAAKGBGTSLDWRLEQPEKTEENLRSLSDSPFRFFAAGNVAFAKWLKNSGFFD 360  
Qy 361 EEFNHWGGEDVFGYRLFRYGSFKTTIDGIMAYHQBPCKENETDREAGNITLDMREK 420  
Db 361 EEFNHWGGEDVFGYRLFRYGSFKTTIDGIMAYHQBPCKENETDREAGNITLDMREK 420  
Qy 421 VPIYKRLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480  
Db 421 VPIYKRLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480  
Qy 481 DNTLEVINKLYGNPNRVRIMSKPNGGIIASASNAVSAFAKGYIIGOLDSDDDYLPDAVELC 540  
Db 481 DNTLEVINKLYGNPNRVRIMSKPNGGIIASASNAVSAFAKGYIIGOLDSDDDYLPDAVELC 540  
Qy 541 LKEFLKDKTKLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
Db 541 LKEFLKDKTKLACVYTTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600  
Qy 601 TDGFNEKIENAVDYDMFLKLSVKGPKHLNKI CYNRVLHGDNTSIKKGIGQKKNHFVVVN 660  
Db 601 TDGFNEKIENAVDYDMFLKLSVKGPKHLNKI CYNRVLHGDNTSIKKGIGQKKNHFVVVN 660  
Qy 661 QSLNRQGITYYNYDEFDLDESRYKIFNKTAEYQEEIDILKDIKIIQNKDAKIAVSIFYP 720  
Db 661 QSLNRQGITYYNYDEFDLDESRYKIFNKTAEYQEEIDILKDIKIIQNKDAKIAVSIFYP 720  
Qy 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKXHLTPDKKEILAFYHKHQVNILLNNDISYY 780  
Db 721 NTNLGLVKKLNNIIEYNKNI FVILVHVDKXHLTPDKKEILAFYHKHQVNILLNNDISYY 780  
Qy 781 TSNRLIKTEAHLNINKLSQLNCEYII FDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840  
Db 781 TSNRLIKTEAHLNINKLSQLNCEYII FDNHDSL FVKND SYAYMKKYDVGWNFSA LTH 840  
Qy 841 DWIEKINAHPPPKKLI KTYFNDNDLKS MNVKGASQGMFTYALAHELLITIIKEVITSCQS 900  
Db 841 DWIEKINAHPPPKKLI KTYFNDNDLKS MNVKGASQGMFTYALAHELLITIIKEVITSCQS 900  
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKLOWTNEQIESAKRGENI 960  
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKLOWTNEQIESAKRGENI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972

```
RESULT 3
US-09-437-277-3
; Sequence 3, Application US/09437277
; Patent No. 644447
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCE: 5820.551
; CURRENT APPLICATION NUMBER: US/09/437,277
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 3
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-09-437-277-3

Query Match      87.9%; Score 4490.5; DB 2; Length 965;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 843; Conservative 62; Mismatches 60; Indels 7; Gaps 2;

QY      1 MNTLSQAIKAYNSNDYQALALFKESAEIYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 60
DB      1 MNTLSQAIKAYNSNDYQALALFKESAEIYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 60
QY      61 KEEKVNVCDSPDLATQALLSNVKKLVLSDESKNTLKNKKWLLTEKKSENAEVRVALVP 120
DB      54 EDKKNVCDSPDLATQALLSNVKKLVLSDESKNTLKNKKWLLTEKKSENAEVRVALVP 113
QY      121 KDFPKDLVLAFLPDHVNDFTYKKRKGKLGKPEHQHVGLSIIVTTFNRPAILSTLACL 180
DB      114 KDFPKDLVLAFLPDHVNDFTYKKRKGKLGKPEHQHVGLSIIVTTFNRPAILSTLACL 173
QY      181 VNQKTHYFEFVITDDGSEDLSPITROYENKLDIYRQKNGFQASARNMGLRLAKY 240
DB      174 VNQKTHYFEFVITDDGSEDLSPITROYENKLDIYRQKNGFQASARNMGLRLAKY 233
QY      241 DFIGLLDCMAPNPLVHSHYVAELLEDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL 300
DB      234 DFIGLLDCMAPNPLVHSHYVAELLEDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL 293
QY      301 EVKTNNSVAAGBEGTVSDWRLBQPEKTEKNTLKNKKWLLTEKKSENAEVRVALVP 360
DB      294 ETATNNPSITSGKNSLDWRLBQPEKTEKNTLKNKKWLLTEKKSENAEVRVALVP 353
QY      361 EEFNHWGGEDVEFGYRLFRYGSFFKTIDGIMAYHOEPPEKNETDREAGKNTLDMREK 420
DB      354 EEFNHWGGEDVEFGYRLFRYGSFFKTIDGIMAYHOEPPEKNETDREAGKNTLDMREK 413
QY      421 VPIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRQVDSALNQTVDLEVCINDGST 480
DB      414 VPIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRQVDSALNQTVDLEVCINDGST 473
QY      481 DNTLEVINKLXGNPRVIMSKPNGIGASASNAVSPAKGYIIGQLDSDDYLEPDAVELC 540
DB      474 DNTLEVINKLXGNPRVIMSKPNGIGASASNAVSPAKGYIIGQLDSDDYLEPDAVELC 533
QY      541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWBPFSREKLTAMIAHFRMFTIRAWHL 600
DB      534 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWBPFSREKLTAMIAHFRMFTIRAWHL 593
QY      601 TDFNFKENIENAYDVMFLKSEVGKPKHLNKKIYNRVLHGDNTSICKLGIQKKNHFVVVN 660
DB      594 TDFNFKENIENAYDVMFLKSEVGKPKHLNKKIYNRVLHGDNTSICKLGIQKKNHFVVVN 653
QY      661 QSLNRQGIYNNYDEPDDLDESKYIFNKTAEYQBEIDILDKIIONKDAKIAVSIFYP 720
DB      654 QSLNRQGIYNNYDEPDDLDESKYIFNKTAEYQBEIDILDKIIONKDAKIAVSIFYP 713
QY      721 NTLNGLVKLNNIIYENKNI FVILHVDKNHLTPDKKEILAFYHKHQVNILLNDISYY 780
DB      714 NTLNGLVKLNNIIYENKNI FVILHVDKNHLTPDKKEILAFYHKHQVNILLNDISYY 773
QY      781 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGNNFSALTH 840
DB      774 TSNRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKYDVGNNFSALTH 833
QY      841 DWIEKINAHPPFKKLKITYFENDNDLKSMMNVKGASQGMFTYALAHALLTIIKEVITSQS 900
DB      834 DWIEKINAHPPFKKLKITYFENDNDLKSMMNVKGASQGMFTYALAHALLTIIKEVITSQS 893
QY      901 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEOIESAKRGNI 960
DB      894 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEOIESAKRGNI 953
QY      961 PVNKFIINSITL 972
DB      954 PVNKFIINSITL 965

RESULT 4
US-09-437-277-1
; Sequence 1, Application US/09437277
; Patent No. 644447
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCE: 5820.551
; CURRENT APPLICATION NUMBER: US/09/437,277
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 1
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-09-437-277-1

Query Match      71.9%; Score 3673.5; DB 2; Length 702;
Best Local Similarity 99.7%; Pred. No. 4.6e-313;
Matches 701; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY      1 MNTLSQAIKAYNSNDYQALALFKESAEIYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 60
DB      1 MNTLSQAIKAYNSNDYQALALFKESAEIYGRKIVEFOITCKEKLSAHPSVNSAHLNVN 60
QY      61 KEEKVNVCDSPDLATQALLSNVKKLVLSDESKNTLKNKKWLLTEKKSENAEVRVALVP 120
DB      61 KEEKVNVCDSPDLATQALLSNVKKLVLSDESKNTLKNKKWLLTEKKSENAEVRVALVP 120
QY      121 KDFPKDLVLAFLPDHVNDFTYKKRKGKLGKPEHQHVGLSIIVTTFNRPAILSTLACL 180
DB      121 KDFPKDLVLAFLPDHVNDFTYKKRKGKLGKPEHQHVGLSIIVTTFNRPAILSTLACL 180
QY      181 VNQKTHYFEFVITDDGSEDLSPITROYENKLDIYRQKNGFQASARNMGLRLAKY 240
DB      181 VNQKTHYFEFVITDDGSEDLSPITROYENKLDIYRQKNGFQASARNMGLRLAKY 240
QY      241 DFIGLLDCMAPNPLVHSHYVAELLEDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL 300
DB      241 DFIGLLDCMAPNPLVHSHYVAELLEDLTIIGPRKYIDTQHDIDPKDPLNNASLESPL 300
QY      301 EVKTNNSVAAGBEGTVSDWRLBQPEKTEKNTLKNKKWLLTEKKSENAEVRVALVP 360
DB      301 EVKTNNSVAAGBEGTVSDWRLBQPEKTEKNTLKNKKWLLTEKKSENAEVRVALVP 360
QY      361 EEFNHWGGEDVEFGYRLFRYGSFFKTIDGIMAYHOEPPEKNETDREAGKNTLDMREK 420
DB      361 EEFNHWGGEDVEFGYRLFRYGSFFKTIDGIMAYHOEPPEKNETDREAGKNTLDMREK 420
QY      421 VPIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRQVDSALNQTVDLEVCINDGST 480
DB      421 VPIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRQVDSALNQTVDLEVCINDGST 479
```

```
QY 481 DNTLEVINLKGNNPRVRIMSKNGGIGTASNAASFAKGYIIGOLDSDDYLDSPDAVELC 540
Db 480 DNTLEVINLKGNNPRVRIMSKNGGIGTASNAASFAKGYIIGOLDSDDYLDSPDAVELC 539
QY 541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNWPEFSREKLTMTAMIAHFRMFTIRAWHL 600
Db 540 LKEFLKDKTLACVYTTNRNVPDGLSIANGYNWPEFSREKLTMTAMIAHFRMFTIRAWHL 599
QY 601 TDGFNEKIENAVDYDMPKLSEVGKFKHLNKICYNRVLHGDNTSIKKGIGTQKKNHFFVVN 660
Db 600 TDGFNEKIENAVDYDMPKLSEVGKFKHLNKICYNRVLHGDNTSIKKGIGTQKKNHFFVVN 659
QY 661 QSLNRQGITVYNYDEPDLDSESRKYIFNKTAEQEIEDILKDI 703
Db 660 QSLNRQGITVYNYDEPDLDSESRKYIFNKTAEQEIEDILKDI 702

RESULT 5
US-09-107-532A-6889
; Sequence 6889, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6889:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...721
; SEQUENCE DESCRIPTION: SEQ ID NO: 6889:
US-09-107-532A-6889
Query Match 5.9%; Score 301.5; DB 2; Length 721;
Best Local Similarity 21.2%; Pred. No. 3.1e-17;
Matches 153; Conservative 121; Mismatches 259; Indels 187; Gaps 28;
```

```
QY 269 DLTIIG-----PRKYIDTQHIDPKDFLNNSLLESLP-----EYKTNNS-----VAAGK 312
Db 30 DLLIVGAWIDEVTKELPTIKVEKNVIAETHVRDLINHLYNLDVKTOSGFKVRISGGKM 89
QY 313 EGTVSLDWRLEQPEKTENLRLSDS--PFRFFAAGNVAFAKKWLNLSKSGFFPDDEEFNHGGEDV 371
Db 90 RGKAILDFQTARHONGIAVKLANGKYPY-----DDGISSWERKKRLKKGINVARTHGV 143
QY 372 EGYRLFRYGSFKTTIDGI--MAYHQEPGKENETDREAGKNITLDIRMEKVPYIYRKLL 429
Db 144 KKAIRRVKLELPGSIDIYAEWISRHEKPDLEQR-----REVQGFAYR--- 186
QY 430 PIEDSHINRVPLVSIYIPAYNC--ANYIORCVDSALNQTVVLDLEVLCIENDGSTNTL--EVI 487
Db 187 -----PLISILMPYVNVKLEKICISVLDQTYDHWELCISDASTDPARKCL 236
QY 488 NKLYGNNPRVRIM--SKPNGGIASASNAAVSFAGYYIIGOLDSDDYLDSPDAVELCLKEFLK 546
Db 237 ESYQAKDDRIKVVFRQENGHISLATNSALEMAEGEFIALDNDDELPPFALYEVAKVLNV 296
QY 547 DKTILACVYTTNRNVPDGLSIANGYNWPEFSREKLTMTAMIAHFRMFTIRAWHLTDPFNE 606
Db 297 HPELDLYSDEDKIDADGNRFPDFHK--ADMSPDTLMGNNYISHLGVYRTSIVKELGGFRK 355
QY 607 KIENAVDYDMFLKLSVGVKFKHLNKICYNRVLHGDNTSIKKGIGTQKKNHFFVVNQSLNRQ 666
Db 356 GYEGSQDYDLVRVTEIQIPAEHIYHI--DRVLY-----HWRTIPGSTASN 398
QY 667 GITVYNYDEPDLDSESRKYIFNKTAEQEIEDILKDIKIIONKDAKI---AVSIFYPNTL 723
Db 399 G-----EAKSYI-----YDSGVKALTDALSRRNKIGSVHPRISGFYEITY 439
QY 724 NGLVKLNNILIEYKNIF-----VI-----VLHVDKXHLTDPDIKKEILAFYH 765
Db 440 DVLQEDLVSVIIPTKNGYEDLTKCVDSIIETKTSYPNYEIIAADNGSTDPKM--QELFAEY-- 497
QY 766 KHQVN---ILLNNDISYVTSNRLIKTEAHLNKLNSQLNLNCEYIIFONHDSLFVKND-- 821
Db 498 KHQLKDRFIV-----ELIDIPFNYSRINNLAEEKANGKYFLFLNNDTEVIEPDW 546
QY 822 -----SYAY-----MKKYD-----V 831
Db 547 MTAMVSYAQFDRIQCVGAKLFYPPDDTTOHAGVLLGIGGVAGHALNNYDRTHCGYFGRLVI 606
QY 832 GNFPSALTHDWI-----EKINAHPPPKLKIPTYNDNDLKSMMVKGASQGMFTYALAH 887
Db 607 DVNYLAVTAACMMVKAAADFNVAVNGFDBILEVAFNDVDL---CLKVVELGRYVNYAHQAE 663

RESULT 6
US-09-634-238-247
; Sequence 247, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 331
```

```
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-247

Query Match      5.9%; Score 300; DB 2; Length 331;
Best Local Similarity 28.6%; Pred. No. 1.2e-17;
Matches 90; Conservative 53; Mismatches 130; Indels 42; Gaps 11;

Qy 439 VPLSVIIPAYNCANYIQRCDVSALNQTVDLVLCICNDGSDTNTLKVINKLYGNPRVR 498
Db 6 MPLSVIIIPVYNEKYLQRCIDSLFAQTYNIEIIVLVDGSDAKSLICKNAQQDERVR 65
Qy 499 IMSKPNGGIISASNAAYSFRAKGYIGOLSDSDYLEPDAVELCLKEFLKDKTCLACVYITNR 558
Db 66 VFSKNGGADTRNFGVSVARGQWISFVDPDDYVDYDIEYLYGILVKSNATMSI-CQHR 124
Qy 559 NVNPDGSLIANGYNWPE-----FSREKLTAMIAHFRMFTIRAWHLTDG-FNE 606
Db 125 NVYKNGKIQTNLYEGPAVLDSHTAVKLLYDDQIDTSVWAKLYPAWVFKKIHPKGRLE 184
Qy 607 KIENAVDYDFLKLSEV---GKFKHLNKICYNVHLGDNISIKKLG-----QK 653
Db 185 DI--AATYKTFPLASDSIANGSEAKYSYPRYSIVN-DQFSLHLKDLIDMTQWACEVKK 241
Qy 654 NHFVVVNSLNROGITVNY-----DEPDLDSESKYIFNKTAAYOEIDILDKIKI- 705
Db 242 ---VYPDLQIASQRRVYAYISTLNQMNQVQGYOEIREQLISKIKELRK--PVLEDHKAP 296
Qy 706 IQNKDAXIAVSIFYP 720
Db 297 IRDKVAICLIGFSYP 311

RESULT 7
US-09-134-000C-5749
; Sequence 5749, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5749
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5749

Query Match      5.6%; Score 287.5; DB 2; Length 842;
Best Local Similarity 19.5%; Pred. No. 6.9e-16;
Matches 191; Conservative 147; Mismatches 315; Indels 327; Gaps 42;

Qy 156 OHVGLSIIVTFNRPAISITLACLNVQKTHYPFEVIVTDDGSDQLSPFIROYENKLDI 215
Db 8 ENVKSVIVPVYNEVETYLEEALMSLNQ-TLKEIFLIINDGSTONSQKILIE----- 59
Qy 216 RYVRQKNGFQSAARNMGLRLAKYDFIIGLLDCDMPNPLVHVSVAELLEDLDTIIGP 275
Db 60 --IAQDDPRFRVFNKNGG--IGKAPNLGVSEAK-----GEYIAEFSDDYVALHAY 107
Qy 276 RXYIOT---QHIDPKDFLNASLLESLEPVKTNNSVAAKGECTVSLD--WRL-EQFEXTE 329
Db 108 ERLYNTAKSHHAD-----VRCNWFESSEEEVERDILMQVPDKYNQI 151
Qy 330 NLRLSDSPRPFAAGNAPFAKKWLNKSGF-FDEEFNHWGGEDVEFGYRLFRYGSFFK--- 385
Db 152 DLKTTDLIVQVY-PWNAIYKSKMIEKENVTWDEEIKSYGDT-----GLFWKINS 199

386 -----TIDGINAYHQEPPEKGENETDRBAGKNITLDMREKVPYIYR----- 426
200 ASQNVIFIKDCLVYRQDNP-----NSTVNVATKVPFLFOQFKLIRSNLIEQ 247
427 -----KLLPIED----- 433
248 NKFERYKGYFQKMFKYFWAIEKLTHLRDESVEYIQKAVDFRQALETDQLNDIDFEY 307
434 -----SHINRVPLSVIYIPAYNCANYIQRCDVSALNQTVDLVLCICND 477
308 IKOFYQIANDPAAYEDYLKNLYKVSVMPIHNASKYLRQTLTETVCESQSLREIILVEN 367
478 GSTDNTLEVINKLYGNPRVRIMSKPNGGIISASNAAYSFRAKGYIGOLSDSDYLE----- 533
368 GSTDNTMDIINEFAVKDPRIITGISIGKSNPGHARNVIGISMARGRYLQFLDADDDHFEANLL 427
534 -----PAVELCLKEFLKDKTCLACVYITNRNVPDGSILANG--YNNPEFSEK 580
428 QDAYRAYDSATDILLFGMKELPNGEVHVH-----NP-----LLTNGGRMSGEEISLDE 478
581 LTTAMIAHFRMFTIRAWHLTDGTFNEKIEANAVDYDMFL---KLSEVGKFKHLNKICYNRV 637
479 VTPYLYDKLFLLEYIKENNLV-----LEQFVGEDAYFTYTALLGTEKIVALNKYLLTRI 533
638 LHGDNTSIIKKGIOKKNHVVVNQSL-----NR-----QGITVYNYDEPD--DLDE 681
534 VRQDGL-MSTYGMNRYRDEFNLHDKMLLEYLKHAPNRTEAYRLKIINTLNWFIIDMNRVDQ 592
682 SRKYIFNKTAAYOEIDILDKIKIIONKDAKIAVSIFYPNTLNGL--VKLNNIIEYNKN 739
593 AFKERF-----YOE-----LKE-KYIQLGLDLVKKEKYSNDPEQVERITRILQNLLE 642
740 IFVIV---LHVDKNHLPDIK---KEILAFYHKHGVN-----ILNNDISYVTS 782
643 IYQNIYKDFGKKTFTIIPNVHIQBERGKVIFGQEKTOGTAEMFIIADND-----TS 698
783 NRLIKTEAHLNSINKLSQNLNCEYIIFDNHDSLFVKNSDYAYNMKKYDVGNFSAETHDW 842
699 N-----ASGVDFVYMGDNTKII---HDSLLVS---LLIKKEGTTLKSIVLOAEW 742
843 IEKINAHPPFKLIKTYFNNDNLKSMNVKSGASQGMFTYALAHELL--TIKEVITSQS 900
743 -----EKG-----YTLQENMYTYFDNVFT----- 763
901 IDSVPYNTEDIW-----FOFALLILEKKTGHVENKTSITLYMPWERKQWNEQI 951
764 -----IWAGYTKYAAFDYVNRILTSREGE-----THFSVVRQNGYIQT 804
952 ESAKRGENIPVNFINSIT 971
805 MTSIGNELTPINKIEGNEPT 824

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
```

```
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/107,532A
;   FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/085,598
;   FILING DATE: 14 May 1998
;   APPLICATION NUMBER: 60/051571
;   FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ariniello, Pamela Deneke
;   REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-5277
; INFORMATION FOR SEQ ID NO: 5123:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 333 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
;   ORGANISM: Enterococcus faecium
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (B) LOCATION 1...333
; SEQUENCE DESCRIPTION: SEQ ID NO: 5123:
US-09-107-532A-5123

Query Match      5.2%; Score 264.5; DB 2; Length 333;
Best Local Similarity 23.3%; Pred. No. 1.5e-14;
Matches 85; Conservative 66; Mismatches 129; Indels 85; Gaps 12;

QY 442 VSIYIPAYNCANYIQCVDSSALNQTVVDLVCIQNDGSTDNTLEVINKLYGNNPRVRIMS 501
Db 13 ISIIVPVYVVEKYLKCVDSILQGTFTDFELLIDGSTDNGSSICDELAKTNRIKVIH 72

QY 502 KPGNGIASNAAVSFAGKYIYIQLSDDDYLEPDAVELCLKEFLK---DKTLACVYTTNR 558
Db 73 KENGGLSDARNIGIEVAKGDFIGFIDSDVDYDEDMVAFYNNILKYDAELSMGCIYDVHK 132

QY 559 N-----VNPDSLIANGYNWPFSPREKLITTA-MIAHHFRMFTIRAWHLTDGPFNEKEN-- 610
Db 133 NKEIKLTPFSQLVTKSEAIELVDGLKVYVANAVSKLYK-----KELFENVR 179

QY 611 -----AVDYDMFLKLSEVGKFKHLNKCYNRVVLHGDNSTSIKKGIGQKNHFVVVQSLN 664
Db 180 YPKGKTAEADAANVLKI-----INQCKNI-----HVDTS-----QKYYVHRGDSIT 220

QY 665 RQGITYYNYDEFDLDESRYIFNKTAEOEID-----ILKDIKIIQNKDAKIAV 715
Db 221 SKKFTKKDFDIIDVWNEKEMWIKNYPQMDKVHTRVCWAYFVVVLKLVLTBEK----- 274

QY 716 SIPYPNTLGLVKLANIIEYKNIFVILVHDNHLTPDIKEIILAFYHKHQVILLNN 775
Db 275 -----GLYQEKQVREYLDINDFFI-----IKNRLTFFQKISM-LLLTF 313

QY 776 DISYY 780
Db 314 GIAAY 318

RESULT 9
US-09-134-000C-5087
; Sequence 5087, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5087
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5087

Query Match      4.9%; Score 250.5; DB 2; Length 534;
Best Local Similarity 21.2%; Pred. No. 5.7e-13;
Matches 114; Conservative 91; Mismatches 189; Indels 145; Gaps 21;

QY 295 LLESPEVKTNNSSAAKGEGTSLDWRLEQFKEKTENLRSLSDSPFRFAAGNVAFKAKWLN 354
Db 21 IFDSIYRDKTNNLTITG-----WALDTIYK-----ESP--TFTINNENQVSAY-N 63

QY 355 KSGFFDEEPN--HWGGEDVEFGYRIFRYGSPFKTIDGI-----MAYHQB----- 397
Db 64 IORVLREDVNOIYQTEPAIEAG-----FVVTLEGIKQKKVLPFPFQSSAHVITVDFP 115

QY 398 -----PKENETDR-----EAGKNIITLIDIMEKVPYI-----YRK 427
Db 116 LNKKYPVIFGTEDKVTRLMIKAKGFKYNAKNGISHTIORAKIEKLUNQASYPNWLARNE 175

QY 428 LPIED-----SHINRVLVSIYIPAYNC-ANYIQCVDSSALNQTVVDLVCIQNDGSTD 481
Db 176 VLDIEAMTQEIATFHYQPKISIAMPVYNVEEKWLRCLCIDSILNQVYNWELCWADASTD 235

QY 482 -NTLEVINKLYGNNPRVRIM-SKPNGGIASNAAVSFAGKYIYIQLSDDDYLEPDAVEL 539
Db 236 PNWKILTEYQQLDERIRVVFREQNGHISEATNSALAIATGSEFVALLDNDDELAINAFYE 295

QY 540 CLKEFLKDKTLACVYTTNRVNPDSLIANGYNWPFSPREKLITTA-MIAHHFRMFTIRAWH 599
Db 296 VVKLVNENPELDLIVSDEKIDMDGNRSDPAFK-PDWSDDLGLGTNYIISHLGVYRRSILE 354

QY 600 LTDGFEKLENAVDYDMFLKLSE---VGKFKHLNKCYNRVVLHGDNSTSIKKGIGQKN 654
Db 355 EIGGFRKYGESQDYDLVLRFTTEKTKERIKHFKVLYYWRMLPTSTAVDQSGKYAPEA 414

QY 655 HFVVNQSLNRQGI-----TYNYDE-----FDDLDESRYIF 687
Db 415 GLRAVQDALVRRINGHATHGAANGLYDVYDIESEKLVSIIPTKNGYKDVQRCVSSII 474

QY 688 NKT-----AEYQ-----EEDILKDIKIIQNKDAKIA 714
Db 475 EKTYYONYEIIWADNGSTDPKMHLYAEFEQQLPGRFFVESIDIPFNFTINNRAAKKA 533

RESULT 10
US-09-107-532A-6181
; Sequence 6181, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;   STREET: 100 Beaver Street
;   CITY: Waltham
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02354
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: CD/ROM ISO9660
;   COMPUTER: PC
```

```
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107.532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...327
; SEQUENCE DESCRIPTION: SEQ ID NO: 6181:
US-09-107-532A-6181

Query Match 4.8%; Score 244.5; DB 2; Length 327;
Best Local Similarity 26.0%; Pred. No. 8.4e-13;
Matches 85; Conservative 59; Mismatches 100; Indels 83; Gaps 15;

Qy 442 VSIYIPAYNCANYQRCVDSALNQTVDLEVCICNDGSDTNTLEVINLGNPRVRIMS 501
Db 10 ISIIVPVYVKYKURKCVDSILAQTFTDFELVDDGSPDMSGKICDEYAEKDNVRVH 69
Qy 502 KPNGGSIASNAAVSFAKGYVIGQDSDDYLEPAVELCLKEFLK---DKTLACVY---- 554
Db 70 KENGGLSARAGIDVARGKVLGFVDSDDYIDEDMYEI-LYENLKIHDADISSVELIPFY 128
Qy 555 -TTNRNVNPDGSLIA-----NGYNWPEFSREKLTMTAMIAHFRMFTIRA 597
Db 129 GDRYKKAKEKKVITLKKKAISVLEGTQFYAYAWNKLYRKEL-----FKD 175
Qy 598 WHLTDFGNEKIENA-VDYDMFLK-----LSEVGKFKHLNKCYNRVLHGDNTSIKLG 651
Db 176 NRYLDG--KTFEDAVIITDLFQTEKIVVSNEEKFYIQR-----NDSIMGKFS 223
Qy 652 KQNHFWVQNSLNROGIYNYNDEPDDLDES--RK-----YIFNK---TAYQSE--EI 697
Db 224 MNFVIVIAQWYNKEKI-----LDAPDLHDSYRCLWAFYVLDKWLSSSYQIIPRKK 279
Qy 698 DILDKDIQON-----KDAKIAV 715
Db 280 TWIEFLKKNRNPIYTKGFTKSRKIAI 306

RESULT 11
US-09-134-000C-6392
; Sequence 6392, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
```

```
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6392
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-6392

Query Match 4.7%; Score 241.5; DB 2; Length 330;
Best Local Similarity 23.9%; Pred. No. 1.6e-12;
Matches 84; Conservative 64; Mismatches 116; Indels 87; Gaps 14;

Qy 439 VPLVSIYIPAYNCANYQRCVDSALNQTVDLEVCICNDGSDTNTLEVINLGNPRVR 498
Db 7 MPKISIIIPVYVYKYLEKCVRSILAQTFTDFELVDDGSPDSSGAMCQFAEQDQVRK 66
Qy 499 IMSPKNGGSIASNAAVSFAKGYVIGQDSDDYLEPAVELCLKEFLK---DKTLACVYT 555
Db 67 VIHKEGGLSDARNAGIEIATGYLGFVDSDDYIADDMYELLYTNIVKEDADLSICGIYD 126
Qy 556 TNRNVNPDGSLIANGYNWPEFSREKLTMTAMIAHFRMFTIRAHLTDGFNEKIENAVDYD 615
Db 127 VYEGKEPIVKSILQG-----TFSREALLLILQGN--IISVHA----- 162
Qy 616 MFLKLSSEVGKFKHLNKCYNRVLHGDNTSIKLGIOKKNHFVVVQNSLNROGIYNYNDE 675
Db 163 -----VNKL-YKKLFADLRYPK--GKYHEDSFIIVDLLSECCQKVS----- 200
Qy 676 FDDLDESRKYIF-----NKTAYQSE--EIDILDKDIQONKDAKIAVS----- 716
Db 201 ---IDSTQKYVYVYHMGSIINTETPSDKQFIEAWKXNELK-----LKGKGAIVIEAAHQ 253
Qy 717 IFYPNTI-----NGLVKK-LNNIIEYKNIFVILVHVDKQHLTPDIKK 758
Db 254 VCFANFLVDLKILISNAPKKRKYQIVRYLRENFIFIM---KQKVFTYSRK 301

RESULT 12
US-08-597-236-10
; Sequence 10, Application US/08597236
; Patent No. 5733765
; GENERAL INFORMATION:
; APPLICANT: STINGELE, Francesca
; APPLICANT: MOLLET, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
; TITLE OF INVENTION: EXOPOLYSACCHARIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americans
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597,236
; FILING DATE:
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95201669.9
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Farucci A. Allan
; REGISTRATION NUMBER: 30256
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
```



```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-597-236-10

Query Match 4.7%; Score 238.5; DB 1; Length 324;
Best Local Similarity 23.1%; Pred. No. 2.8e-12;
Matches 87; Conservative 64; Mismatches 136; Indels 89; Gaps 12;

QY 441 LVSIIYPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTNTLEVINKLYGNNPRVRIM 500
Db 6 LISIPIPVNVVEKYLEKCLQSQVQNTYNNFEVILVNDGSTSSLSICEKFNQDKRFSVP 65
QY 501 SRPNGIASASNAVSPFAKYIYGOLDSDDYLEPDAVE-----LCLKEFLKDK 548
Db 66 SKENGGMSSARNFGIKKAGSGFITFVDSDDYIVKDYLSHLVAGIKSETSVCSKFFLVD 125
QY 549 TLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMTTIRAWHLTDGPFNEKI 608
Db 126 -----KGSLLTK-----KEAPKKKSEVVSIEESIKILLQ----- 155
QY 609 ENAVDYDFMLKSEVCKPKHLNKCYNRVLHGDNTSIKKLGIOKQNHVFNQSLNRQGI 668
Db 156 QNGYDLAVWGKLYPVSPFTTIS-FPEGKLYEDMGTYTKLLKLASEVWFL----- 203
QY 669 TYNYDEPDLDSESKYIFNKTAEQEIEDILKDIKIIQNCKDAKIAVSIYPNTLGLVK 728
Db 204 -----DAYDAYVQVRPNSSIMNSSFNLKKLDIIEWHME-----NDILA 242
QY 729 KLNIIIEYNKN-IFV-----IVLHVDKNHLTPDIKEILAFYHKHQVNILLNDISYYSN 783
Db 243 QFPNLALYVKNRAFAAEVKIFLEIPKEKEFEQAOKL-----WH-----DIKKNRKAPFMTKG 295
QY 784 RLIKTE--AHLNINK 797
Db 296 ARLKNRLGASLSFLGK 311

RESULT 13
US-08-746-682A-10
; Sequence 10, Application US/08746682A
; Patent No. 5786184
; GENERAL INFORMATION:
; APPLICANT: STINGBLE, Francesca
; APPLICANT: MOLLET, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
; TITLE OF INVENTION: EXOPOLYSACCHARIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americans
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,682A
; FILING DATE: 14-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/597,236
; FILING DATE: 20-JUN-1995
; APPLICATION NUMBER: EP 95201669.9
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci A., Allan
; REGISTRATION NUMBER: 30256
; INFORMATION FOR SEQ ID NO: 10:

```

QY 557 NRNVNPGSLIANGYNWPEFSREKLTAMIAHHRMTTIRAWHLTDGNEKIENAVDYDM 616  
Db 683 EDKITENRRFP-NAFYKSDWNPELILNHNVIITFPVVVKRDLLEKVGGLSAYNGAQDYDF 741  
QY 617 FLKLSE-VGFKHLNLCYN-RVLHGDNSTIKKLGIQKKNHFVVVQ------SLNRQGI- 668  
Db 742 VLRAEQATKIKHPCGMWYHRAIE-SSALNPESKGYAVVAGQKAVQAATERGLK 797  
QY 669 -----TY-YYND-----EFDLDESRYIFNKT-----ASYQ 694  
Db 798 AQVEIAEFYGSYKINLYLHVPMVSLIITNDTENMSSYLRQLLEKTAITYNTEILLPARFE 857  
QY 695 EEDILKQ-----IKLQNKDAKIAVSIFYPNTLGLVKKLNNI----- 733  
Db 858 NQINQIDRLRYVSTETRHGMIQAAGEYVALLNAGLVP-TKNDWLKELMNIQOQETSGL 916  
QY 734 -----IEYNKNI FIVLHVDKNHL-----TPDIKKEILAFYHKHVNILLNNDISYY 780  
Db 917 VTGRVVDARYRVETVGVSDTDKRLLYPEKGTGP-----KSLGVYYR-----IALPRNIQAA 969  
QY 781 TSRLIKTEAHLNKNKLSQNLNCEYIIIFDNHDSLFVKNDS-----YAYMK 827  
Db 970 TEDCLL-----FNK--QLYLNLEGI-----NESLGKEMWGVLDLSLQFASAG 1008  
QY 828 KYDVGMNFSALTHDWIEKINAHF---PPFKLIKTY 859  
Db 1009 KRNVYVSAILKAD--ERMQNHDKGYSYKLAEKW 1041

RESULT 15  
US-08-961-083-200  
; Sequence 200, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961.083  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 200:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 674 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-961-083-200

Query Match 4.5%; Score 231.5; DB 2; Length 674;

Best Local Similarity 20.9%; Pred. No. 3.9e-11;  
Matches 102; Conservative 79; Mismatches 171; Indels 135; Gaps 17;  
QY 458 CVDSALNQTVVLEVCICNDGSGTDNTLEVINKLYGNPRVIRMSKNGGIGASASNAVSF 517  
Db 1 CUDSIITQYKNIEIVVNDGSGTDSAGEICKFSEMDHRLIYIEQENAGLSAARTGLNN 60  
QY 518 AKGYIIGQLDSDDYLEPDVAVELCK---EFLKDKTKLACVYTTNRN----- 559  
Db 61 MSGNYVTFVDSDDWIEQDYVETLYKKI VEQADIAVGNVYSFNESEGMFYFHLGDSYVE 120  
QY 560 -VNPDGSLIANGYNWPEFSREKLTAMIAHHRMTTIRAWHL-----TDGP-NEKI 608  
Db 121 KYVDNVSIFENLYE---TQEMKSPALISAWGKLYKARLFEQRLFDIGKUGEDGYLNQKV 176  
QY 609 ENAVDYMFLKLSGVGKFKHLNLCY-NRVLHGD-----NTSIKK 647  
Db 177 -----YLLSE--KVYLNKSLYAIRKGSLSRVWTEKWMHALVDAMSERITLLAN 225  
QY 648 LGIQKKNHFVVNQSL-----NRQG-----ITYNYD-----BFDDLDESRYIFNK 689  
Db 226 MGYPLEKHLAVYRQMLEVSLANGQASGLSDTATYKEPEMKQRLNQLSRQSESEKKAIVL 285  
QY 690 TABYQBEIDILDKIKIIONKDAKIAVSIFYPNTLGLVKKLNNIIEYNKNI FIVLHVDK 749  
Db 286 AANYGYVDQVLTITKISYCHNRSIRFYLIHSDPPNEMIKQLNKRLE-----KFDS 335  
QY 750 NHLTPDIKKEILAFYHKHVNILLNNDISYVTSNRLIKTEAHLNKNKLSQNLNCEYII 809  
Db 336 EIINCRVTSEIISY-----KSDISYTVFLRYFIADF-----VQEDKALYLDCLVV 382  
QY 810 FDNHDSLFVKN-DSY-----AYMKYDVGMNFSALTH 840  
Db 383 TKNLDDLFAFDLDQYPLAAVRDFGGRAYFGQEIFNAGVLLVNNAFWKKNNTOKLIDVTN 442  
QY 841 DWIEKIN 847  
Db 443 EWHDKVD 449

Search completed: January 6, 2006, 16:06:20  
Job time : 48 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 8, 2006, 23:00:16 : Search time 1157 Seconds  
(without alignments)  
612.490 Million cell updates/sec

US-10-642-248-2

Title: 5108

Sequence: 1 MNTLSQAIKAYNSNDYQLA.....SAKGENIPVKNKFIINSITL 972

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool\_p/US10642248/runat\_06012006\_125013\_26983/app\_query.fasta\_1.1159  
-DB=Published Applications NA New -OFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNIT5=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10642248 @cgn 1\_1184 @runat\_06012006\_125013\_26983  
-NCPUS=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.\*

1: /cgn2\_6/ptodata/1/pubpna/US08 NEW PUB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US06 NEW PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US07 NEW PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/PCT NEW PUB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US09 NEW PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10 NEW PUB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq2.\*  
9: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq3.\*  
10: /cgn2\_6/ptodata/1/pubpna/US60 NEW PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	2920	7	US-11-172-145-1
2	5104	99.9	2937	7	US-11-124-215-2
3	5104	99.9	2937	7	US-11-120-422-9
4	4502.5	88.1	2979	7	US-11-172-145-3
5	3697	72.4	2112	7	US-11-172-145-11
6	3692	72.3	2112	7	US-11-172-145-17
7	3692	72.3	2112	7	US-11-172-145-18
8	3692	72.3	2112	7	US-11-172-145-19

9	3692	72.3	2112	7	US-11-172-145-20
10	3471	68.0	1980	7	US-11-172-145-13
11	3336	65.3	1980	7	US-11-172-145-14
12	3225	63.1	1830	7	US-11-172-145-15
13	3116	61.0	1764	7	US-11-172-145-16
14	235	4.6	2736	7	US-11-194-246-190
15	211.5	4.1	37500	6	US-10-522-037-1
16	210.5	4.1	5859	7	US-11-102-497-1
17	210.5	4.1	5859	7	US-11-102-497-7
18	202	4.0	1774	6	US-10-510-386-103
19	139.5	3.9	1851	7	US-11-172-145-5
20	133.5	3.8	1854	7	US-11-172-145-7
21	182	3.6	2990	6	US-10-793-626-3899
22	169	3.2	6507	6	US-10-485-517-75
23	161.5	3.2	918	6	US-10-467-657-1317
24	156	3.1	3202	6	US-10-793-626-3774
25	150.5	2.9	3021	6	US-10-793-626-153
26	149.5	2.9	2475	6	US-10-131-826A-195
27	148.5	2.9	981	6	US-10-467-657-2407
28	142.5	2.8	8503	7	US-11-124-368A-45
29	142	2.8	3504	7	US-11-052-554A-505
30	141.5	2.8	3167	6	US-10-793-626-4117
31	141	2.8	8512	7	US-11-124-368A-46
32	140.5	2.8	1767	7	US-11-052-554A-718
33	139.5	2.7	3285	6	US-10-793-626-3448
34	139	2.7	12732	6	US-10-802-796-1
35	136.5	2.7	6014	7	US-11-102-476-45
36	135.5	2.7	5925	6	US-10-615-668-4
37	132.5	2.6	15071	6	US-10-793-626-2963
38	132	2.6	3438	6	US-10-793-626-1431
39	130.5	2.6	540	6	US-10-873-528-299
40	130.5	2.6	3549	6	US-10-793-626-3796
41	129.5	2.5	3204	6	US-10-793-626-3940
42	129	2.5	3344	6	US-10-793-626-4102
43	129	2.5	4605	7	US-11-102-476-3
44	127	2.5	3068	6	US-10-793-626-3824
45	126.5	2.5	14991	6	US-10-346-706B-18

ALIGNMENTS

RESULT 1

US-11-172-145-1  
; Sequence 1, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: Deatgelis, Paul  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.



```
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
Db 1921 GATACACATCAATTAAGAACTTGGCATTCAGAAAGAAACCAATTTGTTGTAGTCAAT 1980
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680
Db 1981 CAGTCATTAATAGACAGGCATAACTATTATTAATATGACGAATTTGATGATTTAGAT 2040
QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleu 700
Db 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCCTGAATATCAAGAGAGATTTGATATCTTA 2100
QY 701 LysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2101 AAGATATTAATAATCATCCAGAAATAAGATGCCAAATCGCAGTCAGTATTTTATCCC 2160
QY 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 2161 AATACATTAACGGCTTAGTGAATAAACTAAACAATATTAATGAATAATAATAATAATA 2220
QY 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2221 TTCGTTATTTGTTTACATGTTGATAAGAAATCATCTTACACCAGATATCAAAAAAGAAATA 2280
QY 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
Db 2281 CTAGCCCTTCTATCATTAACATCAAGTGAATATTTTACTTAATAATGATATCTCATATTTAC 2340
QY 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2341 ACGAGTATATAGATTAATAAAAACTGAGGCGCATTTAAGTAATATTAATAAATTAAGTCAG 2400
QY 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerIlePheValLysAsn 820
Db 2401 TTAATCTAAATTTGTGAATACATCATCTTTTGTATAATCATGACAGCCTATTGTTAAAAAT 2460
QY 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2461 GACAGCTATGCTTATGAAAAAATATGATGTGCGCATGAAATTTCTCAGCATTAACACAT 2520
QY 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2521 GATTGGATCGAGAAATCAATCGCATCCACCATTTAAAAAGCTCATTAATAACTTATTTT 2580
QY 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2581 AATGACAAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGATGTTTATGAGC 2640
QY 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTAATAAAGAGTATCATCATCTTTGCCAGTCA 2700
QY 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2701 ATTGATAGTGTCCAGAAATTAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAATC 2760
QY 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2761 TTAGAAAGAAAAACCGCCCATGTATTTAATAAACAATCGACCCCTGACTTATATGCGCTGG 2820
QY 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2821 GAACGAAATTAACAATGGAACAAATGAACAAATTTGAAGTGAACAAAGAGGAGGAGAAATAATA 2880
QY 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2881 CCTGTTAACAGTTCATTTAATAGTATAACTCTA 2916
```

## RESULT 2

US-11-124-215-2

; Sequence 2, Application US/11124215

; Publication No. US20050266460A1

; GENERAL INFORMATION:

```
; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND
; FILE REFERENCE: 35541.101
; CURRENT APPLICATION NUMBER: US/11/124.215
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-124-215-2
Alignment Scores:
Pred. No.: 0 Length: 2937
Score: 5104.00 Matches: 971
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.92% Indels: 0
Dbs: 7 Gaps: 0
```

US-10-642-248-2 (1-972) x US-11-124-215-2 (1-2937)

```
QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 19 ATGATATCATTTATCAAGCAATTAACCATATTAACAGCAATGATATCAATATAGCCTC 78
QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATTTATTTGAAAGTCGCGGAAATCTATGACGGAATAATTTGTGAATTTTCAAAATTACC 138
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 139 AAATGCCAAGAAAAAATCTCTCAGCATCTTCTGTGTTAATTCAGCACATCTTTCTGTAAAT 198
QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 199 AAAGAAGAAAAAGTCATGTTTGGATAGTCGGTAGATATTGCAACACACACTGTACTTT 258
QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 259 TCCAAACGTAAAAAATTTAGTACTTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 318
QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 319 AAATTTGCTCACTCAGAGAAGAAATCTGANAATGCGAGGTAAGAGCGGTCCGCCCTTTGATCCA 378
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 379 AAAGATTTTCCCAAGATCTGGTTTTTACGCCCTTTTACCTGATCATGTATTAATGATTTTACA 438
QY 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 439 TGGTACAAAAACGGAAGAAAAAGACTTTGGCAAAAAACCTGAAACATCAACATGTGTGCTCTT 498
QY 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 499 TCTATTATCGTTTACAACATTTCAATCGACCAGCAATTTTATCGATTACATTAGCCTGTTTA 558
QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATTCGTGACAGATGATGGTAGTCAGAA 618
QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
```

Db 619 GATCTATACCGATCATTCGCCAATATGAAATAAATGGATATTCGCTAGCTCAGACAA 678  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 679 AAAGATAACGGTTTTCAAGCCAGTGGCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 738  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
Db 739 GACTTTATGGCTTACTCGACTGTGATATGGCGCAAAATCCATTATGGGTTTCATTCTTAT 798  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 799 GTTGCAGAGCTATTAGAAAGATGATTTAAACATCAITGGTCCAGAAATAATCATCGAT 858  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 859 ACACAACATATTGACCCAAAGACTTCTTAAATAACGCGAGTTTGGCTTGAATCATTACCA 918  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
Db 919 GAAGTGAAACCAATAATAGTTTGGCGCAAAAGGGGAAGCAAGTTTCTCTGGATTGG 978  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGAACANITCGAAATAACAGAAATCTCCGCTTATCCGATTCGCCCTTCCGTTTT 1038  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp 360  
Db 1039 TTTGCGCGGGTAATGTTTTCGCTTAAATAATGGCTAAATAATCCGGTTTCTTTGAT 1098  
Qy 361 GluGluPheAsnHisIleTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1099 GAGGAATTTAATCACTGGGGTGGAGAAGATGGGAATTTGGATATCGCTTATTCCGTTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1159 GGTAGTTTCTTTAAACTATTGATGGCATTTATGGCTTACCCTCAAGAGCCACCCAGGTAAA 1218  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAATGAACCGATCGTGAAGCGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1278  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAACTTTTACCAATAGAAATTCGCATATCAATAGAGTACCT 1338  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAATTTATATCCAGCTTATTAACGTGCAAACTATATTAACCGTTGCGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1399 AGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTCTTAACGATGGTTCAACA 1458  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1459 GATAAATACCTTAGAAGTGATCAATTAAGCTTTATGGTAATAATCTCAGGTCAGCATGTG 1518  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1519 TCTAACAACAAATGGCGAATAGCTCAGCATCAATGCAAGCCGTTTCTTTTGTCTAAGGT 1578  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTGGGCAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCAAGTTGAACCTGTG 1638  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1639 TTAAGAAGAAATTTTAAAGATATAAACGCTAGCTTGTGTTTATACCACTTAATAGAAACGTC 1698  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580

Db 1699 AATCCGGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTTCACGAGAAAAA 1758  
Qy 581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTyrHisLeu 600  
Db 1759 CTCACAACGGCTATGATGCTCCACCTTTAGAAATGTTACAGATTAGAGCTTGGCATTTA 1818  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCAATGAAAAAATGAAATGGCGTAGCATGACATGTTCTCCTCAAACTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1938  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1939 GATAACACATCAATTAAGAAACTTGGCAATTCAAAAGAAAAACCAATTTGTGTAGTCAAT 1998  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 1999 CAGTCATTAAATAGACAGCATCACTTATTATAATTATGACGAATTTGATGATTTAGAT 2058  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2118  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2119 AAAGATATTAAAAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTTTATFCCC 2178  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2179 AATACATTAAACCGCTTAGTGAAAAAACAATAACAATATTATTGAATATAATAAATAATA 2238  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2239 TTCGTTATTGTTCTACATGTTGATAAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2298  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAATAATGATATCTCATATFAC 2358  
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2359 ACAGTAATAGATTAAATAAAACTGAGCGCCATTTAAGTAATATTATAAATTAAGTCAG 2418  
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2419 TTAATCTAAATTTGTAATACATCATTTTTTGATAAATCATGCAGCCCTATTTCGTTAAAAAT 2478  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2539 GATTGATCGAGAAAAATCAATGGCATCCACCAATTTAAAAAGCTCATTAACACTATTTT 2598  
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2599 AATGACAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGACG 2658  
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAAGTCATCATCTTCGCCAGTCA 2718  
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920  
Db 2719 ATTGATAGTGTGCCAGAAATAAACAACGAGGATTTTGGTTCCATTTTGACACTTTTAATC 2778  
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940  
Db 2779 TTAGAAAAAGAAAAACCGCCCATGTATTATTAATAAACACGACCTGACTTATATGCTTGG 2838



```
Qy 941 GluArgLysLeuGlnTTPThrAsnGluGlnLeuGluSerAlaLysArgGlyGluAsnIle 960
Db 2839 GAAGGAAATTTACAAATGGACAAATGAACAATTTGAAAGTGCAGGAGGAGGAAATATA 2898

Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2899 CCTGTTAAAGTTCAATTATTAATAGTATAACTCTA 2934

RESULT 3
US-11-120-422-9
; Sequence 9, Application US/11120422
; Publication No. US20050287646A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kshama
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION
; TITLE OF INVENTION: IN BACILLUS SUBTILIS
; FILE REFERENCE: 3554.049
; CURRENT APPLICATION NUMBER: US/11/120,422
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/09/879,959
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 01/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: pasteurella multocida
US-11-120-422-9

Alignment Scores:
Pred. No.: 0 Length: 2937
Score: 5104.00 Matches: 971
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.92% Indels: 0
DB: 7 Gaps: 0

US-10-642-248-2 (1-972) x US-11-120-422-9 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 19 ATGAATACATTTATCACAAGCAATAAAGCATATATAACAGCAATGACTATCAATTAGCACTC 78

Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATTTATTTGAAAGTCGCGGAAATCTATGGACGGAATTTGTTGAATTTCAAATTACC 138

Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 139 AAATGCCAGGAAAGAACTCTAGACATCTCTCTGTTAATTCAGCNACATCTTCTGTAAT 198

Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 199 AAAGAAGAAAGTCAATGTTTGGATAGTCGTTAGATATTGCAACACAACTGTTACTT 258

Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 259 TCCACGTAAGAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTTAAAAAATAAATGG 318

Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 319 AAATTTGCTCAGTGAAGAAATCTGAAATTCGGAGGTGAAGCCGTCGCCCTTGATACA 378

Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 379 AAAGATTTTCCCAAGAACTGGTTTATAGCGCTTTTACCTGATCATGTTAATCATGTTTACA 438
```

```
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 439 TGGTACAAAAAGCGAAAGAAAGACCTTGGCATAAAAACCTGAACATCAACATGTTGGTCTT 498

Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 499 TCTATTATCGTTACAAACATTTCAATCGACCGCAATTTTATCGATTACATTAGCTGCTTTA 558

Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 559 GTAAACCAAAAAACACATTTACCGTTTGAAGTTATCGTGACAGATGATGTTAGTACAGAA 618

Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 619 GATCTATCACCGATCATTTCCCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 678

Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 679 AAAGATAACGGTTTTCAAGCCAGTGGCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 738

Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db 739 GACTTTATTCGCTTACTCGACTGTGATTCGCGCAATCCATTATGCGTTTCATTCCTTAT 798

Qy 261 ValAlaGluLeuLeuGluAspAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 799 GTTCGACAGAGCTATTAGAAGATGATGATTAAACAATCATTCGTCCAGAAAAATACATCAT 858

Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 859 ACACAACATATTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTTGAATCATTTACA 918

Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320
Db 919 GAAGTGAAACCAATAATATAGTTGTCGCGCAAAAGGGAGGAACAGTTCTCTCGATTGG 978

Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 979 CGCTTTAGAACAAATTCGAAAAAACAAGAAATCTCGCTTATCCGATTTCGCCCTTTCCGTTT 1038

Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPheAsp 360
Db 1039 TTTGCGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAATCCGGTTTCTTTGAT 1098

Qy 361 GluGluPheAsnHisTrpGlyGlyValGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1099 GAGGAATTTAATCACTCGGGTGGAGAGAGATGGGAATTTGGATATCGCTTATTCGTTTAC 1158

Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1159 GGTAGTTTCTTTAAAACTATTGATGGCATTATGGCTACCATCAAGAGCCACCAGGTAAA 1218

Qy 401 GluAsnGluThrAspArgGluAlaGlyAsnIleThrLeuAspIleMetArgGluLys 420
Db 1219 GAAAAATGAAACCGATCGTGAACGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAG 1278

Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTTCGATATCAATAGAGTACCT 1338

Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1398

Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1399 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1458

Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1459 GATAATACCTTAGAAGATGATCAATAAGCTTTTATGGTAAATAATCTCTAGGTAGCATCATG 1518
```

QY 501 SerlySProHengGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly 520  
DB 1519 TCTAAACCAATGGCGAATAGCCTCAGCATCAATGACCGGTCTCTTTGCTAAAGGT 1578  
QY 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
DB 1579 TATTACATGGCGAGTAGATTGAGATTGATCTTGAGGCTGATGAGTGAAGTGTG 1638  
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
DB 1639 TTTAAAGAAATTTTAAAGATATAAACGCTAGCTGTGTGTATATACCACTAATAGAAACGTC 1698  
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
DB 1699 AATCCGATGGTATTAATCGCTTAATGGTTACAAATGGCCAGCAATTTTTCACGAGAAAA 1758  
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
DB 1759 CTCAACACGGCTATGATGCTCACCATTTAGATGTTACGATTAGAGCTTGCCATTTA 1818  
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
DB 1819 ACTGATGGATCAATGAAAAATTTGAAATGCCGTAGACTATGACATGTTCTCAAACTC 1878  
QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
DB 1879 AGTGAAGTTGGAAATTTAAACATCTTAATAAAAAATCGCTATACCGGTGATTACATGGT 1938  
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
DB 1939 GATACACATCAATTAGAAACTTGGCATTCNAAGAAACCAATTTTGTGTAGTCAAT 1998  
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
DB 1999 CAGTCATTAATACACAAGGCATAAATTTATTAATGATGACGAATTTGATGATTTAGAT 2058  
QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
DB 2059 GAAAGTAGAAGTATATTTCAATTAACCCGCTGAATATCAAGAAAGAGATTGATATCTTA 2118  
QY 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
DB 2119 AAAGATATTAATATCATCCAGATTAAGATGCCAAATCGCAGTCAGTATTTTATCCC 2178  
QY 721 AsnThrLeuAsnGlyLeuValLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
DB 2179 AATACATTAACCGCTTAGTGAAAAAACTAAACAATATTTATGAATATAATAAAATATA 2238  
QY 741 PheValIleValLeuHisValAspLysAsnHisIleLeuThrProAspIleLysLysGluIle 760  
DB 2239 TTCGTTATTTGTTCTACATGTTGATAAGAAATCATCTTACCCAGATATCAAAAAAGAAATA 2298  
QY 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
DB 2299 CTAGCCTTCTATCATTAACATCAAGTGAATATTTTACTAATAATGATATCTCATATTAC 2358  
QY 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
DB 2359 ACGAGTAATAGATTAAATAAAACTGAGCGCATTTAAGTAATATAATAAATTAAGTCAG 2418  
QY 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
DB 2419 TTAATCTAAATTTGTAATACATCATTTTTCATTAATCATGACGCCCTATTCGTTAAAAAT 2478  
QY 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
DB 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGCATGAATTTCTCAGCATTAACACAT 2538  
QY 841 AspTrpIleGluLysIleAsnAlaHisProProPheLysLysLeuIleLysThrTyrPhe 860  
DB 2539 GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTAAAGAGCTCATTTAAACCTATTTT 2598  
QY 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880

DB 2599 AATGACATGACTTAAAGATATGATGTGAAGGGGCATCAACGGTATGTTATGACG 2658  
QY 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
DB 2659 TATGCGTAGCGCATGAGCTTCTGACGATTAATAAGAAAGTCATCATCATCTTCCAGTCA 2718  
QY 901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920  
DB 2719 ATTGATAGTGTGCCAAGATATAACACTGAGGATATTTGGTTCCAAATTTGCACCTTTAATC 2778  
QY 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940  
DB 2779 TTAGAAAAGAAACCCGCCATGATTTAATAAAACATCGACCTGACTTATATGCTTGG 2838  
QY 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
DB 2839 GAACGAAATTTACAATGGACAAATGAACAAATTTGAAAGTGCAAAAAAGAGGAGAAATATA 2898  
QY 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
DB 2899 CCTGTTAACAAAGTTTCATTATTAATAGTATAACTCTA 2934

RESULT 4  
US-11-172-145-3  
; Sequence 3, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 2979  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-3

Alignment Scores:  
Pred. No.: 0 Length: 2979  
Score: 4502.50 Matches: 845  
Percent Similarity: 93.21% Conservative: 61  
Best Local Similarity: 86.93% Mismatches: 59  
Query Match: 88.15% Indels: 7  
DB: 7 Gaps: 2

US-10-642-248-2 (1-972) x US-11-172-145-3 (1-2979)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 61 ATGAATACATATATCACAGCAATATAAGCATATAACAGCAATGACTATGTAATAGCACTC 120  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 121 AAATATATTGAGAAAGTCTGCTGAAACCTTACGGCGCAAAATCGTTGAATTCCAAATATATC 180  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 181 AAATGTAAGAAAAACCTC-----TCGACCAATCTC-----TATGTAAGT 219  
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 220 GAAGATAAAAAACACAGTGTTCGATAGCTCATTTAGATATCGCAACACAGCTCTTACTT 279  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 280 TCCAACGTAAAAAATTAACCTCTATCCGAATCAGAAAAAACAAGCTTTAAAAAATAAATGG 339  
Qy 101 LysLeuLeuThrGluLysLeuSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 340 AAATCTATCATCTGGGAAAAATCGAGAACCGCAAAATCAGAAAGGTGGAACTAGTACCC 399  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 400 AAAGATTTTCTTAAGATCTTGTTCTGCTCCATTCGACATCATGTTTAATGATTTTACA 459  
Qy 141 TrpTyrLysLysArgLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
Db 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATAAGCCTGTAAATTAAGAAATATCGGTCTT 519  
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 520 TCTATTATTATTCCTACATTTAATCGTAGCCGTATTTTAGATATTAACGTTAGCCGTGTTG 579  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 580 GTCAATCAGAAAAACAACACTACCCATTTGAAGTCTGTTGTCAGATGATGTTAGTAAAGGAA 639  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 640 AACTTACTTACCATTGTGCAAAAAATACGAAACAAAACTTGACATAAAGTATGTAAAGCAA 699  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 700 AAAGATTATGGATATCAATTTGTGTCAGTTCAGAACTTAGGTTTACGTACGACGAAAGTAT 759  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
Db 760 GATTTTGCTCGATTCYAGACTGCGATATGGCACCACAACTTATGGGTTCAITCTTAT 819  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 820 CTTACAGAACTATTAGAACAATGATATGTTTAAATTTGGACCTAGAAAAATATGCGAT 879  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 880 ACTCATATATTATACCGCGAAACAATTCCTTAACGATCCCATATTTAATAGAATCACTACTC 939  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 940 GAACCGCTCAAAATAACATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 1000 AGATTAGAACATTTCAAAAAAACCGATAATCTACGCTCTATGATGATCTCCGTTGCTTAT 1059  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPheAsp 360  
Db 1060 TTTAGTTGCGGTAATGTTGTCATTTTCTAAAGAAATGCTTAAATAAAGTAGGTTGGTTCGAT 1119  
Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380

Db 1120 GAAGAAATTTAATCATTTGGGGGGCGAAGATGTGAATTTGGTTACAGATTTATTTGCCAAA 1179  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1180 GGCTGTTTTTTCAGAGTAATTTGACGGCGGAATGGCATACCATCAAGAACCACCTGGTAAA 1239  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1240 GAAAAATCAAAACAGACCCGGAAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTAAGAAAAG 1299  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGATTCACATATTTATAGAAATACCT 1359  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1360 TTAGTTTCTATTTATATCCCGCTTATAACTGTGCAAAATATATTTCAAGATGTTGTAGAT 1419  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1479  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1480 GATAATACCTTAGAAGTGTATCAATAAGCTTTATGTTATTAATCTTAGGTTAGCATCATG 1539  
Qy 501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1540 TCTAAACCAATGCGGNAATAGCCTCAGCATCAATGCAGCCGTTCTTTTTCGTTAAAGGT 1599  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1600 TATTACATTTGGCAGTTAGATTACATGATTTATCTTGAGCCTGATGCGATTTGAACTGTGT 1659  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1660 TTAAAGAAATTTTAAAGAGATAAAACGCTAGCTGTGTGTTATACCATTAATAGAAACGTC 1719  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1720 AATCCGATGTTGCTTAATCGCTTAATGGTTACAAATTTGGCCAGAAATTTTTCAGAGAAAA 1779  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1780 CTCACACGGCTATGATTTGCTCACCATTTTGAATTTTACGATTTAGAGCTTTGGCATTTA 1839  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1840 ACGGATGGATTTAAACGAAATATTGAAACCCCGTGGATTATGACATGTTCTCTTAAACTC 1899  
Qy 621 SerGluValGlyLysPheLysLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1900 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATTAACCGGTTATACATGCT 1959  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1960 GATAACACATCCATTTAAGAACTCGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 2019  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 2020 CAGTCATTTAAATAGACAAGGCATCAATTTATATATATATATGACAAATTTGATGATTTAGAT 2079  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2080 GAAAGTGAAGATATATCTTCAATAAACCGCTGAATATCAAGAAGAAATGATATTTTA 2139  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2140 AAAAGATCTTAAACTCATTTCAAAATAAAGATGCAAAATCGCAGTCAGTATTTTCTATCCC 2199  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740

```
Db 2200 AATACATTAAAGCGCTTAGTGAAAAAACTAAACAATATTATTGAATATAATAAAAAATATA 2259
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2260 TTGCGTTATTCTTACATGTTGATAAGAAATCATCTTACACGACATCAAAAAAGAAATA 2319
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAspIleSerTyrTyr 780
Db 2320 TTGCGCTTCTATCATAGCACCAGTGAATATTTTACTAAATATGACATCTCATATTAC 2379
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2380 ACGAGTAATAGACTAATAAAAACTGAGCACAATTAAAGTAATATTAATAATTAAAGTCAG 2439
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2440 TTAATCTAAATTGTGAATACATCATTTTGTGAATCATGACAGCCTATTTCGTTAAAAAT 2499
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2559
Qy 841 AspTyrIleGluLysIleAsnAlaHisProProPheLysLysLeuIleLysThrTyrPhe 860
Db 2560 GATTGGATCGAGAAAAATCAATCGCATCCACCATTTTAAAAAGCTGATTAAACCTATTTT 2619
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2620 AATGACAATGACTTAAGAAAGTATGAATGTGAAGGGGCATCACAGGATGTTTATGAAG 2679
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2680 TATGCGCTACGCGATGAGCTTCTGACGATTATTAAAGAAAGTCATCACATCTCGCAATCA 2739
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920
Db 2740 ATTGATAGTGTCCAGAAATATAACACTGAGGATATTTGGTTCCAATTTGCACTTTAAATC 2799
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940
Db 2800 TTAGAAAAAGAAAAACCGCCATGTATTTTAAATAAAACATCGACCCCTGACTTATATGCCTGG 2859
Qy 941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2860 GAACGAAAAATACAAATGGACAAATGAACAAATTCAAAGTGCAAAAAAGGCGAAAAATATC 2919
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCGGTTAAACAGTTTCATTATTAAATAGTATAACGCTA 2955
```

## RESULT 5

```
US-11-172-145-11
; Sequence 11, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; FILE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
```

```
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-11

Alignment Scores:
Pred. No.: 5,27e-314 Length: 2112
Score: 3697.00 Matches: 703
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.38% Indels: 0
DB: 7 Gaps: 0

US-10-642-248-2 (1-972) x US-11-172-145-11 (1-2112)
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 1 ATGAATACATTATCAACAAGCAATAAAAGCATATATAACAGCAATGACTATCAATTAGCACTC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTATTGAAAGTCGCGGAAATCTATGAGCGGAAATGTTGAAATTTCAAAATTACC 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AAATGCAAGAAAAAATCTTCAGCACATCTTCTGTTAAATTCAGCACATCTTCTGTAAT 180
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAAGAAGAAAAAGTCAATGTTTGCAGTAGTCCGTTAGATATTGCAACACAACTGTTACTT 240
Qy 81 SerAsnValIleLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db 241 TCAACAGTAAAAAATATTAGTACTTTCTGACTCGGAAAAAACACGTTAAAAAATAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTGCTCACTCAGAGAAGAAATCTGAAATCGGAGGTAAGAGCGGTCCGCTTGTACCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAAGATTTTCCCAAGATCTGGTTTTAGCGCCTTTTACCTGATCATGTATATGATTTTACA 420
Qy 141 TrpTyrLysLysArgLysLysArgLysGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 421 TGTACAAAAAGCGAAAGAAAGACATTGGCATAAAACTGCAATCATCAACATGTTGTCCTT 480
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTACAACATTTCAATCCAGCAGCAATTTTATCGATTACATTAGCTGTTTA 540
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAAACACATTAACCCGTTTGAAGTTTATCGTGACAGATGATGTCAGGAA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 601 GATCTATCACCGATCATTTCCCAATATGAAATTAATTTGGATATTCTCTACGTCAGACAA 660
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
```

Db	661	AAAGATAACGGT	TTTCAAGCCAGTGC	CGCTCGGAATATGGGATTACGCTTAGCAAAATAT	720
Qy	241	AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr			260
Db	721	GACTTTATGGCTTACTCGACTGTGATATGGCCCAATCCATTTATGGGTTTCATCTTAT			780
Qy	261	ValAlaGluLeuLeuGluAspAspLeuThrIleGlyProArgLysTyrIleAsp			280
Db	781	GTTCGAGAGCTATTAGAGATGATGATTTAAACAATCATTTGGTCCCAAGAAATAACATCAT			840
Qy	281	ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro			300
Db	841	ACACAACATATTGACCCAAAAGACTTCTTAAATAACCGGAGTTTGTGGAATCATATTACA			900
Qy	301	GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr			320
Db	901	GAAGTGAACCAATTAATAGTGTTCGCCGAAAGGGGAAGAACAGTTTCTCTGGATTGG			960
Qy	321	ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe			340
Db	961	CGCTTAGAACCAATTCGAAAACAGAAATCTCCGCTTATCCGATTCGCTTTTCGGTTT			1020
Qy	341	PheAlaIaGlyAsnValAlaPheAlaLysTyrLeuAsnLysSerGlyPhePheAsp			360
Db	1021	TTTGGCGGGTAAATGTTGCTTCGCTAAATAATGGCTAAATAATCCGGTTTCTTTGAT			1080
Qy	361	GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr			380
Db	1081	GAGGAATTTAATCATCTGGGGTGGAGAAGATGGGAATTTGGGATATCGCTTATTCGGTTAC			1140
Qy	381	GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys			400
Db	1141	GGTAGTTTCTTTAAACTATTCATGATGGCATATGGCTACCATCAGAGCCACAGGTAA			1200
Qy	401	GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys			420
Db	1201	GAATGAACCGATCGTGAAGCGGGAATAATTTAGCTCGATATATGAGAGAAAG			1260
Qy	421	ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisLeasnArgValPro			440
Db	1261	GTCCCTTATATCTATAGAAACTTTTACCAGATAGAGATTCGCATATCAATAGATACCT			1320
Qy	441	LeuValSerIleTyrProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp			460
Db	1321	TTAGTTTCAATTTATATCCAGCTTATTAATCTGTGCACACTATATCAAGTTGCGTAGAT			1380
Qy	461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr			480
Db	1381	AGTGCACTCAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAACCGATGTTCAACA			1440
Qy	481	AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet			500
Db	1441	GATAATACCTTAGAAGTATCAATAGCTTTATGGTAATTAATCCTTAGGGTACGCATCATG			1500
Qy	501	SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly			520
Db	1501	TCTAAACCAATAGCCGGAATAGCTCAGCATCAATGACGCGTTTCTTTGCTAAGGT			1560
Qy	521	TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys			540
Db	1561	TATTACATTTGGGAGTTAGATTACAGATGATTTATCTTGAGCCTGATCGATTGAACGTGT			1620
Qy	541	LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal			560
Db	1621	TTAAAGAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC			1680
Qy	561	AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys			580
Db	1681	AATCCGGATGGTATGCTTAATCGCTTAATGGTTACATTTGCCAGAAATTTTACAGAGAAA			1740
Qy	581	LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTyrHisLeu			600
Db	1741	CTCACAAACGGCTATGATGCTCACCACTTTAGAAATGTTTACCGATTAGAGCTTGGCATTTA			1800

Qy

601

ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu

620

Db

1801

ACTGATGGATTCAATGAAAAAATTTGAAAAATGCCGTAGACTATATGACATGTTCTTCAAACTC

1860

Qy

621

SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly

640

Db

1861

AGTGAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGGTATTACATGGT

1920

Qy

641

AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn

660

Db

1921

GATTAACACATCAATTAAGAACTTTGGCATTCAAAAGAAAAAACCATTTTGTGTAGTCAAT

1980

Qy

661

GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp

680

Db

1981

CAGTCATTAATAGCAAGGCATACTTATTATTAATATATGACGAATTTTGATGATTTAGAT

2040

Qy

681

GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu

700

Db

2041

GAATGTAAGAAAGTATATTTTCAATAAACCCTGAATATCAAGAAAGAGATTGATATCTTA

2100

Qy

701

LysAspIle

703

Db

2101

AAAGATATT

2109

RESULT 6

US-11-172-145-17

Sequence 17, Application US/11172145

Publication No. US20050272696A1

GENERAL INFORMATION:

APPLICANT: DeAngelis, Paul

TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC

TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS

FILE REFERENCE: 3554.104

CURRENT APPLICATION NUMBER: US/11/172,145

CURRENT FILING DATE: 2005-06-30

PRIOR APPLICATION NUMBER: 60/584,442

PRIOR FILING DATE: 2004-06-30

PRIOR APPLICATION NUMBER: 10/642,248

PRIOR FILING DATE: 2003-08-15

PRIOR APPLICATION NUMBER: 60/404,356

PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 60/479,432

PRIOR FILING DATE: 2003-06-18

PRIOR APPLICATION NUMBER: 60/491,362

PRIOR FILING DATE: 2003-07-31

PRIOR APPLICATION NUMBER: 10/195,908

PRIOR FILING DATE: 2002-07-15

PRIOR APPLICATION NUMBER: 09/437,277

PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 60/107,929

PRIOR FILING DATE: 1998-11-11

PRIOR APPLICATION NUMBER: 09/283,402

PRIOR FILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/080,414

PRIOR FILING DATE: 1998-04-02

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.3

SEQ ID NO 17

LENGTH: 2112

TYPE: DNA

ORGANISM: Pasteurella multocida

US-11-172-145-17

Alignment Scores:

Pred. No.: 1.45e-313

Score: 3692.00

Percent Similarity: 100.00%

Best Local Similarity: 99.86%

Query Match: 72.28%

Length: 2112

Matches: 702

Conservative: 1

Mismatches: 0

Indels: 0

Gaps: 0

DB:

US-10-642-248-2 (1-972) x US-11-172-145-17 (1-2112)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 1 ATGAATACATTTATCACAGCAATAAAGCATATATACAGCAATGACTATCAATTAGCACTC 60  
Qy 21 LysLeuPheGluLysSerAlaGluLeuTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 61 AAATTTATTTGAAAGTCCGGGGAATCTATGGACGGAAATTTGTGTGAATTTCAAAATACC 120  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 121 AAATGCAAGAAAGAACTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTCTGTAAAT 180  
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 181 AAAGAAGAAAGTCAATTTGTCGATAGTCCGTTAGATATTGCAACACACACTGTTACTT 240  
Qy 81 SerAsnValLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 241 TCCAAACGTAAAGAAATTTAGTACTTCTGACTCGGAAAGAAACACGTTAAAGAAATAAATGG 300  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 301 AAATTTGCTCACTGAGAGAAATCTGAAATGCGGAGGTAGAGCGGTCGCCCTTGTACCA 360  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 361 AAAGATTTTCCCAAGATCTGGTTTAGCGCCTTTACCTGATCATGTTAATGATTTTACA 420  
Qy 141 TrpTyrLysLysArgLysLeuArgLysProGluHisGlnHisValGlyLeu 160  
Db 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACATGTTGGTCTT 480  
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 481 TCTATTATCGTTTACACATTCATCGACCAGCAATTTATCGATTACATTAGCCCTGTTA 540  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 541 GTAAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Qy 201 AspLeuSerProIleIleArgGlnTyrClnAsnLysLeuAspIleArgTyrValArgGln 220  
Db 601 GATCTATACCGATCATTCGCGCAATATGAAATAAATTTGGATATTCGCTACGTGAGACAA 660  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 661 AAAGATAACGGTTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT 720  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
Db 721 GACTTTTATGGCTTACTCAACTGTGATATGCGCCAAATCCATTTATGGGTTTCATCTTAT 780  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 781 GTTCGAGAGCTATTAGAGATGATGATTAAACAATCATTTGTCCTCAAGAAATAATCATCGAT 840  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 841 ACACACATATTGACCCAAAGACTTCTTAAATAACGGGAGTTTGTGTAATCATTACCA 900  
Qy 301 GluValLysThrAsnAsnSerValAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 901 GAAGTGAAGAACCAATAATAGTGTTCGCCCAAAAGGGGAAAGAACAGTTTCTCTCGAATTGG 960  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 961 CGCTTTAGAACCAATTCGAAAAAACAGAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTT 1020  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
Db 1021 TTTGCGGGGGTAAATGTTGCTTTTCGTAAAGAAATGGCTAAATAATCCGGTTTCTTTGAT 1080

Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1081 GAGAAATTAATCACCTGGGGTGGGAAGATGTGGAAATTTGGATATCGCTTATTCGGTTAC 1140  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1141 GGTAGTTTCTTTAAACTATTGATGCAATTATGCGCTACCATCAAGAGCCACCAGGTAAA 1200  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1201 GAAATGAAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260  
Qy 421 ValProTyrIleTyrArgLysLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1261 GTCCCTTATATCTATAGAAAACTTTTACCNAATAGAAGATTCGCATATCAATAGATACCT 1320  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1321 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1381 AGTGCACCTGAATCAGACTGTGTTGATCTCGAGGTTGTATTGTAAACGATGGTTCAACA 1440  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1441 GATAATACCTTTAGAAGTGATCAATAAGCTTTATGGTAATAANTCCTAGGGTACCGATCATG 1500  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1501 TCTAAACCAATCGCGGAATAGCTCAGCATCAATGAGCCGCTTCTTTTGTAAAGGT 1560  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLysGluProAspAlaValGluLeuCys 540  
Db 1561 TATTACATTCGGCAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCAAGTTGAACGTGT 1620  
Qy 541 LeuLysGluPheLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1621 TTAAGAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTTTATACCACTAATAGAAACGTC 1680  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1681 AATCCGGATGTTAGCTTAATCGCTAATGGTTTACAATTTGCCCAGAAATTTTCCAGGAAAA 1740  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1741 CTCACACGGCTATGATTCCTCACCCTTTAGAAATGTTCCAGATTAGAGCTTGGCATTTA 1800  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1801 ACTGATGATTTCAATGAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCCCAAACTC 1860  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1861 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1920  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660  
Db 1921 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACCACTTTTGTGTAGTCAAT 1980  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 1981 CAGTCATTAAATGACAGGCATAACTTATTATAATTTATGACGAATTTGATGATTAGAT 2040  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTGATATCTTA 2100  
Qy 701 LysAspIle 703  
Db 2101 AAAGATATT 2109



## RESULT 7

```

US-11-172-145-18
; Sequence 18, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-18

```

Qy	121	LysAspPheProLysAspLeuValLeuAlaProLeuProAsnHisValAlaAspPheThr	140
Db	361	AAAGATTTTTCCCAAGAAGATCTGGTTTATAGCGCCTTTACCTGATCATGTGAATGATTTACA	420
Qy	141	TTPTYzLyLysArgIyLysArgLeuGlyVileLYeProGLuHieGLNHisValGIyLeu	160
Db	421	TGGTCACAAAAGCGAAGAAAGACTTGGCATAAAAACCTGAACATCAACATGATGTGCTCTT	480
Qy	161	SerIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCyLeu	180
Db	481	TCTATTATCTGCATCAACATTCAGCCAGCAATTTTATCGATTACATTAGCCTGTTTA	540
Qy	181	ValAsnGlnYseThrHisTyPrOPheGLuValIleValThrAspAspGlySerGlnGlu	200
Db	541	GTAACCAAAAAACACATACCCTGTTTGAAAGTTATCGTGACAGATGNTGGTAGTCAGAA	600
Qy	201	AspLeuSerProIleIleArgGinTyrgLuAsnLysLeuAspIleArgTyrrValArGLin	220
Db	601	GATCTATCACCGATCATTCGCCAATAATGAAAAATAATTTGGATATTCGCTACGTCAGACAA	660
Qy	221	LysAspAsnGlyPheGlnIlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLyeTyrr	240
Db	661	AAAGATAACGGTTTTTCAAGCCAGCTGGCGCTCGGAATATGGGATTAGCCTTAGCAAATAAT	720
Qy	241	AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyrr	260
Db	721	GACTTTATGGCTTACTCGACTGTATATATGGCCCAATCCATTATGGGTTCATTTCTTAT	780
Qy	261	ValAlaGLuLeuLeuGluAspAspAspLeuThrIleIleGlyProArgLysTyrrIleAsp	280
Db	781	GTTCGACAGCTATTAGAAGATGATGATTTAACAAATCATTCGTCCAAGAAATACATCGAT	840
Qy	281	ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro	300
Db	841	ACACAACATATTGACCCCAAGAAGACTTCTTAAATAACGCGAGTTTGGCTTGAATCATTTACCA	900
Qy	301	GluValLysThrAsnAsnSerValAlaAlaLysGlyVLuGlyThrValSerLeuAspTrp	320
Db	901	GAAGTGAACCAATAATAGTGTTCGCGCAAAAGGGGAAGAACAGATTTCTCTGGATTGG	960
Qy	321	ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerPropheArgPhe	340
Db	961	CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCTTCCCCTTTT	1020
Qy	341	PheAlaLaGLyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp	360
Db	1021	TTTCGCGCGGGTAATGTGTCTTCGCTTAAAAAATGGCTAAATAATCCGGTTTTCTTTGAT	1080
Qy	361	GluGluPheAsnHisTrpGlyGIyLUaspValGluPheGlyTyrrArgLeuPheArgTyrr	380
Db	1081	GAGGAATTTAATCACTCGGGTGGAGAGAGATGTGGAAITTTGGATATCTGCTTATTCGGTTAC	1140
Qy	381	GlySerPhePheLysThrIleAspGlyIleMetAlaTyrrHisGlnGluProProGlyLys	400
Db	1141	GGTAGTTTCTTTAAACATAITTAGTGGCATATATGGCCTTACCATCAAGAGCCACCAGGTAAA	1200
Qy	401	GluAsnGlnThrAspArgGluAlaGLyAsnIleThrLeuAspIleMetArgGluLys	420
Db	1201	GAATAATGAACCGATCGTGAAGCGGGAAAAATAATACGCTCGATATATGAGAGAAAAG	1260
Qy	421	ValProTyrrIleTyrrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro	440
Db	1261	GTCCCTTATATCTAGAAAACCTTTTACCAATAGAAGATTCGCATATCAATAGAGTAGCTCT	1320
Qy	441	LeuValSerIleTyrrIleProAlaTyrrAsnCysAlaAsnTyrrIleGlnArgCysValAsp	460
Db	1321	TTAGTTTTCAATTTATATCCCCAGCTTATAACTGTGCAAACTATATTTCAACGTTGCGTAGAT	1380
Qy	461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480
Db	1381	AGTGCACTGAATCAGACTGTTGTGTGATCTCGAGGTTTGTATTTCGTACCGATGGTTCACA	1440



```
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProAsgValArgIleMet 500
Db 1441 GATATATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATAATCTTAGGGTAGCATCATG 1500
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAATGCGGAATAGCCTCAGCATCAATGCAGCGCTTCTTTTGCTTAAAGGT 1560
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrIleGluProAspAlaValGluLeuCys 540
Db 1561 TATTACATGGCGAGTTAGATTTCAGATGATTATCTTGAGCCGTGATGCAGTTGAACCTGTGT 1620
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1621 TTTAAAGAAATTTTAAAGATATAAAGCGCTAGCTTGTTTATACCACTAATAGAAAGGTC 1680
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580
Db 1681 AATCCGGATGGTAGCTTAATCGCTAAATGGTTTACAATTTGCCAGAAATTTTCACGAGAAAAA 1740
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1741 CTCAACCGGCTATGATGTGCTCACCACTTTTAAAGATGTTTACGATTAGAGCTTGCGCATTTA 1800
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1801 ACTGATGATTCATGTAAAGAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAACTC 1860
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1861 AGTCAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGGTGATTACATGGT 1920
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660
Db 1921 GATAACACATCAATTAAGAAACTTGGCATTCAAAAGAAAAACCACTTTTGTGTAGTCAAT 1980
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 1981 CAGTCATTAATAGACAGGCTAACTTATTATTAATATGCAATTTTGTATGATTAGAT 2040
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100
Qy 701 LysAspIle 703
Db 2101 AAAGATATT 2109

RESULT 8
US-11-172-145-19
; Sequence 19, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; FILE OF INVENTION: GLYCOSAMINOGLUCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172.145
; CURRENT FILING DATE: 2005-06-30
; PRIOR FILING DATE: 2005-06-30
; PRIOR FILING DATE: 2004-06-30
; PRIOR FILING DATE: 2003-08-15
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2004-07-15
; PRIOR FILING DATE: 2003-06-18
; PRIOR FILING DATE: 2003-07-31
; PRIOR FILING DATE: 2003-07-31
; PRIOR FILING DATE: 2002-07-15
; PRIOR FILING DATE: 2002-07-15
; PRIOR FILING DATE: 1999-11-01
```

```
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-19

Alignment Scores:
Pred. No.: 1,45e-313 Length: 2112
Score: 3692.00 Matches: 702
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.86% Mismatches: 0
Query Match: 72.28% Indels: 0
DB: 7 Gaps: 0

US-10-642-248-2 (1-972) x US-11-172-145-19 (1-2112)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 1 ATGAATACATTATCACAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTATTGAAAAGTCGGCGGAAATCTATGACGCGGAAATTTGTTGAATTTCAAAATFACC 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AAATGCAAGAAAAAATCTCTCAGCACATCTCTTCTGTTAAATTCAGCACATCTTCTGTAAAT 180
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeu 80
Db 181 AAAGAGAAAAAAGTCAATGTTTCGGATAGTCCTGTAGATATTGCAACACACTGTTACTT 240
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 241 TCCACGCTAAAAAATATTAGTACTTTCTGACTCGGAAAAAACACGTTTAAAAAATAAATGG 300
Qy 101 LysLeuLeuThrGlnLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTGCTCACTGAGAAGAAATCTGAAAAATCGGAGGTAAGAGCGGTGCGCCTTGTACCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAAGATTTTCCCAAGATCTGGTGTTTAGCCGCTTTACCTGATCATGTATATGATTTTACA 420
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATATAAACCTGAAACATCAACATGTTGTCTT 480
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTTACAACATTTCAATCGACCAGCAATTTTATCGATTATACATTAGCCCTGTTTA 540
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAAACACATTAACCGTTTGAAGTTATCTGTGACAGATGATGTAGTCAGNA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 601 GATCTATCACCGATCATTCGCCAATATGAAAAATAAATTGGATATTTCGCTACGTACAGCAA 660
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 661 AAAGATAACGGTTTTCAAGCCAGTGGCGCTCGGAATATATGGATTTACGCTTAGCAAAATAT
```

QY 241 AspPheileGlyLeuLeuAaspCysAaspMetAlaProAenProLeuTrpValHisSerTyr 260  
Db 721 GACITTTATGGCTTACTCGACTGTGATATGGCGCAATCCATTAATGGTTCAITCTTAT 780  
QY 261 ValAlaGluLeuLeuGluAaspAaspLeuThrIleleGlyProAaGlyTyrIleAasp 280  
Db 781 GTTCAGAGCTATTAGAAAGATGATGATTAAACAATCATTTGGTCCAGAAAAATACATCGAT 840  
QY 281 ThrGlnHisIleAaspProLysAaspPheLeuAenAenAlaSerLeuLeuGluSerLeuPro 300  
Db 841 ACACAACATATGACCCAAAAGACTTCTTAATAACCGAGTTTGCCTTGAATCAATACCA 900  
QY 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAaspTrp 320  
Db 901 GAAGTGAACCAATATAGTTTGGCGCAAAAGGGAGAAACAGTTTCTCTGATGG 960  
QY 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAaspSerProPheAArgPhe 340  
Db 961 CGCTTAGAACCAATTCGMAAAACAGMAAATCTCGCTTATCCGATTCGCCCTTTCGGTTTT 1020  
QY 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPheAasp 360  
Db 1021 TTTGCGCGGGTAATGTTGCTTTCGCTAAAAAATGGCTAAATAATCCGGTTTCTTTGAT 1080  
QY 361 GluGluPheAenHisTrpGlyGluAaspValGluPheGlyTyrArgLeuPheAArgTyr 380  
Db 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC 1140  
QY 381 GlySerPhePheLysThrIleAaspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1141 GGTAGTTCTTTAAACTATTGATGGCATTTATGGCTACCATCAAGACCCACAGGTAAA 1200  
QY 401 GluAenGluThrAaspArgGluAlaGlyLysAenIleThrLeuAaspIleMetArgGluLys 420  
Db 1201 GAAATGAACCGATCGTGAACGGGAAAAAATATTACGCTCGATATTATCAGAGAAAG 1260  
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAaspSerHisIleAenArgValPro 440  
Db 1261 GTCCCTTATATCTATAGAAACTTTTACCAATAGAAAGATTGCAATATCAATAGAGTACT 1320  
QY 441 LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnAArgCysValAasp 460  
Db 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
QY 461 SerAlaLeuAenGlnThrValValAaspLeuGluValCysIleCysAenAaspGlySerThr 480  
Db 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTGTAACGATGGTTCAACA 1440  
QY 481 AspAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet 500  
Db 1441 GATAATACCTTAGAAGTGATCAATAAAGCTTTTATGGTAATAATCTTAGGGTACGCATCATG 1500  
QY 501 SerLysProAenGlyGlyIleAlaSerAlaSerAenAlaAlaValSerPheAlaLysGly 520  
Db 1501 TCTAAACCAATGGCGGAATACCTCAGCATCAATGACGCGGTTCTTTGCTAAAGT 1560  
QY 521 TyrTyrIleGlyGlnLeuAaspSerAaspTyrLeuGluProAaspAlaValGluLeuCys 540  
Db 1561 TATTACATTTGGCGAGTTAAATTCAGATGATTAATCTTTGAGCCTGATGCGAGTTGAATGTGT 1620  
QY 541 LeuLysGluPheLeuLysAaspLysThrLeuAlaCysValTyrThrAenAArgAenVal 560  
Db 1621 TTTAAAGAAATTTTAAAGATAAACGCTAGCTGTGTTTATACCACCTAATAGAACGTC 1680  
QY 561 AenProAaspGlySerLeuIleAlaAenGlyTyrAenTrpProGluPheSerArgGluLys 580  
Db 1681 AATCCGATGGTAGCTTAATCCCTAATGTTACATTTGCTACATTTGCCAGAAATTTACAGAGAAA 1740  
QY 581 LeuThrThrAlaMetIleAlaIstHisPheAArgMetPheThrIleAArgAlaTrpHisLeu 600  
Db 1741 CTCACACGGCTATGATGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1800  
QY 601 ThrAaspGlyPheAenGluLysIleGluAenAlaValAaspTyrAaspMetPheLeuLysLeu 620

Db 1801 ACTGATGATTCATGAAAAAATTTGAAAAATGGCGTAGACTATGACATGTTCTCTCAAACTC 1860  
QY 621 SerGluValGlyLysPheLysHisLeuAenLysIleCysTyrAenArgValLeuHisGly 640  
Db 1861 AGTGAAGTTGGAAATTTAAACATCTTAATAAATCTGCTATAACCGCTGTATTACATGGT 1920  
QY 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValAen 660  
Db 1921 GATAACACATCAATTAAGAAACTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
QY 661 GlnSerLeuAenArgGlnGlyIleThrTyrTyrAenTyrAepGluPheAaspLeuAasp 680  
Db 1981 CAGTCATTAATAAGCAAGCATAACTTATATAATATGACGAATTTGATGATTTAGAT 2040  
QY 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluGluIleAaspIleLeu 700  
Db 2041 GAAAGTAGAAGTATATTTTCATTAACCCGCTGAATATCAAGAAGAGATTGATATCTTA 2100  
QY 701 LysAaspIle 703  
Db 2101 AAAGATATT 2109

RESULT 9  
US-11-172-145-20  
; Sequence 20, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; FILE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172.145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; LENGTH: 2112  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-20

Alignment Scores:  
Pred. No.: 1,456-313 Length: 2112  
Score: 3692.00 Matches: 702  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.86% Mismatches: 0  
Query Match: 72.28% Indels: 0  
DB: 7 Gaps: 0

US-10-642-248-2 (1-972) x US-11-172-145-20 (1-2112)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
DB 1 ATGAATACATTTATCACAGCAATATAAGCAATATAACAGCAATGACTATCAATTAGCACTC 60  
QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
DB 61 AAATTTATTTCAAAGTCGGCGGAAATCTATGGACGGAATAATGTTGAATTTCAAATTACC 120  
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
DB 121 AAATGCAAGAAAAAATCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTCTGTAAT 180  
QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
DB 181 AAAGAAGAAAGTCAATGTTTCGGATAGTCGGTATGATATTGCAACACAACTGTTACTT 240  
QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
DB 241 TCCACGTAATAAAAAATTTAGTACTTTCTGACTCGGMAAAAAACAGTTTAAAAAATAATGG 300  
QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaArgAlaValAlaLeuValPro 120  
DB 301 AAATTCGTCACTGAGAAGAAATCTGAAAAATCGCGAGGTAAGCGGTGCGCTTGTACCA 360  
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
DB 361 AAAGATTTTCCCAAGATCTGGTTTTAGCCCTTTACCTGATCATGTTAATGATTTTACA 420  
QY 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
DB 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAACCTCGAACATCAACATGTTGGTCTT 480  
QY 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
DB 481 TCTATTATCGTTTCAACATTTCAATTCGACCACCAATTTATTCGATTTACATTTAGCTGTTA 540  
QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
DB 541 GTAAACCAAAAAACACATTTACCCTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA 600  
QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
DB 601 GATCTATACCGATCATTCGCCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 660  
QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
DB 661 AAAGATAAACGGTTTTCAGCGCAGTCGCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT 720  
QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
DB 721 GACTTTTATGGCTTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGGTTCAATCTTAT 780  
QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
DB 781 GTTGCAGAGCTATTAGAGATGATGATTTAAACATCATTTGGTCCAGAAAATACATCGAT 840  
QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300  
DB 841 ACACAACATATTGACCCCAAGACTTCTTAAATAAACCGCAGTTTGGCTTGAATCATTTACCA 900  
QY 301 GluValLysThrAsnAsnSerValAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
DB 901 GAAAGTAAAAACCAATTAATAGTGTGGCGCAAAAGGGAAGGAACAGTTTCTCTGGATTTG 960  
QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
DB 961 CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCGCTTATCCGCTTTCGCCCTTTCCGCTTT 1020  
QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysGlyTrpLeuAsnLysSerGlyPheAsp 360  
DB 1021 TTTGCGCGGGTAATGTTGCTTTTCGCTTAAAAAATGGCTAAATAAATCAATTCGGTTCTTTGAT 1080  
QY 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380

DB 1081 GAGGAATTTAATCACTGGGGTGGAGNAGATGTGGAATTTGGATATCGCTTATTTCCGTAC 1140  
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
DB 1141 GGTAGTTTTCTTTAAACATATTGATGGCATTTATGGCTACCATCAAGAGCACCAGGTAAA 1200  
QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
DB 1201 GAAAAATGAACCGATCGTGAAGCGGAAAAAATATTACCGCTCGATATTATGAGAGAAAAG 1260  
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
DB 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTTCCGATATCAATAGAGTACCT 1320  
QY 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
DB 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
QY 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
DB 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA 1440  
QY 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
DB 1441 GATAATACCTTAGAGTGATCAATAAGCTTTATGGTAATACTCTAGGGTACGCATCATG 1500  
QY 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
DB 1501 TCTAAACCAAAATGGCGGAATAGCTCAGCATCAAAATGCAGCGGTTTCTTTTGTAAAGGT 1560  
QY 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
DB 1561 TATTACATTTGGCGAGTTAGATTTCAAAATGATTTATCTGAGCGCTGATCGAGTTGAACGTGT 1620  
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
DB 1621 TTAAAGAATTTTAAAGATAAAGCTAGCTGTGTTTATACCACTAATAGAAAACGTC 1680  
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
DB 1681 AATCCGATGGTAGCTTTAATCGCTAATGGTTACAATTTGCCAGAAATTTTTCAGAGAAAAA 1740  
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
DB 1741 CTCACAAACGGCTATGATTTGCTCACCACCTTTAGAAATGTTCCAGATTAGAGCTTTGGCATTTA 1800  
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
DB 1801 ACTGATGGATTCANTGAAAAAATTTGAAAATGCGGTAGACTATGACATGTCTCTCAACATC 1860  
QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
DB 1861 AGTGAAGTTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGTGTATTACATGGT 1920  
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
DB 1921 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAAGAAAAAACCATTTTCTGTAGTCAAT 1980  
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
DB 1981 CAGTCNTTAATAGACAGCGCATTAATTAATTAATTAATGACGAATTTGATGATTTAGAT 2040  
QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu 700  
DB 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATAATCAAGAAGAGATTTGATATCTTA 2100  
QY 701 LysAspIle 703  
DB 2101 AAAGATATT 2109

RESULT 10

US-11-172-145-13

```
; Sequence 13, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-13

Alignment Scores:
Pred. No.: 3,2e-294 Length: 1980
Score: 3471.00 Matches: 658
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.95% Indels: 0
DB: 7 Gaps: 0

US-10-642-248-2 (1-972) x US-11-172-145-13 (1-1980)
QY 46 LeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsnLysGluGluLysVal 65
DB 4 CTCTCAGCACATCTCTCTGTTTAATTCAGCACATCTCTCTGTTTAATTAAGAGAGAGAGATC 63
QY 66 AsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeuLeuSerAsnValLysLys 85
DB 64 AATGTTGCGATAGTCGTTAGATATTGCAACACAACTGTTACTTTTCAACGCTAAAGAAA 123
QY 86 LeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysThrLysLeuLeuThrGlu 105
DB 124 TTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGAAAAATGCTCACTGAG 183
QY 106 LysLysSerGluAsnAlaGluValArgAlaValAlaLeuValProLysAspPheProLys 125
DB 184 AAGAATCTGAATAATCGCGAGGTAGAGCGGTGCGCCCTTGTTACCAAGAGATTTCCTCAAA 243
QY 126 AspLeuValLeuAlaProLeuProAspHisValAsnAspPheThrTrpTrpLysLysArg 145
DB 244 GATCTGTTTATAGCCCTTACTCATGATGTTTAATGATTTTACATGGTACAAAAGCGA 303
QY 146 LysLysArgLeuGlyLysProGluHisGlnHisValGlyLeuSerIleIleValThr 165
DB 304 AAGAAAGACTTGGCATAAAACCTGAACATCAACATGTTGGTCTTTCTATTATTCGTTACA 363
QY 166 ThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeuValAsnGlnLysThr 185

364 ACATTCAATCGACAGCAATTTTATCGATTACATTAGCCCTGTTTAGTAAACCAAAAAACA 423
186 HisTy-ProPheGluValIleValThrAspAspGlySerGlnGluAspLeuSerProIle 205
424 CATTAACCCGTTTGAAGTTATCGTCAGACATGATGTTAGTCAGGAAGATCTATCACCAGTC 483
206 IleArgGlnTyArgGlnLysLeuAspIleArgTyValArgGlnLysAspAsnGlyPhe 225
484 ATTCCGCAATATGAAAAATAAATTCGATATTCGCTACGTCAGACAAAAAGATAACGGTTTT 543
226 GlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyArgPheIleGlyLeu 245
544 CAAGCCAGTCGCGCTCGGAATATGGGATTAACGTTAGCAAAATATGACTTTATTTGGCTTA 603
246 LeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyValAlaGluLeuLeu 265
604 CTGACTGTGATATGGCCCAATCCATTAATGGGTTCAATCTTATGTTGCAGAGCTATTA 663
266 GluAspAspLeuThrIleIleGlyProArgLysTyIleAspThrGlnHisIleAsp 285
664 GAAGATGATGATTAACAATCAATTCGTCAGAAAAATACATCGATACACAACTATTGAC 723
286 ProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuProGluValLysThrAsn 305
724 CCAAAAGACTTCTTAAATAACGCGAGTTTCTTGAATCATTTACCAGAGTGAACCAAT 783
306 AsnSerValAlaLysGlyGluGlyThrValSerLeuAspTrpArgLeuGluGlnPhe 325
784 AATAGTGTGTCGCGCAAAAGGGAAGAACAGATTCTCTGGATGGCGCTTAGAACAAATTC 843
326 GluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhePheAlaGlyAsn 345
844 GAAAAACACAGAAATCTCCGCTTATCGGATTCGCTTTTCCGTTTTTTTTCGCGCGGTAAT 903
346 ValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAspGluGluPheAsnHis 365
904 GTTGTCTTCGCTAAAAAATGGCTAAATAATCCGGTTCTTTTGAATGAGGAATTAATCAC 963
366 TrpGlyGlyGluAspValGluPheGlyTyArgLeuPheArgTyArgTySerPhePheLys 385
964 TGGGTGCGAGAAAGATGGAATTTGGATATCGCTTATTCGTTACGGTAGTTTCTTTAAA 1023
386 ThrIleAspGlyIleMetAlaTyHisGlnGluProProGlyLysGluAsnGluThrAsp 405
1024 ACTATTGATGCAATTTATGGCTTACCATCAAGAGCCACAGGTAAGAAAAATGAACCGAT 1083
406 ArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLysValProTyIleTy 425
1084 CGTGAAGCGGAAAAAATATTTACGCTCGATATTAAGAGAAAAAGGTCCTTATATCTAT 1143
426 ArgLysLeuLeuProIleGluAspSerHisIleAsnArgValProLeuValSerIleTy 445
1144 AGAAACATTTTACCACATAGAAAGATTTCGATATCAATAGAGTACCTTTAGTTTCAATTTAT 1203
446 IleProAlaTyAsnCysAlaAsnTyIleGlnArgCysValAspSerAlaLeuAsnGln 465
1204 ATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGATAGTGCACCTGAATCAG 1263
466 ThrValValAspLeuGluValCysIleCysAsnAspGlySerThrAspAsnThrLeuGlu 485
1264 ACTGTGTTGATCTCGAGGTTTGTATTTGTAAACGATGTTTCAACAGATTAATACCTTAGAA 1323
486 ValIleAsnLysLeuTyArgAsnAsnProArgValArgIleMetSerLysProAsnGly 505
1324 GTGATCAATAGCTTTATGGTAATAATCTTAGGTCAGCATCATGCTCTAAACCAANTGGC 1383
506 GlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGlyTyTyIleGlyGln 525
1384 GGAATAGCTCAGCATCAATGACGCGCTTTCTTTTGTAAAGGTTATTTACATTGGCGAG 1443
526 LeuAspSerAspAspTyArgLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeu 545
```

Db 1444 TTAGATTGAGATGATTATCTTGAGCCTGATGTCAGTTGAACTGTGTTTTAAAGAATTTTTA 1503  
Qy LysAspLysThrLeuAlaCysValTyrThrThraAsnArgAsnValLeuAsnProAspGlySer 565  
Db 1504 AAAGATAAAACGCTAGCTGTGTTTATACCACTAATAGAAACGTCATCCGGATGGTAGC 1563  
Qy LeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLysLeuThrThraAlaMet 585  
Db 1564 TTAATCGCTAATGTTTCAATTTGCCAGAAATTTTCAGGAAAAACCTCACACGGCTATG 1623  
Qy IleAlaHisHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPheAsn 605  
Db 1624 ATGCTCACCATTTAGAAATGTTACCGATTAGAGCTTGGCATTTAACTGATGATTCAT 1683  
Qy GluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeuSerGluValGlyLys 625  
Db 1684 GAAAAAATTGAAATGCGTAGACATATGACATGTTCTCAAACTCAGTGAAGTTGAAAA 1743  
Qy PheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAspAsnThrSerIle 645  
Db 1744 TTTAAACATCTTAAATAAATCTGCTATAACCGTGTATTACATGTTGATAACATCATNT 1803  
Qy LysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsnGlnSerLeuAsnArg 665  
Db 1804 AAGAACTTGGCATTCAAAAGAAAAACCATTTTGTGTAGTCAATCAGTCATTAATAGA 1863  
Qy GlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAspGluSerArgLysTyr 685  
Db 1864 CAAGGCATAACTTATTATAATATTAGCAAAATTTGATGATTTAGATGAAGTAGAAGTAT 1923  
Qy IlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeuLysAspIle 703  
Db 1924 ATTTTCAATAAACCGCTGAATATCAAGAAGAGATTGATATCTTAAAGATATT 1977

## RESULT 11

US-11-172-145-14  
; Sequence 14, Application US/11172145  
; Publication No. US2005027696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 1902  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
; US-11-172-145-14

## Alignment Scores:

Pred. No.:	2,09e-282	Length:	1902
Score:	3336.00	Matches:	632
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	65.31%	Indels:	0
DB:	7	Gaps:	0

US-10-642-248-2 (1-972) x US-11-172-145-14 (1-1902)

Qy	72	LeuAspIleAlaThrGlnLeuLeuSerAsnValLysLysLeuValLeuSerAspSer	91
Db	4	TTAGATATTGCCAACACAACTGTTACTTTCACAGCTAAAAAATTAGTACTTCTTGACTCG	63
Qy	92	GluLysAsnThrLeuLysAsnLysTrpLysLeuLeuThrGluLysLysSerGluAsnAla	111
Db	64	GAATAAAACACGTTAAAAAATAAATGGAATTTGCTCACTGAGAAGAAATCTGAAAAATGCG	123
Qy	112	GluValArgAlaValAlaLeuValProLysAspPheProLysAspLeuValLeuAlaPro	131
Db	124	GAGGTAAAGAGCGGTCCGCTTTGTACCAAGAATTTTCCCAAGATCTGGTTTATGGCCCT	183
Qy	132	LeuProAspHisValAsnAspPheThrTrpTyrLysLysArgLysLysArgLeuGlyIle	151
Db	184	TTACCTGATCATGTTTAATGATTTTACATCGTACAAAAAGGAAAGAAAGACTTGGCATA	243
Qy	152	LysProGluHisGlnHisValGlyLeuSerIleIleValThrThrPheAsnArgProAla	171
Db	244	MAACCTGAACATCAACATGTTGCTCTTCTATTATCGTTACAACATTCATTCACACGCA	303
Qy	172	IleLeuSerIleThrLeuAlaCysLeuValAsnGlnLysThrHisTyrProPheGluVal	191
Db	304	ATTTTATCATTTACATTAGCCTGTTTAGTAAACCAAAAAACACATTTACCGTTTGAAGTT	363
Qy	192	IleValThrAspAspGlySerGlnGluAspLeuSerProIleArgGlnTyrGluAsn	211
Db	364	ATCGTCACAGATGATGTTAGTACGGAAGATCTATCACCGATCATTCGCCAATATGAAT	423
Qy	212	LysLeuAspIleArgTyrValArgGlnLysAspAsnGlyPheGlnAlaSerAlaAlaArg	231
Db	424	AAATTGGATATTGCTTACGTCAGACAAAAAAGATAACGGTTTTCAAGCCAGTGCCTCGG	483
Qy	232	AsnMetGlyLeuArgLeuAlaLysTyrAspPheIleGlyLeuLeuAspCysAspMetAla	251
Db	484	AATATGGGATTACGCTTAGCAAAATATGACTTTATTGGCTTACTCGACTGTGATATGGCG	543
Qy	252	ProAsnProLeuTrpValHisSerTyrValAlaGluLeuLeuGluAspAspLeuThr	271
Db	544	CCAAATCCATTATGGGTTTCATTCTTATGTTGCAGAGCTATTAGAAGATGATGATTAACA	603
Qy	272	IleIleGlyProArgLysTyrIleAspThrGlnHisIleAspProLysAspPheLeuAsn	291
Db	604	ATCATTTGGTCCAAAGAAATACATCGATACACACATATTGACCCCAAAAGACTTCTTAAAT	663
Qy	292	AsnAlaSerLeuLeuGluSerLeuProGluValLysThrAsnAsnSerValAlaAlaLys	311
Db	664	AACGCGAGTTTGGCTTGAATCATTTACCAGAAAGTGAACCAATTAATAGTGTTCGCGAAAA	723
Qy	312	GlyGluGlyThrValSerLeuAspTrpArgLeuGluGlnPheGluLysThrGluAsnLeu	331
Db	724	GGGGAAGGAACAGTTTCTCTGGATTGCGCTTAGAACAAATTCGAAAAACAGAAAAATCTC	783
Qy	332	ArgLeuSerAspSerProPheArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLys	351
Db	784	CGCTTATCCGATTTCGCTTTTCCGTTTTTTTGGCGGGTAAATGTTGCTTTTCGCTAAAAA	843
Qy	352	TrpLeuAsnLysSerGlyPhePheAspGluGluPheAsnHisTyrGlyGlyGluAspVal	371
Db	844	TGCTTAAATAAATCCGGTTCTTTTGTATGAGGAATTTAATCACTGGGGTGGAGAAGATGTG	903
Qy	372	GluPheGlyTyrArgLeuPheArgTyrGlySerPhePheLysThrIleAspGlyIleMet	391

Db 904 GAATTTGGATATCGCTTATTCCGTACGGTAGTGTCTTTAAACATATTGATGGCATTTATG 963  
Qy 392 AlaTyrHisGlnGluProGlyLysGluAsnGluThrAspArgGluAlaGlyLysAsn 411  
Db 964 GCCTACCATCAAGAGCCACCGGTAAAGAAATGAACCGATCGTGAAGCGGGNAAAT 1023  
Qy 412 IleThrLeuAspIleMetArgGluLysValProTyrIleTyrArgLysLeuLeuProIle 431  
Db 1024 ATTACGTCGATATTATGAGAGAAAGTCCTCTTATATCTATATAGAAAATTTTACCAATA 1083  
Qy 432 GluAspSerHisIleAsnArgValProLeuValSerIleTyrIleProAlaTyrAsnCys 451  
Db 1084 GAAGATTGCGCATATCAATAGAGTAGTACCTTTAGTTTCAATTTATATATCCAGCTTAACTGT 1143  
Qy 452 AlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGlu 471  
Db 1144 GCAAACTATATTCAACGTTGGGTAGATAGTCGACTGAATCAGACTGTTGTGTCTCGAG 1203  
Qy 472 ValCysIleCysAsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyr 491  
Db 1204 GTTTGTATTGTAACGATGGTTCAACAGATAATACCTTTAGAAGTGATCAATAAGCTTTAT 1263  
Qy 492 GlyAsnAsnProArgValArgIleMetSerLysProAsnGlyGlyIleAlaSerAlaSer 511  
Db 1264 GGTAAATATCTAGGTACGCATCATGCTCTAAACCAAAATGCGGAATAGCCTCAGCATCA 1323  
Qy 512 AsnAlaValSerPheAlaLysGlyTyrIleGlyGlnLeuAspSerAspAspTyr 531  
Db 1324 AATGCGCCGTTCTTTGCTAAAGGTTATTACATTTGGCGAGTTAGATTTCAGATGATTAT 1383  
Qy 532 LeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLysAspLysThrLeuAla 551  
Db 1384 CTTGAGCCTGATGAGTGGTGAATCTGTGTTAAAGAAATTTTAAAGATAAATGCTAGCT 1443  
Qy 552 CysValTyrThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyr 571  
Db 1444 TGTGTTTATACCACTAATAGAAAGCGTCAATCGGATGGTAGCTTAATCGCTAAATGGTTAC 1503  
Qy 572 AsnTyrProGluPheSerArgGluLysLeuThrAlaMetIleAlaHisPheArg 591  
Db 1504 AATTGGCCAGAAATTTTCACGAGAAAACTCAACGCGCTATGATTGCTCACCATTTAGA 1563  
Qy 592 MetPheThrIleArgAlaTyrHisLeuThrAspGlyPheAsnGluLysIleGluAsnAla 611  
Db 1564 ATGTTCCAGATTAGAGCTTGCAATTAATCTGATGATTCATGATAAATAATGAAATGCC 1623  
Qy 612 ValAspTyrAspMetPheLeuLysLeuSerGluValGlyLysPheLysHisLeuAsnLys 631  
Db 1624 GTAGACTATGACATGTTCTCAAACTCAGTGAAGTTGGAAAAATTTAAACATCTTAATAA 1683  
Qy 632 IleCysTyrAsnArgValLeuHisGlyAspAsnThrSerIleLysLeuLysGlyIleGln 651  
Db 1684 ATCTGCTATAACCGGTGTTATTACATGGTGATTAACACATCAATTAAGAAACTTTGGCAATCAA 1743  
Qy 652 LysLysAsnHisPheValValValAsnGlnSerLeuAsnArgGlnGlyIleThrTyrTyr 671  
Db 1744 AAGAAAAACCATTTTGTGTAGTCAATCAGTCATTAATAGAACAGGATTAATTTAT 1803  
Qy 672 AsnTyrAspGluPheAspLeuAspGluSerArgLysTyrIlePheAsnLysThrAla 691  
Db 1804 AATTATGCAATTTTATGATGATTAGATGAAGTAGAAGATATATTTCAATAAAACCGCT 1863  
Qy 692 GluTyrGlnGluLysLeuAspIleLeuLysAspIle 703  
Db 1864 GAATATCAAGAGAGATTGATATCTTAAAGATATT 1899

## RESULT 12

US-11-172-145-15  
; Sequence 15, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC

; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15  
; LENGTH: 1830  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-15

## Alignment Scores:

Pred. No.: 1,08e-272 Length: 1830  
Score: 3225.00 Matches: 608  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 63.14% Indels: 0  
DB: Gaps: 0

US-10-642-248-2 (1-972) x US-11-172-145-15 (1-1830)

Qy 96 LeuLysAsnLysTyrPheLysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAla 115  
Db 4 TTAATAAATAAATGAAATTCCTCACTGAGAAGAAATCTGAAATTCGGAGGTAAAGCG 63  
Qy 116 ValAlaLeuValProLysAspPheProLysAspLeuValLeuAlaProLeuProAspHis 135  
Db 64 GTCGCCCTGTACCAAAAGATTTTCCCAAGATCTGGTTTATAGCGCCTTTACCTGATCAT 123  
Qy 136 ValAsnAspPheThrTyrTyrLysArgLysLysArgLeuGlyIleLysProGluHis 155  
Db 124 GTTAATGATTTTATGTTACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAT 183  
Qy 156 GlnHisValGlyLeuSerIleValThrThrPheAsnArgProAlaIleLeuSerIle 175  
Db 184 CAACATGTGGTCTTCTTCTATTATCGTTACAAATTCATTCAGCAGCAAGCAAGCAATTTATCGATT 243  
Qy 176 ThrLeuAlaCysLeuValAsnGlnLysThrHisTyrProPheGluValIleValThrAsp 195  
Db 244 ACATTAGCCTGTTTAGTAAACCAAAACACATTTACCGCTTTTGAAGTTTATCGTGACAGAT 303  
Qy 196 AspGlySerGlnGluAspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIle 215  
Db 304 GATGATAGTAGGAGATCTATACCGCATCATTCGCCATATGAATAATTAATTTGATATT 363  
Qy 216 ArgTyrValArgGlnLysAspAsnGlyPheGlnAlaSerAlaIleArgAsnMetGlyLeu 235  
Db 364 CGCTACGTCAGCAAAAGATAACGGTTTTCAAGCCAGTCGCGCTCGCAATATGGGATTA 423  
Qy 236 ArgLeuAlaLysTyrAspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeu 255



424	Db	CGCTTAGCAAAATATGACTTTATTTGGCTTACTCGACTGTGTGATATGGCGGCCAAATTCCAATTA	483
256	Qy	TipValHisSerTyRValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyPro	275
484	Db	TGGGTTCAATCTTAATGTTGCAGACTATTAGAAGATGATGATTTTAAACATCATTTGGTCCA	543
276	Qy	ArgLysTyRLeuAspThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeu	295
544	Db	AGAAAAATACATCGATACACAACATATTGACCCAAAGACTTCTCTTAAATAACGCGAGTTTG	603
296	Qy	LeuGlnSerLeuProGluValLysThrAsnAsnSerValAlaLysGlyGluGlyThr	315
604	Db	CTTGAATCATTTACCAGAAGTGAAACCAATAATAGTGTTCGCCGAAAGGGGAGGAACA	663
316	Qy	ValSerLeuAspTrpArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAsp	335
664	Db	GTTTCTCTGGATTGGCGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCCGCTTATCCGAT	723
336	Qy	SerProPheArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLys	355
724	Db	TCGCCTTTCCGTTTTTTTGGCGGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAA	783
356	Qy	SerGlyPhePheAspGluGluPheAsnHisTrpGlyGlyLeuAspValGluPheGlyTyR	375
784	Db	TCCGGTTCTTTGATGAGGAATTTAAATCACTGGGGGTGAGAAGATGTGGAATTTGGATAT	843
376	Qy	ArgLeuPheArgTyRArgLysSerPhePheLysThrIleAspGlyIleMetAlaTyRHisGln	395
844	Db	CGCTTATTTCCGTTACGGTAGTGTCTTTTAAACTATTGATGCATATTGGCTTACCATCAA	903
396	Qy	GluProProGlyLysGluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAsp	415
904	Db	GAGCCACCGGTAAAGAAAAATGAAACCGATCGTGAAGCGGGAAAAAATATTACGCTCGAT	963
416	Qy	IleMetArgGluLysValProTyRILETyRArgLysLeuLeuProIleGluAspSerHis	435
964	Db	ATTATGAGAGAAAAAGGTCCTTATATCTATAGAAAAACTTTTACCAAATAGAAGATTTCGAT	1023
436	Qy	IleAsnArgValProLeuValSerIleTyRILEProAlaTyRAsnCysAlaAsnTyRILE	455
1024	Db	ATCAATAGAGTACCTTTAGTTTTCAAATTTATATCCAGCTTATACTGTGCAAACTATATT	1083
456	Qy	GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys	475
1084	Db	CAACGTTGCGTAGATAGTGCACATGACAGACTGTTGTTGATCTCGAGGTTTGTATTGTT	1143
476	Qy	AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyRArgLysAsnAspPro	495
1144	Db	AACATGCGTTCAACAGATAATATACCTTAGAAGTGATCAATAGCTTTTATGGTAATAATCCT	1203
496	Qy	ArgValArgIleMetSerLysProAsnGlnGlyIleAlaSerAlaSerAsnAlaAlaVal	515
1204	Db	AGGGTAGCATCATGTCTTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCAAGCGGT	1263
516	Qy	SerPheAlaLysGlyTyRILEGlnLeuAspSerAspAspTyRLeuGluProAsp	535
1264	Db	TCTTTTGCTAAAGGTTATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTAGCCCTGAT	1323
536	Qy	AlaValGluLeuCysLeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyRThr	555
1324	Db	GCAGTTGAACCTGTCTTTAAAAAGAAATTTTAAAAAGATAAAACCGCTAGCTTGTGTTTATACC	1383
556	Qy	ThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyRAsnTrpProGlu	575
1384	Db	ACTAATAGAAACGTCAAATCCGGATGGTAGCTTAATCGCTAATGTTTACAATTTGCCACAGAA	1443
576	Qy	PheSerArgGluLysLeuThrThrAlaMetIleAlaHisPheArgMetPheThrIle	595
1444	Db	TTTTTCACGAGNAAAACTCACAAACGGCTATGATTTGCTTACCACCTTTTAGATGTTCCAGATT	1503
596	Qy	ArgAlaTrpHisLeuThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyRAsp	615
1504	Db	AGACCTTGGCAATTTAACTGTGATTTCAATGAAATAATTTGAAATATGCGTAGATATGAC	1563

Qy	616	MetPheLeuIysLeuSerGluValGlyLysPheLysHisLeuAsnIysIleCysTyrAsn	635
Db	1564	ATGTTCCTCAAACTCGATGAAGTTGGAAATTTAAACATCTTAAATAAAATCTCTATAAC	1623
Qy	636	ArgValLeuHisGlyAspAsnThrSerIleLysLysLeuGlyIleGlnIysLysAsnHis	655
Db	1624	CGTGTATTACATGGTGNTAACACATCANTTAGAAACTTGGCATTCAAAGAANAACCAT	1683
Qy	656	PheValValValAsnGlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGlu	675
Db	1684	TTTGTGTAGTCAATCAGTCATTAAATAGACAAGGCATAACTATTATTAATTATGACGAA	1743
Qy	676	PheAspAspLeuAspGluSerArgLysTyrIlePheAsnIysThrAlaGluTyrGlnGlu	695
Db	1744	TTTGATGATTTAGATGAAGTAGAAGATATATTTTCAATATAAACCCGCTGATATATCAAGAA	1803
Qy	696	GluIleAspIleLeuIysAspIle	703
Db	1804	GAGATTGATATCTTAAAGATATT	1827

RESULT 13

```

US-11-172-145-16
; Sequence 16, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-16

```

Alignment Scores:		
Pred. No.:	3.73e-263	Length: 1764
Score:	3116.00	Matches: 586
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	61.00%	Indels: 0
DB:	7	Gaps: 0

US-10-642-248-2 (1-972) x US-11-172-145-16 (1-1764)

QY 118 LeuValProLysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsn 137







us-10-642-248-2.p2n.rnpbn

Db	18568	CTCGTGTGGTGATGCTGCCGGTGTTCAAATGCGGAGCGGTACATCGCCAGGGCCGTGCAG	18509
Qy	461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480
Db	18508	TCCGGCTCTCCAGACACTTACAGCCCGTGAAGTGATCGTCTGACGACGGATCGACC	18449
Qy	481	AspAsnThrLeuGluValIleAsnIleAsnLeuTyrGlyIleAsnAsnProArgValArgIleMet	500
Db	18448	GACGGCACGCGACACATCTGCGAGATTTCGGCGGC-----GCCATCACGGTGATC	18398
Qy	501	SerLeuProAsnGlyGlyIleAlaSerAsnAlaValSerPheAlaIleGly	520
Db	18397	TCTCAGCCCAACCGGGGCTTGC CGCGCCGCCAATCGGCATCGCCGCGCGCGAGGG	18338
Qy	521	TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys	540
Db	18337	GAATTCTGTGGCGTGTCTGACGCGCGAGCACTGTGGGATCCGGCCCAAGATTTCGCGGCGAG	18278
Qy	541	LeuIleGluPheLeuIleAspIleThrLeuAlaCysValTyrThrAsnArgAsnVal	560
Db	18277	GTCGATCTCTTCGACAGCAGCGCGACTGGAGTTCATTTCATCCGGGGCGCGCGTCAATC	18218
Qy	561	AsnProAspGlySerLeulle-----AlaAsnGlyTyrAsnTrp	573
Db	18217	GACGAGCCGGCGAGGTCTTCGCGACGCTCGATCTTCGCGCGCTCGAGGGCGGTGCTC	18158
Qy	574	ProGluPheSerArgGluIleThrThrAlaMetIleAlaHisPheArgMetPhe	593
Db	18157	CCCGACCTCTCTTCGAAACGCGGTGACGGCT-----TCGTCGGTC	18116
Qy	594	ThrIleArgAlaTrpHisIleu---ThrAspGlyPheAsnGluIleGluAsnAlaVal	612
Db	18115	ATGGTCAAGCGCGCGTGTCTCCGGCAGGAGATGTTCCGACCGGATCCACGGCGTCCAG	18056
Qy	613	AspTyrAspMetPheLeuIleAsnSerGluValGlyIlePheIleHisLeuAsnIle	632
Db	18055	GACTGGGACCTTGCTGTGCGCTCTCGCGAAGGGCCCGTGGTTCATCCCGGAACCC	17996
Qy	633	CysTyrAsnArgValLeuHisGlyAspAsnThrSer	644
Db	17995	CTGACGATTACAGGCTGCACGACCAACATCATGTCG	17960

Search completed: January 9, 2006, 02:48:08  
Job time : 1262 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 8, 2006, 20:53:59 ; Search time 1557 seconds  
(without alignments)  
5162.386 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSNDYQLA.....SAKRGENIPVKNFIINSITL 972

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Maximum Match 0%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool\_p/US10642248/runat\_06012006\_125012\_26951/app\_query.fasta\_1.1159  
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=p2n.rnpbm  
-MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40 cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct  
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext  
-HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10642248 @CGN 1 1 1549 @runat\_06012006\_125012\_26951 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA\_Main.\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	5108	100.0 2920 5	US-10-217-613-2
2	5108	100.0 2920 7	US-10-642-248-1
3	5108	100.0 2937 5	US-10-011-768B-8
4	5108	100.0 2937 5	US-10-011-771B-8
5	5108	100.0 2937 10	US-11-109-855-8
6	5104	99.9 2916 6	US-10-326-185-94
7	5104	99.9 2916 10	US-11-096-190-8

8	5104	99.9	2937	3	US-09-879-359-9	Sequence 9, Appli
9	5104	99.9	2937	5	US-10-172-527-9	Sequence 7, Appli
10	5104	99.9	2937	6	US-10-309-560-7	Sequence 9, Appli
11	4502.5	88.1	2979	3	US-09-842-484A-3	Sequence 3, Appli
12	4502.5	88.1	2979	7	US-10-642-248-3	Sequence 3, Appli
13	4502.5	88.1	2979	9	US-10-197-153-4	Sequence 4, Appli
14	4502.5	88.1	2979	10	US-11-042-530-3	Sequence 3, Appli
15	4490.5	87.9	2979	3	US-09-842-484A-1	Sequence 1, Appli
16	4490.5	87.9	2979	5	US-10-184-485-4	Sequence 4, Appli
17	4490.5	87.9	2979	10	US-11-042-530-1	Sequence 1, Appli
18	3968	77.7	2271	7	US-10-642-248-20	Sequence 20, Appl
19	3705	72.5	2136	7	US-10-642-248-51	Sequence 51, Appl
20	3697	72.4	2112	7	US-10-642-248-71	Sequence 71, Appl
21	3697	72.4	2112	9	US-10-197-153-2	Sequence 2, Appli
22	3694	72.3	2112	7	US-10-642-248-45	Sequence 45, Appli
23	3694	72.3	2112	7	US-10-642-248-46	Sequence 46, Appli
24	3693	72.3	2112	5	US-10-184-485-2	Sequence 2, Appli
25	3693	72.3	2112	7	US-10-642-248-16	Sequence 16, Appl
26	3693	72.3	2112	7	US-10-642-248-18	Sequence 18, Appl
27	3693	72.3	2112	7	US-10-642-248-33	Sequence 33, Appli
28	3693	72.3	2112	7	US-10-642-248-36	Sequence 36, Appli
29	3693	72.3	2112	7	US-10-642-248-40	Sequence 40, Appli
30	3693	72.3	2112	7	US-10-642-248-42	Sequence 42, Appl
31	3693	72.3	2112	7	US-10-642-248-48	Sequence 48, Appl
32	3692	72.3	2112	7	US-10-642-248-11	Sequence 11, Appl
33	3692	72.3	2112	7	US-10-642-248-12	Sequence 12, Appl
34	3692	72.3	2112	7	US-10-642-248-34	Sequence 34, Appli
35	3692	72.3	2112	7	US-10-642-248-37	Sequence 37, Appli
36	3692	72.3	2112	7	US-10-642-248-39	Sequence 39, Appli
37	3692	72.3	2112	7	US-10-642-248-43	Sequence 43, Appli
38	3692	72.3	2112	7	US-10-642-248-47	Sequence 47, Appli
39	3692	72.3	2112	7	US-10-642-248-49	Sequence 49, Appli
40	3690	72.2	2112	7	US-10-642-248-17	Sequence 17, Appli
41	3690	72.2	2112	7	US-10-642-248-19	Sequence 19, Appli
42	3690	72.2	2112	7	US-10-642-248-35	Sequence 35, Appli
43	3690	72.2	2112	7	US-10-642-248-38	Sequence 38, Appli
44	3690	72.2	2112	7	US-10-642-248-41	Sequence 41, Appli
45	3690	72.2	2112	7	US-10-642-248-44	Sequence 44, Appli

ALIGNMENTS

RESULT 1  
US-10-217-613-2  
; Sequence 2, Application US/10217613  
; Publication No. US20030113845A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL  
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND U:  
; FILE REFERENCE: 35541.081  
; CURRENT APPLICATION NUMBER: US/10/217,613  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 2920  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-10-217-613-2

Alignment Scores:  
Pred. No.: 0  
Score: 5108.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Length: 2920  
Matches: 972  
Conservative: 0  
Indels: 0

DB:	5	Gaps:	0
US-10-642-248-2 (1-972) x US-10-217-613-2 (1-2920)			
Qy	1	MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu	20
Db	1	ATGAATACATTTATCACAAAGCAATAAAGCATATACAGCAATGACTATCAATTAGCACTC	60
Qy	21	LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr	40
Db	61	AAATTTATTGAAAGTCGGCGGAAATCTATGGACGGAAAAATTTGTGAATTTCAAATTTACC	120
Qy	41	LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn	60
Db	121	AAATGCAAGAAAAAATCTCTAGCACATCCCTCTCTGTAAATCAGCACATCTTCTGTAAAT	180
Qy	61	LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu	80
Db	181	AAAGAAGAAAAAGTCAATGTTTGGATAGTCCGTTAGTATTTGCAACACAACTGTTACTT	240
Qy	81	SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp	100
Db	241	TCCAAACGTAAAAAAATTTAGTACTTTCTGACTCGGAAAAAAACACGTTAAAAAAATAAATGG	300
Qy	101	LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaValAlaLeuValPro	120
Db	301	AAATTTGCTCACTGAGAAAGAAATCTGAAATAATCGGAGGTAAAGCGCGTTCGTCCTTGTACCA	360
Qy	121	LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr	140
Db	361	AAAGATTTTCCAAAGATCTGTTTGTAGCGCTTTACTTGATCATGTTAATGATTTTACA	420
Qy	141	TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu	160
Db	421	TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACATGTTGGTCTT	480
Qy	161	SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu	180
Db	481	TCTATTATTCGTTACAAACATTCATCGACCACCAATTTTTCGATTACATTAGCTCGTTTA	540
Qy	181	ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu	200
Db	541	GTAACCCAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Qy	201	AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln	220
Db	601	GATCTATCACCGATCATTCGCCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA	660
Qy	221	LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr	240
Db	661	AAAGATACCGGTATTTCAAGCCAGTCGCGCTCGGAATATGGGAATACGCTTAGCAAAATAT	720
Qy	241	AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr	260
Db	721	GACTTTATTCGCTTACTCGACTGATGATGGGCCAATCAATATGGGTTCACTCTAT	780
Qy	261	ValAlaGluLeuLeuGluAspAspLeuThrIleLeGlyProArgLysTyrIleAsp	280
Db	781	GTTTCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCCAAGAAAAATACATCAT	840
Qy	281	ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro	300
Db	841	ACACAACATATTGACCCAAAAAGACTTCTTAATAACGCGAGTTTGGCTTGAATCAATACCA	900
Qy	301	GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp	320
Db	901	GAACTGAAACCAATATATAGTTTGGCCGCAAAAGGGAGGAAACAGTTTCTCTGGATTGG	960
Qy	321	ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe	340
Db	961	CGCTTAGAACAAATTCGAAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT	1020
Qy	341	PheAlaAlaGlyAsnValAlaPheAlaLysIleTrpLeuAsnLysSerGlyPheAsp	360

Db	1021	TTTGGCGCGGTAAATGTTGCTTTCGCTAAAAAATGCTAAATAAATCCCGTTCCTTTGAT	1080
Qy	361	GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr	380
Db	1081	GAGGAATTTAATCACTGGGTGGAGAAGATGTGGAATTTTGGATATCGCTTATTTCCGTTAC	1140
Qy	381	GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys	400
Db	1141	GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCAAGGTAAA	1200
Qy	401	GluAsnGlnThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGlyLys	420
Db	1201	GAAATGAAACCCGATCGTGAAGCGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG	1260
Qy	421	ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro	440
Db	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTTCGCATATCAATAGAGTACCT	1320
Qy	441	LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp	460
Db	1321	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTGCGTAGAT	1380
Qy	461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480
Db	1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTGTATTGTAAACGATGGTTCAACA	1440
Qy	481	AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet	500
Db	1441	GATAATACCTTTAGAAAGTGATCAATAAGCTTTATGGTAAATAATCTTAGGGTACGCATCATG	1500
Qy	501	SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly	520
Db	1501	TCFAAACCAAAATGGCGAATAGCCTCAGCATCAAAATCAAAATGCAGCCGTTCTTTTGTCTAAAGGT	1560
Qy	521	TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys	540
Db	1561	TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGAGTTGAACCTGT	1620
Qy	541	LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal	560
Db	1621	TTAAAAGAAATTTTAAAAGATAAAACGCTAGCTTGTGTTTATATACCACTAATAGAAACGTC	1680
Qy	561	AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGlyLys	580
Db	1681	AAATCCGAGTGGTAGCTTAATCGCTTAATGGTTTACAATTTGGCCAGAAATTTTCCAGAGAAAA	1740
Qy	581	LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu	600
Db	1741	CTCACAAACGCTATGATGCTCACCACTTTAGAAATGTTACAGATTAGAGCTTGGCATTTA	1800
Qy	601	ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu	620
Db	1801	ACTGATGGATTTCAATGAAAAAATGAAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC	1860
Qy	621	SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly	640
Db	1861	AGTGAAGTTGGAAAAATTTAAACATCTTTAAATAAATCTGCTATTAACCGGTATTACATGGT	1920
Qy	641	AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn	660
Db	1921	GATAACACATCAATTAAGAAACCTTGGCATTCAAAAGNAAAAACCAATTTTGTGTAGTCAAT	1980
Qy	661	GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp	680
Db	1981	CAGTCATTAATAAGAACATCACTTATATAAATATGACGAATTTGATGATTTAGAT	2040
Qy	681	GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu	700
Db	2041	GAAAGTAGAAGATATATTTTCAATAAACCAGCTGAATATCAAGAAGAGATTGATATCTTA	2100
Qy	701	LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro	720

```
Db 2101 AAGATATTAATAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2160
Qy 721 AenThrLeuAenGlyLeuValLysLysLeuAenAenllelleGluTyrAenLysAenlle 740
Db 2161 AATACATTTAAACGGCTAGTGGAAAAAATAAACAATATATTATGTAATATAAATAAATA 2220
Qy 741 PheValIleValLeuHleValAspLysAenHleLeuThrProAspLleLysLysGluIle 760
Db 2221 TTCGTTATGTTTACATGTTGATAAGAAATCATCTTACACCAAGATATCAAAAAAGAAATA 2280
Qy 761 LeuAlaPheTyrHisLysHisGlnValAenlleLeuLeuAenAenAspLleSerTyrTyr 780
Db 2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATAATATATATCTCATATTTAC 2340
Qy 781 ThrSerAenArgLeuIleLysThrGluAlaHisLeuSerAenlleAenLysLeuSerGln 800
Db 2341 ACAGTAATAGATTAAATAAATACTGAGCGCATTTTAAGTAATATTAATAAATTAAGTCAG 2400
Qy 801 LeuAenLeuAenCysGluTyrIleIlePheAenHleAspSerLeuPheValLysAen 820
Db 2401 TTAATCTAAATTTGTAATATACATCATTTTGTATATCATGACAGCTATTCGTTAAAAAT 2460
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAenPheSerAlaLeuThrHis 840
Db 2461 GACAGCTATGCTTATATGAAAAATATGATGTCGCATGAATTTCTCAGCATTAACACAT 2520
Qy 841 AspTrpIleGluLysIleAenAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2521 GATTGGATCGAGAAAATCAATCGCATCCACCATTTAAAAAGCTCATTTAAAACTTATTTT 2580
Qy 861 AenAenAenAenAenLeuLysSerMetAenValLysGlyValSerGlnGlyMetPheMetThr 880
Db 2581 AATGCAATGACTTAAAGATATGAATGTGAAGGGCATCAACAGGTATGTTATGACG 2640
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900
Db 2641 TATGCGCTAGCGCATGAGCTTCGACGATTTATTAAGAAGTCATCACATCTTGCCAGTCA 2700
Qy 901 IleAspSerValProGluTyrAenThrGluAenPheIleTrpPheGlnPheAlaLeuLeu 920
Db 2701 ATTGATAGTGTCCAGATATATACACTGAGGATATTTGTTTCCAATTTGCACTTTTAATC 2760
Qy 921 LeuGluLysLysThrGlyHisValPheAenLysThrSerThrLeuThrTyrMetProTrp 940
Db 2761 TTAGAAAAGAAAACCGCGCATGTATTTAATAAACAATGACCTGACCTATATATGCTTGG 2820
Qy 941 GluArgLysLeuGlnTrpThrAenGluGlnIleGluSerAlaLysArgGlyGluAenlle 960
Db 2821 GAACGAAATTAACATGGCAAAATGAACAAATTTGAAGTGCAGAAAAGAGAGAGAAATATA 2880
Qy 961 ProValAenLysPheIleIleAenSerIleThrLeu 972
Db 2881 CCTGTTAAACAAGTTCATTATTATTAAGTATAAATCTCTA 2916
RESULT 2
US-10-642-248-1
; Sequence 1, Application US/10642248
; Publication No. US20040132143A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METHO
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 3554.097
; CURRENT APPLICATION NUMBER: US/10/642,248
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
```

```
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/842,484
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-10-642-248-1
Alignment Scores:
Pred. No.: 0 Length: 2920
Score: 5108.00 Matches: 972
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-10-642-248-2 (1-972) x US-10-642-248-1 (1-2920)
Qy 1 MetAenThrLeuSerGlnAlaIleLysAlaTyrAenSerAenAspTyrGlnLeuAlaLeu 20
Db 1 ATGATATCATTTATACAGCAATATAACAGCATATACAGCAATGATATCAATATGACATC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTTATTTGAAAAGTCGCGCAATCTATGACGCAAAATTTGTTGAATTTTCAAAATTACC 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen 60
Db 121 AAATGCAAAAGAAAACCTCTCAGCACATCTCTCTGTTAAATCAGCACATCTTTCTGTAAAT 180
Qy 61 LysGluGluLysValAenValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAAGAAGAAAAGTCAATGTTTGCATAGTCCGTTAGATATTGCAACACACACTGTTACTT 240
Qy 81 SerAenValLysLysLeuValLeuSerAspSerGluLysAenThrLeuLysAenLysTrp 100
Db 241 TCCACGCTAAAAAATTTAGTACTTTTCTGACTCGGAAAAAACACGCTTAAAAAATAAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTTGCTCACTGAGAAGAAAATCTGANAATGCGGAGGTAAGACGCGTCCGCTTTGATCCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAenAspPheThr 140
Db 361 AAAGATTTTCCCAAGATCTGGTTTATGCGCTTTACCTGATCATGTTAATGATTTTACA 420
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 421 TGGTACAAAAAGCGAAGAAAAGACTTGGCATAAAAACCTGAAACATCAACATGTTGTCTT 480
Qy 161 SerIleValThrThrPheAenArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATGCTTACCAACATTCATCGACCAAGCAATTTTATGATTTACATTTAGCCTGTTA 540
Qy 181 ValAenGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATTCGTGACAGATGATGCTAGTAGMA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAenLysLeuAspIleArgTyrValArgGln 220
```



Db 601 |||||GATCTATACCGATCATTCGCCAATATGAAATAAATGGATATTCGCTACGTCAGACAA 660  
Qy 221 LysAspAenGlyPheGlnAlaSerAlaAArgAenMetGlyLeuAArgLeuAlaLysTyr 240  
Db 661 AAAGATAACGGTTTCAAGCCAGTGGCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 720  
Qy 241 AspPheIleGlyLeuLeuAapCysAspMetAlaProAenProLeuTyrValHisSerTyr 260  
Db 721 GACTTTTATGGCTTACTCGAATGATGATGGCGCAATCAATATGGGTTCAATCTTAT 780  
Qy 261 ValAlaGluLeuLeuGluAAspAspLeuThrIleIleGlyProAArgLysTyrIleAasp 280  
Db 781 GTTGCAGAGCTATTAGAGATGATGATTAACATCATTTGGTCCAGAAATATACATCGAT 840  
Qy 281 ThrGlnHisIleAapProLysAAspPheLeuAenAenAlaSerLeuLeuGluSerLeuPro 300  
Db 841 ACACAACATATTGACCCAAAGACTTCTTAAATAACGCGAGTTTGCCTTGAATCATTTACCA 900  
Qy 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAaspTyr 320  
Db 901 GAAGTGAACCAATATAGTTTGGCCGCAAAAGGGGAAGCAAGTTTCTCTGGATTGG 960  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAaspSerProPheAArgPhe 340  
Db 961 CGCTTAGACANATTCGAATAAACAAGAAATCTCCGCTTATCCGATTTCCGCTTTCCGTTTT 1020  
Qy 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPheAasp 360  
Db 1021 TTTGCGGCGGTAATGTTGCTTTCCGCTAAAAATGGCTTAATAAATCCGGTTTCTTTGAT 1080  
Qy 361 GluGluPheAenHisTrpGlyGluAaspValGluPheGlyTyrArgLeuPheAArgTyr 380  
Db 1081 GAGAAATTTAATCACTCGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGCTTAC 1140  
Qy 381 GlySerPhePheLysThrIleAaspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1141 GGTAAGTTCTTTAAACTATTGATGGCATTATGGCTTACCATTCAAGGCCACAGGTANA 1200  
Qy 401 GluAenGluThrAaspArgGluAlaGlyLysAenIleThrLeuAaspIleMetArgGluLys 420  
Db 1201 GAAATGAAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG 1260  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAaspSerHisIleAenArgValPro 440  
Db 1261 GTCCCTTATATCTATAGAAAATCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
Qy 441 LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAasp 460  
Db 1321 TTAGTTTCAATTTATATCCAGCTTATTAACCTGTGCNAACTATATTTCAACGTTGCGTAGAT 1380  
Qy 461 SerAlaLeuAenGlnThrValValAaspLeuGluValCysIleCysAenAaspGlySerThr 480  
Db 1381 AGTGCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTACAGCTGTTCAACA 1440  
Qy 481 AspAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet 500  
Db 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTATTAATCTCTAGGGTACGGATCATG 1500  
Qy 501 SerLysProAenGlyGlyIleAlaSerAlaSerAenAlaAlaValSerPheAlaLysGly 520  
Db 1501 TCTAAACCAATATGGCGAATAGCTTCAGATCAATATGACGCCGTTTCTTTTGTCTAAGGT 1560  
Qy 521 TyrTyrIleGlyGlnLeuAaspSerAaspTyrLeuGluProAaspAlaValGluLeuCys 540  
Db 1561 TATTACATTTGGCAGTTAGATTTCAGATGATTTCTTGAGCTGTATGCGAGTTTGAACCTGTGT 1620  
Qy 541 LeuLysGluPheLeuLysAaspLysThrLeuAlaCysValTyrThrAenAArgAenVal 560  
Db 1621 TTAAGAAGAAATTTTAAAGATATAAACCGCTAGCTGTGTGTTTATACCACTTAATAGAAACGTC 1680  
Qy 561 AenProAaspGlySerLeuIleAlaAenGlyTyrAenTyrProGluPheSerArgGluLys 580

Db 1681 AATCCGGATCGTAGCTTAATCGCTAATGGTTACAATTTGGCCAGAAATTTTTCACGAGAAAAA 1740  
Qy 581 LeuThrThrAlaMetIleAlaHisHisPheAArgMetPheThrIleArgAlaTyrHisLeu 600  
Db 1741 CTCACAAACCGCTATGATGCTCCACTTTAGAAATGTTTACGATTAGAGCTTGGCATTTA 1800  
Qy 601 ThrAaspGlyPheAenGluLysIleGluAAspAlaValAaspTyrAaspMetPheLeuLysLeu 620  
Db 1801 ACTGATGGATTCAATGAAAATTTGAAAATCGCGTAGACTATGACATGTTCTCTCAAACTC 1860  
Qy 621 SerGluValGlyLysPheLysHisLeuAenLysIleCysTyrAenArgValLeuHisGly 640  
Db 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT 1920  
Qy 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValValAen 660  
Db 1921 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAACCATTTTGTGTAGTCAAT 1980  
Qy 661 GlnSerLeuAenAArgGlnGlyIleThrTyrTyrAenTyrAaspGluPheAaspAaspLeuAasp 680  
Db 1981 CAGTCATTAATATAGACAGGCATCACTTATTAATTAATGACGAATTTGATGATTTAGAT 2040  
Qy 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluGluIleAaspIleLeu 700  
Db 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA 2100  
Qy 701 LysAaspIleLysIleGlnAenLysAaspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2101 AAAGATATTAAAAATCATCCAGAAATAAGATGCCAAAATCCGCTCAGTATTTTTTATCCC 2160  
Qy 721 AenThrLeuAenGlyLeuValLysLysLeuAenAenIleIleGluTyrAenLysAenIle 740  
Db 2161 AATACATTAACCGCTTAGTGAATAAACAATTAACAATATTATTGATTAATATAAATAATA 2220  
Qy 741 PheValIleValLeuHisValAaspLysAenHisLeuThrProAaspIleLysLysGluIle 760  
Db 2221 TTCGTTATTGTTCTACATGTTGATAAGATCATCTTACACACAGATATCAAAAAAGAAATA 2280  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAenIleLeuAenAenAaspIleSerTyrTyr 780  
Db 2281 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATTAATGATATCTCATATTAC 2340  
Qy 781 ThrSerAenAArgLeuIleLysThrGluAlaHisLeuSerAenIleAenLysLeuSerGln 800  
Db 2341 ACAGTAAATAGATTAAATAAATCTGAGCGCATTTAAGTAAATTAATTAATTAAGTCAG 2400  
Qy 801 LeuAenLeuAenCysGluTyrIleIlePheAaspAenHisAaspSerLeuPheValLysAen 820  
Db 2401 TTAATCTAAATTTGTGAATACATCAATTTTGTGAATCATGACAGCTTATTCGTTAAAAAT 2460  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAaspValGlyMetAenPheSerAlaLeuThrHis 840  
Db 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCCGCATGAATTTCTCAGCATTAACACAT 2520  
Qy 841 AspTrpIleGluLysIleAenAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2521 GATTGGATCGAGAAATCAATGGCATCCACCATTTTAAAGCTCATTAACCTATTTT 2580  
Qy 861 AenAaspAenAaspLeuLysSerMetAenValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2581 AATGACAATGACTTAAAAAGTATGAATGTGAAGGGGCATCACAAAGGTATGTTTATGACG 2640  
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2641 TATGCGCTAGCGATGAGCTTCTGACGATTAATAAGAAAGTCATCACTCTGCGCAGTCA 2700  
Qy 901 IleAaspSerValProGluTyrAenThrGluAaspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2701 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCATTTTGCATTTTAAATC 2760  
Qy 921 LeuGluLysLysThrGlyHisValPheAenLysThrSerThrLeuThrTyrMetProTyr 940  
Db 2761 TTAGAAAAAGAAAACCGGCCATGTATTTAATAAAACATCGACCTGACTTATATGCTTGG 2820

Qy 941 GluArgLysLeuGlnTrrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Db 2821 GAACGAAATTTACAAATGACAAATTAACAAATTTGAAGTGCAGAAAGGAGAAATATA 2880  
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2881 CCTGTTAAAGTTCAATTTAATAGTATATACTCTA 2916

RESULT 3  
US-10-011-768B-8  
; Sequence 8, Application US/10011768B  
; Publication No. US20030073221A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kehana  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/10/011,768B  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pastuerella Multocida  
US-10-011-768B-8

Alignment Scores:  
Pred. No.: 0 Length: 2937  
Score: 5108.00 Matches: 972  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-642-248-2 (1-972) x US-10-011-768B-8 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 19 ATGAATACATATTATCAAGCAATAAAGCATATATAAGCAATAGACTATCAATATGACATC 78  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 79 AAATTTATTTGAAGTTCGGCGGAATCTATGACGCGMAAATTTGTTGAATTTCAAAATTACC 138  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 139 AAATGCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTCTTCTGTAAT 198  
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 199 AAAGAAGAAAAAGTCAATGTTTGGCATAGTCCTGATATTTGCAACACACTGTACTT 258  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 259 TCCACGTAATAAATAATAGTACTTCTGACTCGGAAAAAACAACGTTAAATAAATG 318  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 319 AAATGCTCACTCAGAGAAGAAATCTGAAATGCGAGGTAAAGAGCGTCCGCTTGTACCA 378  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 379 AAAGATTTTTCCCAAGATCTGGTTTTAGCGCCTTTACCTGATCATGTTAATGATTTTACA 438  
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160

439 TGGTACAAAAGCGAAGAAAAGACTTGGCATAAAACCTGAAACATCAACATGTTGGTCTT 498  
161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
499 TCTATTATCTGTACCAATTCATCGACAGCAATTTTATCGATTATACATTAGCGCTGTTA 558  
181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
559 GTAAACCAAAAAACACATTATCCCGTTTGAAGTTATCTGTGACAGATGATGGTAGTCAGAA 618  
201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
619 GATCTATACCGATCATTCGCCAATATGAATAATTAATTTGATATTCGCTAGCTCAGACAA 678  
221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
679 AAAGATAACGGTTTTCAAGCCAGTCGCCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 738  
241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrrValHisSerTyr 260  
739 GACTTTATTTGGCTTACTCGACTGTGATGTCGCCAATCCATTTAGGGTTTCATTTCTTAT 798  
261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
799 GTTCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGTCCTCAAGAAAAATACATCAT 858  
281 ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300  
859 ACACAACATATTGACCCCAAGACTTCTTAAATTAACGCGAGTTTGTCTTGAATCATTTACCA 918  
301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
919 GAAGTGAACCAATAATAGTTGTCGCCGCAAAAGGGAAGAACAGTTTCTCTGGATTGG 978  
321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
979 CGCTTAGAACAAATTCGAAAAAACAGAAATCTCCGCTTATCCGATTCGCCCTTTCGGTTT 1038  
341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
1039 TTTGCGGCGGTAAATTTGCTTTTCGCTAAAAAATGGCTAAATAATCGGTTTCTTCTGAT 1098  
361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
1099 GAGCAATTTAATCACTGGGTGAGAGATGTGGAATTTGGATATTCGCTTATTCGCTTAC 1158  
381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
1159 GGTAGTTTCTTTAAACACTATTGATGGCATTTATGGCTTACCATCAAGACCCACAGTAAA 1218  
401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
1219 GAAATGAAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1278  
421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
1279 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTGCGCATATCAATAGAGTACCT 1338  
441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
1339 TTAGTTTCAATTTATATCCAGCTTAACTGTGCAAACTATTATCAACGTTTCGCTAGAT 1398  
461 SerAlaLeuAsnGlnThrValValAspLeuValCysIleCysAsnAspGlySerThr 480  
1399 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAGCATGTTCAACA 1458  
481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
1459 GATATACCTTAGAAGTGCATCAATAGCTTTTATGTTGTAATAATTCCTTAGGCTAGCATG 1518  
501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
1519 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACGCGGTTTCTTTTCTTAAGGT 1578

```
Qy 521 TTTyrTleGlyGlnLeuAaspSerAaspTyrLeuGluProAaspAlaValGluLeuCys 540
Db 1579 TATTACATTGGCGAGTTAGATTTCAGATTATCTTGAGCGCTGATGCGAGTTGAACCTGTGT 1638
Qy 541 LeuLysGluPheLeuLysAaspLysThrLeuAlaCysValTyrThrAsnArgAasnVal 560
Db 1639 TTTAAAGAAATTTTAAAGATATAAACCGCTAGCTTGCTGTTTATACCATTAATAGNAACGTC 1698
Qy 561 AsnProAaspGlySerLeuIleAlaAasnGlyTyrAenTrpProGluPheSerArgGluLys 580
Db 1699 AATCCGGATGGTAAATCGCTAAATGGTTTACAATTTGGCCAGAAATTTTCACGAGAAAAA 1758
Qy 581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1759 CTCACACGGCTATGATTGCTCACCATTTTAGAATTTGTCAGATTAGAGCTTGGCATTTA 1818
Qy 601 ThrAaspGlyPheAenGluLysIleGluAasnAlaValAaspTyrAapMetPheLeuLysLeu 620
Db 1819 ACTGATGGATTCAATGAANAATTTGAANAATGCCGTAGACTATGACATGTTCCCTCAAACTC 1878
Qy 621 SerGluValGlyLysPheLysHisLeuAasnLysIleCysTyrAenArgValLeuHisGly 640
Db 1879 AGTGAAGTTGGAAATTTAAACATCTTAAATAAAATCTGCTATAACCGTGTATTACATGTT 1938
Qy 641 AaspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValAasn 660
Db 1939 GATAACACATCAATTAAGAACTTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1998
Qy 661 GlnSerLeuAenArgGlnGlyIleThrTyrTyrAenTyrAapGluPheAaspAaspLeuAasp 680
Db 1999 CAGTCATTAAATGACACAGGCATCACTTATTAATTAATGATGCGAATTTGATGATTTAGAT 2058
Qy 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluGluIleAaspIleLeu 700
Db 2059 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2118
Qy 701 LysAaspIleLysIleGlnAasnLysAaspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2119 AAAGATATTAATAATCATCCAGAAATAAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2178
Qy 721 AsnThrLeuAenGlyLeuValLysLysLeuAasnAenIleIleGluTyrAasnLysAasnIle 740
Db 2179 AATACATTAACGGCTTAGTGAAAAAATACTAAACAATATATTGATATATATAAANAATATA 2238
Qy 741 PheValIleValLeuHisValAaspLysAasnHisLeuThrProAaspIleLysLysGluIle 760
Db 2239 TTCGTATTGTTCTACATGTTGTATAAGAAATCATCTTACCCAGATATCAAAAAAGAAATA 2298
Qy 761 LeuAlaPheTyrHisLysHisGlnValAasnIleLeuAasnAenAaspIleSerTyrTyr 780
Db 2299 CTAGCCCTTCTATCATATAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATATAC 2358
Qy 781 ThrSerAasnArgLeuIleLysThrGluAlaHisLeuSerAenIleAasnLysLeuSerGln 800
Db 2359 ACGAGTAAATAGATTAAATAAAACCTGAGCGCGATTAAAGTAAATATATAAATTAAGTCAG 2418
Qy 801 LeuAasnLeuAenCysGluTyrIleIlePheAaspAasnHisAaspSerLeuPheValLysAasn 820
Db 2419 TTTAAATCTAAATTTGTAATACATCATTTTTTGATAATCATGACAGCCATTTCGTTAAAAAT 2478
Qy 821 AaspSerTyrAlaTyrMetLysLysTyrAaspValGlyMetAasnPheSerAlaLeuThrHis 840
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538
Qy 841 AspTrpIleGluLysIleAasnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2539 GATTGGATCGAGAAAAATCAATCGGCATCCACATTTTAAAAAGCTCAATTAACATTTATTTT 2598
Qy 861 AasnAaspAenAaspLeuLysSerMetAasnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2599 AATGACAATGACTTAAAAAAGTATGAATGTGAAAGGGGCATCACAAAGGTATGTTTATGACG 2658
```

```
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCAATCACAATCTTCCAGTCA 2718
Qy 901 IleAaspSerValProGluTyrAenThrGluAaspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2719 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCCAATTTGCACTTTAAATC 2778
Qy 921 LeuGluLysLysThrGlyHisValPheAasnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2779 TTAGAAAAAGAAAAACCGGCATGTGATTAAATAAAACATCGACCCCTGACTTATATGCTTGG 2838
Qy 941 GluArgLysLeuGlnTrpThrAenGluGlnIleGluSerAlaLysArgGlyGluAasnIle 960
Db 2839 GAACGAAAAATTACAAATGGACAAATGAACAAATTTGAAAGTGCAAAAGAGAGAAATATA 2898
Qy 961 ProValAasnLysPheIleIleAasnSerIleThrLeu 972
Db 2899 CCTGTTAAACAAGTTTCATTATTATATAGTATAACTCTA 2934

RESULT 4
US-10-011-771B-8
; Sequence 8, Application US/10011771B
; Publication No. US20030082780A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H.
; APPLICANT: DeAngelis, Paul
; APPLICANT: Kumari, Kshama
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof
; FILE REFERENCE: 3554.011
; CURRENT APPLICATION NUMBER: US/10/011,771B
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 09/178,851
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: US 60/064,435
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Pastuerella Multocida
US-10-011-771B-8

Alignment Scores:
Pred. No.: 0 Length: 2937
Score: 5108.00 Matches: 972
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-642-248-2 (1-972) x US-10-011-771B-8 (1-2937)
Qy 1 MetAenThrLeuSerGlnAlaIleLysAlaTyrAasnSerAasnAapTyrGlnLeuAlaLeu 20
Db 19 ATGAATACATTATCACAAAGCAATAAAGCAATATAACAGCAATGACTATCAATTAGCACTC 78
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATTTTCAAAAAGTCGGCGGAAATCTATGGACGGAAAAATTTGTTGAATTTCAAAATTACC 138
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAasnSerAlaHisLeuSerValAasn 60
Db 139 AAATGCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTCTTGTAAAT 198
Qy 61 LysGluGluLysValAenValCysAaspSerProLeuAaspIleAlaThrGlnLeuLeuLeu 80
Db 199 AAAGAAAGAAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACACTGTTACTT 258
Qy 81 SerAasnValLysLysLeuValLeuSerAaspSerGluLysAenThrLeuLysAasnLysTrp 100
Db 259 TCCAAACGTAAAAAATTTAGTACTTTTCTGACTCGGAAAAAACACGTTAAAAAATAAATGG 318
```

101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaArgAlaValAlaLeuValPro 120 QY  
139 AAATGTCTCACTGAGAGAAATCTGAAATCGGAGGTAGAGCGGTGTTACCA 378 Db  
121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140 QY  
379 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTGTAATGATTTTACA 438 Db  
141 TrpTyrLysLysArgLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160 QY  
439 TGGTACAAAAGCGAAGAAAGACTTGGCATAAAACCTGAACATCAATGTTGGGCTT 498 Db  
161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180 QY  
499 TCTATATTCGTTCACACATTCATCGACCAACATTTTATCGATTACATTAGCCTGTTA 558 Db  
181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200 QY  
559 GTAAACCAAAAAACACATTTACCCGTTTCAAGTTTATCGTGACAGATGATGTGTACAGAA 618 Db  
201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220 QY  
619 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGATATTCGCTACGTCAGACAA 678 Db  
221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuAlaGluAlaLysTyr 240 QY  
679 AAAGATAACGGTTTTCAAGCAGTCGCCCTCGAATATGGGATTAACGCTTAGCAAAATAT 738 Db  
241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260 QY  
739 GACTTATTTGGCTTACTCGACTGTGATATGGCCCAATCCATTATGGTTTCATTTCTTAT 798 Db  
261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280 QY  
799 GTTCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAAAGAAATATACATCAT 858 Db  
281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300 QY  
859 ACACAACATATTGACCCAAAAGACTTCTTAATAACGCGAGTTTCTGTTGMAATCATTACCA 918 Db  
301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320 QY  
919 GAAAGTGAACCAATTAATAGTTGTCGCCAAAAGGGGAAGAACAGTTTCTCTGGATTGG 978 Db  
321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340 QY  
979 CGCTTAGAACATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTTCCGTTTT 1038 Db  
341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPheAsp 360 QY  
1039 TTTGCGCGGGTAAATGTTGCTTTCGCTTAAAAATGGCTAAATAATCCGGTTCTTTGAT 1098 Db  
361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380 QY  
1099 GAGGAATTTAATCACTGGGTGAGAGAGATGTGGAAATTTGGATATCGCTTATTCGTTAC 1158 Db  
381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400 QY  
1159 GGTAGTTTCTTTAAACATTTGATGGCATTATGGCTACCATCAAGAGCCACAGGTAAA 1218 Db  
401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420 QY  
1219 GAAAAATGAACCGATCGTGAACGGGAAAAATAATTTACGCTCGATATTATGAGAGAAAG 1278 Db  
421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440 QY  
1279 GTCCCTTATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGATACCT 1338 Db  
441 LeuValSerIleTyrProLysThrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460 QY  
1339 TTAGTTTCAATTTATATCCAGCTTATACTGTGCACAACTATATTCAACGTTGCGTAGAT 1398 Db

461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480 QY  
1399 AGTGCACCTGAATCAGACTGTTGTTGATCTCAGGTTTGTATTGTTAAACGATGGTTCAACA 1458 Db  
481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500 QY  
1459 GATAATACCTTAGAAGTGATCAATTAGCTTTATGGTAAATTAATCTCTAGGGTACGCATCATG 1518 Db  
501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520 QY  
1519 TCTAAACCAATGCGGAATAGCCTCAGCTCAATGCAATGCAGCCGTTTCTTTTGTCTAAAGGT 1578 Db  
521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540 QY  
1579 TATTACATTCGGCAGTTAGATTTCAGATTATCTTCAGCGCTGATGCGATTGAATCTGTGT 1638 Db  
541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560 QY  
1639 TTAAGAAGATTTTAAAGATTAACCGCTAGCTGTGTTTATACCACTTATAGAAACGTC 1698 Db  
561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580 QY  
1699 AATCCGATGCTAGCTTAATCGCTTAATGGTTTACAATTTGGCCAGAAATTTTCACGAGAAAA 1758 Db  
581 LeuThrThrAlaMetIleAlaHisIlePheArgMetPheThrIleArgAlaTrpHisLeu 600 QY  
1759 CTCACAACGGCTATGATTGCTCACCACTTTAGAAATGTTTCAAGATTAGAGCTTGGCATTTA 1818 Db  
601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620 QY  
1819 ACTGATGGATTCAATGAAAAAATTTGAAATGCCGTAGACTATGACATGTTTCTCNAACTC 1878 Db  
621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640 QY  
1879 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1938 Db  
641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660 QY  
1939 GATAACACATCAATTAAGAAACTTTGGCATTTCAAAGAAAAAACCAATTTTGTGTAGTCAAT 1998 Db  
661 GlnSerLeuAsnArgGlnGlyIleThrTyrThrAsnTyrAspGluPheAspAspLeuAsp 680 QY  
1999 CAGTCATTAAATAGCAAGGCATTAATCTTATTAATATATGCAATTTTGATGATTTAGAT 2058 Db  
681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700 QY  
2059 GAAAGTAGAAGATATTTTCAATAAACCCTGATATCAAGAAGACAGATTGATATCTTA 2118 Db  
701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720 QY  
2119 AAAGATATTAATAATCATCCAGATAAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 2178 Db  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740 QY  
2179 AATACATTAACCGCTTAGTGAAAAAACTAAACAATATTTTGAATATAATAAAAAATA 2238 Db  
741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760 QY  
2239 TTCGTTATGTTCTACATGTTGTAAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2298 Db  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780 QY  
2299 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2358 Db  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800 QY  
2359 ACGAGTAATAGATTAAATAAAAACTGAGCGCATTTTAAGTAATTAATAAAAAATAAGTCAG 2418 Db  
801 LeuAsnLeuAsnCysGluTyrIlePheAspAsnHisAspSerLeuPheValLysAsn 820 QY  
2419 TTAATCTAAATTTGTAATACATCATTTTGTGTAATCATGACAGCTTATTCGTTAAAAAT 2478 Db  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840 QY

```
Db      2479  GACAGCTATGCTTATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538
Qy      841  AspTrpIleGluLysIleAsnAlaHisProPhelYsLysLeuIleLysThrTyrPhe 860
Db      2539  GATTGGATCGAGAAATCAATGCGCATCCACCATTAAAAAGCTCATTTAAACCTTATTTT 2598
Qy      861  AsnAspIleAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlnGlyMetPheMetThr 880
Db      2599  AATGACAATGACTTTAAAAAGTATGAATGTGAAGGGGCATCACAAGGTATGTTTATGACG 2658
Qy      881  TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db      2659  TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCATCACAATCTTGCCAGTCA 2718
Qy      901  IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db      2719  ATTGATAGTGTGCGAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACATTTTAATC 2778
Qy      921  LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db      2779  TTAGAAAAGAAAACCGGCCATGTATTTAATAAAAAACATCGACCCCTGACTTATATGCGCTTG 2838
Qy      941  GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db      2839  GAACGAAATATACAAATGGACAAATGAACAAATTTGAAAGTGCAAAAGAGGAGAAAATATA 2898
Qy      961  ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db      2899  CCTGTTAAACAAGTTTCATTATTAATAGTATAACTCTA 2934

RESULT 5
US-11-109-855-8
; Sequence 8, Application US/11109855
; Publication No. US20050202540A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H.
; APPLICANT: DeAngelis, Paul
; APPLICANT: Kumari, Kshana
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof
; FILE REFERENCE: 3554.011
; CURRENT APPLICATION NUMBER: US/11/109,855
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US 09/178,851
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: US 60/064,435
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Pastuerella Multocida
US-11-109-855-8

Alignment Scores:
Pred. No.: 0 Length: 2937
Score: 5108.00 Matches: 972
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-642-248-2 (1-972) x US-11-109-855-8 (1-2937)

Qy      1  MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db      19  ATGAATACATTTATCACAGCAATTAAGCATATACAGCAATGATCATATTAAGCACTC 78
Qy      21  LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db      79  AAATTTTGAAGAATCGCGGAAATCTATGCGAGGAAATTTGTTGAATTTCAATTAACC 138
```

```
Qy      41  LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db      139  AAATGCAAGAAAAAATCTTCAGCACATCTCTTGTTAATTCAGCACATCTTCTCTGAAT 198
Qy      61  LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db      199  AAAGAAGAAAAAGTCAATGTTTCGATAGTCCGTTAGATATTGCAACAACAACCTGTACTT 258
Qy      81  SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db      259  TCCAACGTTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAATGG 318
Qy      101  LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db      319  AAATTGCTCACTGAGAAGAAATCTGAAATTCGGAGGTAAAGCGGTGCGCCTTTGTACCA 378
Qy      121  LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db      379  AAAGATTTTCCCAAGATCTGGTTTTAGCGCCTTTTACCTGATCATGTTAATGATTTTACA 438
Qy      141  TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db      439  TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAAACCTGAACATCAACATGTGTGGCTT 498
Qy      161  SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db      499  TCTATTATCGTTACAACATTCATCCAGCAGCAATTTTATCGATTACATTAGGCTGTTTA 558
Qy      181  ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db      559  GTAAACCAAAAAACACATTACCCTGTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA 618
Qy      201  AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db      619  GATCTATACCGCATCTTCGCCAATATGAAAAATAAATTCGATATTCGCTACGTCAGACAA 678
Qy      221  LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db      679  AAAGATAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATACGCTTAGCNAATAT 738
Qy      241  AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260
Db      739  GACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTATGGGTTTCATCTTAT 798
Qy      261  ValAlaGluLeuLeuAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db      799  GTTGCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAAAGAAATACATCAT 858
Qy      281  ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db      859  ACACAACATATTGCCCAAAAGACTTCTTAATTAACGCGAGTTTGCTTGAATCATTTACCA 918
Qy      301  GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320
Db      919  GAAGTGAARACCAATAATAGTGTTCGCGCAAAAGGGGAGGAACAGTTTCTCTGGATTGG 978
Qy      321  ArgLeuGluGlnPheGlnLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db      979  CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTT 1038
Qy      341  PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360
Db      1039  TTTGCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGCTAATAATCCGGTTTCTTTGAT 1098
Qy      361  GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db      1099  GAGGAATTTAATCACATGGGCGTGAGAGATGTGGAATTTTGGATATCGCTTATTCCTCGTTAC 1158
Qy      381  GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db      1159  GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCAGGTAAA 1218
Qy      401  GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
```

Db 1219 GAAATGAAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG 1278  
Qy ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGAAATTCGCATATCAATAGAGTACCT 1338  
Qy LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1398  
Qy SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1399 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTGTAACGATGTTCAACA 1458  
Qy AspAsnThrLeuGluValIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleMet 500  
Db 1459 GATAATACCTTAGAAGTATGATCAATAGCTTTATGTTGTAATATCCTAGGGTACGCATCATG 1518  
Qy SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaIaValSerPheAlaLysGly 520  
Db 1519 TCTTAACCAATGGCGAATAGCCTCAGCATCAATGACGCGTTCCTTTGCTAAAGGT 1578  
Qy TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValIleGluLeuCys 540  
Db 1579 TATTACATTTGGCAGCTTAGATTCAGATGATTCATTGAGCCTGATGTCAGTGTGAACGTGT 1638  
Qy LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560  
Db 1639 TTAAGAAGATTTTAAAAAGATAAAACGCTAGCTGTGTGTTATACCACTAATAGAAACGTC 1698  
Qy AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGlyLys 580  
Db 1699 AATCCGATGGTGTATATCTGCTAATGTTACAAATGGCCGAAATTTTCACGAGAAAAA 1758  
Qy LeuThrThrAlaMetIleAlaHisIlePheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1759 CTCACACGGCTATGATGCTCACCATTTAGAAATGTTACAGATTTAGAGCTTGGCATTTA 1818  
Qy ThrAspGlyPheAsnGlyLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCATCAATGAAAAATGAAAAATGCGTAGACTATGACATGTTCTCCAACTC 1878  
Qy SerGluValGlyLysPheLysIleLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGTT 1938  
Qy AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1939 GATAACACATCAATTAAGAACTTGGCATTTCAAAAGAAAAACCAATTTGTTGTTAGTCAAT 1998  
Qy GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
Db 1999 CAGTCATTAATAGACAGGCATAACTTATTATTAATTTATGACGAATTTGATGATTTAGAT 2058  
Qy GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu 700  
Db 2059 GAAAGTAGAAGTATATTCTCAATAAAACCGCTGAATATCAAGAGAGATGATATCTTA 2118  
Qy LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2119 AAGATATTTAAATCATCATCAAGATAAAGATGCCAAATCGCAGTCAGTATTTTATCCC 2178  
Qy AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2179 AATACATTAACCGCTTAGTGAATAAACTAAACAATATTATTGAATATATAAAAAATA 2238  
Qy PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysGlyLeu 760  
Db 2239 TTGCTTATTGTTCTACATGTTGATAAGATCATCTTACACCATGATATCAAAAAAGATA 2298  
Qy LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780

Db 2299 CTAGCCTTCTATCATATAAACATCAAGTGAATATTTTACTTAATATGATATCTCATATTAC 2358  
Qy ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2359 ACGAGTAATAGATTAAATAAAAACTGAGCGCATTTAAGTAAATATTAATAAATTAAGTCAG 2418  
Qy LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2419 TTAATCTAAATTTGTGAATACATCATTTTGTGATTAATCATGACACCTTATTCGTTAAANAT 2478  
Qy AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2479 GACAGCATGCTTATATGAANAATATGATGTCGCGCATGAATTTCTCAGCATTAACACAT 2538  
Qy AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2539 GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTAAAAAGCTCATTTAAAACTTATTTT 2598  
Qy AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2599 AATGACCAATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGACG 2658  
Qy TyrAlaLeuAlaHisGluLeuLeuThrThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2659 TATCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAGTCATCACATCTTGGCAGTCA 2718  
Qy IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2719 ATTGATAGTGGCAGAAATATAACACATGAGATATTTGGTTCCAATTTGCACATTTTAATC 2778  
Qy LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
Db 2779 TTAGAAAAAGAAAAACCGCCCATGTATTTAATAAAAAACATCGACCTGACTTATATGCTTGG 2838  
Qy GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Db 2839 GAACAAATTTACATGACAAATGAACAAATTTGAAGTGCANAAAGAGGAGGAAATATA 2898  
Qy ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2899 CTTGTTAAACAGTTTCATTTAATAGTATACTCTA 2934  
RESULT 6  
US-10-326-185-94  
; Sequence 94, Application US/10326185  
; Publication No. US20030175902A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloma, Alan  
; APPLICANT: Behr, Regine  
; APPLICANT: Widner, William  
; APPLICANT: Tang, Maria  
; APPLICANT: Sternberg, David  
; APPLICANT: Brown, Stephen  
; TITLE OF INVENTION: Methods for Producing Hyaluronan In a Recombinant Host Cell  
; FILE REFERENCE: 10341.200-US  
; CURRENT APPLICATION NUMBER: US/10/326,185  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/342,644  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 94  
; LENGTH: 2916  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2916)  
; OTHER INFORMATION:  
US-10-326-185-94  
Alignment Scores: 0 Length: 2916  
Pred. No.:



Score:	5104.00	Matches:	971
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.90%	Mismatches:	0
Query Match:	99.92%	Indels:	0
DB:	6	Gaps:	0
US-10-642-248-2 (1-972) x US-10-326-195-94 (1-2916)			
Qy	1	MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu	20
Db	1	ATGAATACATTTATCACAGCAATATAAGCAATATAACAGCAATGACTATCAATAGCACTC	60
Qy	21	LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr	40
Db	61	AAATTATTGAAAGTGGCGGAAATCTATGGACGGAAATTTGTGAATTTCAAAATPACC	120
Qy	41	LysCysLysLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn	60
Db	121	AAATGCCAGAAAACCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTCTGTAAAT	180
Qy	61	LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeu	80
Db	181	AAAGAAGAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT	240
Qy	81	SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr	100
Db	241	TCCAACGTAAATAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTTAAAAAATAAATGG	300
Qy	101	LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValpro	120
Db	301	AAATTGCTCACTGAGAGAAATCTGAAANAATGCGAGAGGTAGAGCGGTGCGCCCTGTACCA	360
Qy	121	LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr	140
Db	361	AAAGATTTTCCCAAGATCTGTTTTAGCGCCTTTTACTGATCATCTGTTAATGATTTTACA	420
Qy	141	TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu	160
Db	421	TGGTACAAAAGCGAAAGAAAGACTTGGCATAAACCCTGAAACATCAATCATGTTGGTCTT	480
Qy	161	SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu	180
Db	481	TCATATTTCGTTACACATTCATCGACCACCAATTTTATCGATTACATTAGCCTGTTTA	540
Qy	181	ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu	200
Db	541	GTAACCAAAAACACATTTACCCGTTTGAAGTTATTCGTGACAGATGATGGTAGTCAGGAA	600
Qy	201	AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln	220
Db	601	GATCTATCACCAGATCATTCGCAATATGAAATAAATTTGGATATTCGCTAGCTCAGACAA	660
Qy	221	LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuA:qLeuAlaLysTyr	240
Db	661	AAAGATTAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT	720
Qy	241	AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr	260
Db	721	GACTTTATGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGTTTCATTTAT	780
Qy	261	ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp	280
Db	781	GTTTCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGTCCTCAAGAAAAATACATCGAT	840
Qy	281	ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro	300
Db	841	ACACAACATATGACCCAAAAGACTTCTTAATAATACCGGAGTTTCTGTTGAATCATTTACCA	900
Qy	301	GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr	320
Db	901	GAAGTGAACCAATAATAGTGTTCGCCCAAAAGGGGAAGCAACAGTTTCTCTGGATTGG	960
Qy	321	ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe	340
Db	961	CGCTTAGAACATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCCTTCCGTTTT	1020
Qy	341	PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp	360
Db	1021	TTTGGCGGGTAATGTTGCTTTTCCGCTAAAAAATGGCTAAATAAATCCGTTTTCTTTGAT	1080
Qy	361	GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr	380
Db	1081	GAGGAATTTAATCACCTGGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGGTTAC	1140
Qy	381	GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys	400
Db	1141	GGTAGTTTTCTTTAAAACTATTGATGGCATTAGCCCTACCATCAAGAGCCACCAGGTAAA	1200
Qy	401	GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys	420
Db	1201	GAAAAATGAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG	1260
Qy	421	ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro	440
Db	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT	1320
Qy	441	LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp	460
Db	1321	TTAGTTTTCAATTTATATCCAGCTTATTAACGTGCAACTATATTCAACGTTGCGTAGAT	1380
Qy	461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480
Db	1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA	1440
Qy	481	AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet	500
Db	1441	GATAAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTTAGGGTACGCATCATG	1500
Qy	501	SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly	520
Db	1501	TCTAACCAANAATGGCGAATAGCCTCAGCATCAANAATGCAGCCGTTCTTTTGTAAAGGT	1560
Qy	521	TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys	540
Db	1561	TATTAACATGGGCAGTTAGATTAGATTGATTATCTTGAGCCTGATGCAGTTGAACCTGT	1620
Qy	541	LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal	560
Db	1621	TTAAAAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTTATACCACATAATAGAAACGTC	1680
Qy	561	AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys	580
Db	1681	AATCCCGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTCACGAGAAAAA	1740
Qy	581	LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrPheLeu	600
Db	1741	CTCACACGGCTATGATGTTGCTCACCACTTTAGAATGTTACAGATTAGAGCTTGGCATTTA	1800
Qy	601	ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu	620
Db	1801	ACTGATGGATTCAATGAAAAAATTTGAAAAATGGCGTAGCATATGACATGTTTCCCTCAAACTC	1860
Qy	621	SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly	640
Db	1861	AGTGAAGTTGGAANAATTTAAACATCTTAATAAATCTGCTATAACCGGTATTACATGGT	1920
Qy	641	AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn	660
Db	1921	GATAACACATCAATTAAGAAACTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT	1980
Qy	661	GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp	680
Db	1981	CAGTCATTAATAAGCAAGGCATAACTTATTATAATTTATGACCAATTTGATGATTTAGAT	2040
Qy	681	GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluLeuAspIleLeu	700



2041 GAAAGTGAAGATATATTTTCAATAAAACCGCTGATATCAAGAGAGATTGATATCTTA 2100  
Db  
701 LysAspIleValIleGluAsnLysAspAlaValIleAlaValSerIlePheTyrPro 720  
Qy  
2101 AAAGATATTAATAATCATCAGAAATAAGATGCCAAATCGGAGTCAGATATTTTATCC 2160  
Db  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Qy  
2161 AATACATTAACGGCTTAGTGAAAAAATCAACCAATATTTATGAATAATAAATAATA 2220  
Db  
741 PheValIleValLeuHisValAspLysAsnHisIleThrProAspIleLysGluIle 760  
Qy  
2221 TTCGTTATTTGTTTACATGTTGATAAGAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
Qy  
2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Db  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Qy  
2341 ACGAGTATAGTATTAATAAACTGAGCGCATTTAAGTAATATTAATAAATTAAGTCAG 2400  
Db  
801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Qy  
2401 TTAATCTAAATTTGTGATACATCATCTTTTGATAATCATGACAGCCTATTGCTTAAAAAT 2460  
Db  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Qy  
2461 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAATTTCTCAGCATTAACAT 2520  
Db  
841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Qy  
2521 GATTGATCGAGAAATCATCGGCATCCACCATTTAAAGACTCATTAACATTTATTT 2580  
Db  
861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Qy  
2581 AATGACATGACTTAAAGATATGAATGTGAAAGGGGCATCAAGGATATGTTATGACG 2640  
Db  
881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Qy  
2641 TATGCGTAGCCGATGAGCTTCGAGATTTATTAAGAAGTCAATCACAATCTTGCCAGTCA 2700  
Db  
901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920  
Qy  
2701 ATTGATAGTGCAGAGATATTAACACTGAGGATATTTGGTTCATTTGACATTTTATC 2760  
Db  
921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940  
Qy  
2761 TTAGAAAAAGAAACCGGCCATGTATTTAATAAAACATCGACCTGACTATATATGCTTGG 2820  
Db  
941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Qy  
2821 GAACGAAAAATTAACAATGGCAAAATGAACAATTTGAAGTGCAAAAGAGGAGAAAAATA 2880  
Db  
961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Qy  
2881 CTTGTTAACAGTTTCATTATTAATAGTATACTCTA 2916  
Db

## RESULT 7

US-11-096-190-8  
; Sequence 8, Application US/11096190  
; Publication No. US20050221446A1  
; GENERAL INFORMATION:  
; APPLICANT: Widner, William  
; APPLICANT: Sloma, Alan  
; APPLICANT: Thomas, Michael D.  
; APPLICANT: Tang, Maria  
; TITLE OF INVENTION: Methods For Producing A Hyaluronic Acid In A Bacillus Cell  
; FILE REFERENCE: 10596.200-US  
; CURRENT APPLICATION NUMBER: US/11/096,190  
; CURRENT FILING DATE: 2005-03-31  
; PRIOR APPLICATION NUMBER: 60/558,507  
; PRIOR FILING DATE: 2004-03-31

; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: Patent in version 3.2

; SEQ ID NO 8  
; LENGTH: 2916  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-096-190-8

Alignment Scores:  
Pred. No.: 0 Length: 2916  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
DB: 10 Gaps: 0

US-10-642-248-2 (1-972) x US-11-096-190-8 (1-2916)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 1 ATGAATACATTTATCACAAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCCTC 60  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 61 AAATTTATTTGAAAAAGTCGCGGAAATCTATGACGCGAAATTTGTGAATTTCAATTTACC 120  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 121 AATGCCAAGAAAAAATCTCAGACATCTTCTGTTAATTCAGCAGATCTTTCTGTAAT 180  
Qy 61 LysGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 181 AAAGAAGAAAAAGTCAATGTTTGGGATAGTCGTTAGATATTGCAACACAATCTGTACT 240  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
Db 241 TCCACGCTAAAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAATGG 300  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 301 AAATGCTCACTGAGAGAAATCTGAAATCGGAGGTAGAGCGGTGCGCTTGTAGCA 360  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 361 AAAGATTTCGCAAGATCTGCTTTTAGCGCTTTACCTGATCATGTTAATGATTTTACA 420  
Qy 141 TrpTyrLysLysArgLysArgLysProGluHisGlnHisValGlyLeu 160  
Db 421 TGGTACAAAAAGCGGAAAAAGACTTGGCATAAACCTGAACATCAACATGTTGGTCTT 480  
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 481 TCTATATCGTTACAACTCAATCGACCAATTTATCGATTACATTAGCCTGTTTA 540  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 541 GTAAACAAAAAACAATTTACCGTTTCAAGTATTCGTGACAGATGATGGTAGTCAGGAA 600  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 601 GATCTTATCACCAGATCATTTGCCCAATATAAATTTGGATATTTCCGTCAGTCAGACAA 660  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 661 AAAGATAACGGTTTTCAGCCGCTGCCCTCGGATATGGGATTTAGCTTACCAAAATAT 720  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
Db 721 GACTTTATTTGGCTTACTCGACTGATGATGCGCCAAATCCATTATGGTTTCACTTCTAT 780  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 781 GTTGCAGAGCTATTAGAAGATGATGATTTAAACAAATCATTTGGTCCCAAGAAAAATACATCGAT 840

Qy 281 ThrGlnHisIleAspProLysAspPheIeuAenAenAlaSerIeuLeuGluSerLeuPro 300  
Db 841 ACAACAATATTGACCCAAAGACTCTCTTAATAACCGGAGTTTGCTTGAATCAATTACCA 900  
Qy 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 901 GAAGTGAACCAATAATAGTTGTCGCCGCAAAAGGGGAGGAACAGTTTCTCTGGATTGG 960  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe 340  
Db 961 CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCCCTTCCGTTTT 1020  
Qy 341 PheAlaAlaGlyAenValAlaPheAlaLysIleTrpIeuAenLysSerGlyPhePheAsp 360  
Db 1021 TTTGCGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATCCGGTTTCTTTGAT 1080  
Qy 361 GluGluPheAenHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1081 GAGGAATTTAATCACTGGGGTGGAGAAGATGTGGAAATTTGGATATCGCTTATTCGGTTAC 1140  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1141 GGTAGTTTCTTTAAACCTATTGATGGCATTATGGCTTACCATCAAGAGCCACCAGGTAAA 1200  
Qy 401 GluAenGluThrAspArgGluAlaGlyLysAenIleThrIeuAspIleMetArgGluLys 420  
Db 1201 GAAATGAAACCGGATCTGGAAGCGGGAAAAAATAATTACGCTCGATATTATGAGAGAAAAG 1260  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAenArgValPro 440  
Db 1261 GTCCCTTATATATAGAAACCTTTTACCATAAGAGATTCGCATATCAATAGATACCT 1320  
Qy 441 LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAsp 460  
Db 1321 TTAGTTTCAATTTATATCCAGCTTATAAATGTGCAAACTATATTCAACGTTCGGTAGAT 1380  
Qy 461 SerAlaLeuAenGlnThrValValAspLeuGluValCysIleCysAenAspGlySerThr 480  
Db 1381 AGTCACATGAATCAGACTGTTGTTGATCTCGAGTTTGTATTGTTAAACGATGGTTCAACA 1440  
Qy 481 AspAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet 500  
Db 1441 GATTAATACCTTAGAAGTGATCAATAGCTTTATGGTAAATAATCTCAGGTACGCATCATG 1500  
Qy 501 SerLysProAenGlyIleAlaSerAenAlaAlaValSerPheAlaLysGly 520  
Db 1501 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCGCGGTTTCTTTTGCTAAAGGT 1560  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrIeuGluProAspAlaValGluLeuCys 540  
Db 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCGATTGAATCTGTG 1620  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAenArgAenVal 560  
Db 1621 TTAAGAAGATTTTAAAGATAAACCGCTAGCTTGTGTTATACCATTAATAGAAAACGTC 1680  
Qy 561 AenProAspGlySerLeuIleAlaAenGlyTyrAenTrpProGluPheSerArgGluLys 580  
Db 1681 AATCCGGATGTAGCTTAATCGCTAAATGGTTTACAATTTGGCCAGAAATTTTCCAGAGAAAA 1740  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1741 CTCACACGGCTATGATTGCTCACCACTTTTAAAGATGTTTACGATTAGAGCTTGGCATTTA 1800  
Qy 601 ThrAspGlyPheAenGluLysIleGluAenAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1801 ACTGATGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCCAACTC 1860  
Qy 621 SerGluValGlyLysPheLysHisLeuAenLysIleCysTyrAenArgValLeuHisGly 640  
Db 1861 AGTGAAGTTGGAAAAATTTAAACATCTTTAAATAATCTGCTATAACCGCTGTATTACATGGT 1920

Qy 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValValAsn 660  
Db 1921 GATTAACACATCAATTAAGAAACTTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1980  
Qy 661 GlnSerLeuAenArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 1981 CAGTCATTTAAATAGACAAGGCATAACTTATTATAATATGACCAATTTTGATGATTTAGAT 2040  
Qy 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100  
Qy 701 LysAspIleLysIleIleGlnAenLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2101 AAAGATATTAAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTTTATCCC 2160  
Qy 721 AenThrLeuAenGlyLeuValLysLysLeuAenAenIleIleGluTyrAenLysAenIle 740  
Db 2161 AATACATTTAAACGGCTTAGTGAATAAACTAAACAATATTATTGAATATAATAAAATATA 2220  
Qy 741 PheValIleValLeuHisValAspLysAenHisLeuThrProAspIleLysLysGluIle 760  
Db 2221 TTCGTTATTGTTCTCATGTTGATAAGAATCATCTTACACCATATCAAAAAAGAAATA 2280  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAenIleLeuLeuAenAenAspIleSerTyrTyr 780  
Db 2281 CTAGCCTTCTATCATTAACATCAAGTGAATATTTTACTAAATTAATGATATCTCATATTAC 2340  
Qy 781 ThrSerAenArgLeuIleLysThrGluAlaHisLeuSerAenIleAenLysLeuSerGln 800  
Db 2341 ACCAGTAATAGATTAATAAAACCTGAGGCGCATTTAAGTAAATATAATAAATAAAGTCAG 2400  
Qy 801 LeuAenLeuAenCysGluTyrIleIlePheAspAenHisAspSerIeuPheValLysAen 820  
Db 2401 TTAATCTTAATTTGTGAATACATCATTTTTTGATAAATCATGACAGCCTATTTCGTTAAANAT 2460  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAenPheSerAlaLeuThrHis 840  
Db 2461 GACAGCTATGCTTATATGAANAANTATGATGCGGATGNAATTTCTCAGCATTAACACAT 2520  
Qy 841 AspTrpIleGluLysIleAenAlaHisProProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2521 GATTGGATCGAGAAATCAATCGCATCCACCATTTTAAAAAGCTCATTTAAACCTTATTTT 2580  
Qy 861 AsnAspAenAspLeuLysSerMetAenValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2581 AATGACAAATGACTTAAAAAAGTATGAATGTGAAGGGGCATCACAGGTATGTTTATGACG 2640  
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTCATCACATCTTGCCAGTCA 2700  
Qy 901 IleAspSerValProGluTyrAenThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2701 ATTGATAGTGTGCAGAAATATAACATCGAGATATTGTTGTTCCAAATTTGCACATTTAATC 2760  
Qy 921 LeuGluLysLysThrGlyHisValPheAenLysThrSerThrIeuThrTyrMetProTrp 940  
Db 2761 TTAGAAAAGAAAAACCGGCCATGTATTATAATAAACATCGACCCCTGACTTATATGCTCTGG 2820  
Qy 941 GluArgLysLeuGlnTrpThrAenGluGlnIleGluSerAlaLysArgGlyGluAenIle 960  
Db 2821 GAACGAAATTTACATGGACAAATGAACAATTTGAAAGTGCNAAGAGAGAGAAATATA 2880  
Qy 961 ProValAenLysPheIleIleAenSerIleThrLeu 972  
Db 2881 CCTGTTAAACAAGTTTCATTATTATAATAGTATAACTTA 2916

## RESULT 8

US-09-879-959-9

; Sequence 9, Application US/09879959

; Patent NO. US20020160489A1

; GENERAL INFORMATION:

; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Khama  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION  
; FILE REFERENCE: 3554.049  
; CURRENT APPLICATION NUMBER: US/09/879,959  
; PRIORITY FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: 09/469,200  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: pasteurella multocida  
US-09-879-959-9

Alignment Scores:  
Pred. No.: 0 Length: 2937  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
Gaps: 0

US-10-642-248-2 (1-972) x US-09-879-959-9 (1-2937)

QY 1 MetAenThrLeuSerGlnAlaIleLysAlaTyraenSerAsnAspTyraGlnLeuAlaLeu 20  
Db 19 ATGAATACATATATCAAGCAATATAAGCATATACAGCAATGACTATCAATATGACATC 78  
QY 21 LysLeuPheGluLysSerAlaGluLeuTyraGluLysIleValGluPheGlnIleThr 40  
Db 79 AAATTTATTTGAAAGAGTCGCGGAAATCTATGGACGCAAAATTTGTTGAAATTTCAAATTACC 138  
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValaenSerAlaHisLeuSerValaen 60  
Db 139 AAATGCCAAGAAATCTCTCAGCACATCCCTCTGTTAAATTCAGCACATCTTTCTGTAAAT 198  
QY 61 LysGluGluLysValaenValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 199 AAAGAAGAAATAGTCAATGTTTCCGATAGTCCGTTAGATATTTGCCACACACTGTTACTT 258  
QY 81 SerAenValLysLysLeuValLeuSerAspSerGluLysAenThrLeuLysAenLysTrp 100  
Db 259 TCCACGTAAATTAATAGTACTTTCTGACTCGGAAAAACACCGTTAAAAATAAATGG 318  
QY 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValaIleValPro 120  
Db 319 AAATTTGCTCACTCAGAAAGAAATCTGAAATTCGCGAGGTAAAGACCGTCCGCTTGTACCA 378  
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValaenAspPheThr 140  
Db 379 AAAGATTTTCCCAAGATCTGGTTTTCGATAGTCCCTTACCTGATCAATGTTAATGATTACA 438  
QY 141 TrpTyraLysLysArgLysArgLeuGluLysProGluHisGlnHisValGlyLeu 160  
Db 439 TGGTACAAAGCGAAAGAAAGACTTTGGCATAAACCTGAACATCAACATGTTGTCCTT 498  
QY 161 SerIleIleValThrThrPheAenArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 499 TCTATTATGTTTACAAATTCATTCAGCAGCAATTTTATCGATTAATAGCTGCTTTTA 558  
QY 181 ValaenGlnLysThrHisTyraProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 559 GTAACCAACAAACAAATTCACCGGTTTGAAGTTATCGTACAGATGATGTTAGTACGAA 618  
QY 201 AspLeuSerProIleLeuArgGlnTyraGluAenLysLeuAspIleArgTyraValArgGln 220  
Db 619 GATCTATACCGATCATTCGCCAATATGAAATTAATTTGGATATTCGCTACGTACAGCAA 678

QY 221 LysAspAenGlyPheGlnAlaSerAlaAArgAenMetGlyLeuArgLeuAlaLysTyra 240  
Db 679 AAAGATAACGGTTTCAAGCCAGTCGCGCTCGGAATATGGATATACGCTTAGCAAAATAT 738  
QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAenProLeuTrpValHiserTyra 260  
Db 739 GACTTTATTTGGCTTACTCGACTGTGATATGCGCAATATCCATTTATGGTTTCATCTTAT 798  
QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyraIleAsp 280  
Db 799 GTTCAGAGCTATTTAGAGATGATGATTAACAATCATTTGTTCCAAAGAAATATACATCAT 858  
QY 281 ThrGlnHisIleAspProLysAspPheLeuAenAenAlaSerLeuLeuGluSerLeuPro 300  
Db 859 ACACAACATATTTGACCCCAAGAGACTTCTTAATAACGCGAGTTTCTTGAATCATTTACCA 918  
QY 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 919 GAAGTGAACCAATATAGTTGTTCCGCCAAAGGGGAAGAACAGTTTCTCTGGATTGG 978  
QY 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGAACATTTCCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTTCGGTTT 1038  
QY 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPheAsp 360  
Db 1039 TTTGCGCGGGTAATGTTGCTTCCGTAATAAATGGCTTAATAATCCGGTTTCTTTGAT 1098  
QY 361 GluGluPheAenHisTrpGlyGlyGluAspValGluPheGlyTyraArgLeuPheArgTyra 380  
Db 1099 GAGGAATTTAATCACTGGGGTGGAGAAATGTTGGAAATTTGGATATCGCTTATTCGGTTAC 1158  
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyraHisGlnGluProProGlyLys 400  
Db 1159 GGTATTTTCTTTAAACTATTTGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAA 1218  
QY 401 GluAenGluThrAspArgGluAlaGlyLysAenIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAATGAACCGATCGTGAAGCGGAAAAATAATATAGCTCGATATTTATGAGAGAAAG 1278  
QY 421 ValProTyraIleTyraArgLysLeuProIleGluAspSerHisIleAenArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAATCTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT 1338  
QY 441 LeuValSerIleTyraIleProAlaTyraAenCysAlaAenTyraIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAAATTTATCCAGCTTATACTGTGCNAACTATATTCNAGCTTTCGCTAGAT 1398  
QY 461 SerAlaLeuAenGlnThrValValAspLeuGluValCysIleCysAenAspGlySerThr 480  
Db 1399 AGTGCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAACCATGTTCAACA 1458  
QY 481 AspAenThrLeuGluValIleAenLysLeuTyraGlyAenAspProArgValArgIleMet 500  
Db 1459 GATAATACCTTAGAAGTGCATCAATAGCTTTTATGTTAATAATCCCTAGGGTAGCATCATG 1518  
QY 501 SerLysProAenGlyGlyIleAlaSerAlaSerAenAlaAlaValaSerPheAlaLysGly 520  
Db 1519 TCTAAACCAATATGGCGAATAGCTTCAGCATCAATATGACGCGTTCTTTTGTCTAAAGGT 1578  
QY 521 TyraTyraIleGlyGlnLeuAspSerAspTyraLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTTGGCAGTTAGATTTCAGATGATTTATCTTGGCTGATGTCAGTTGAATCTGTGT 1638  
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyraThrAenArgAenVal 560  
Db 1639 TTTAAAGAAATTTTAAACATATAACGCTAGCTTGTGTTTATACCACTAATATAAGAACGTC 1698  
QY 561 AenProAspGlySerLeuIleAlaAenGlyTyraAenTrpProGluPheSerArgGluLys 580  
Db 1699 AATCCGGATGGTAGCTTAATCTGTTAATGTTTACATTTGCCAGAAATTTTCACGAGAAATA 1758

Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleAaGlaTrpHisLeu 600  
Db 1759 CTCACACGGCTATGATGCTCACCACTTTAGATGTTGAGATTAGAGCTTGCCATTYA 1818  
Qy 601 ThrAspGlyPheAenGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCAATGAAATAAATGAAAAATGCCCGTAGCATATGATGCTCTCAAACTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAenArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGGAAATTTAAACATCTTAATAAAATCTGCTATAAACCGTGATTACATGGT 1938  
Qy 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValAsn 660  
Db 1939 GATNACACATCAATTAGAAACTTGGCATTCNAAAAGAAAACCAATTTGTTGTAGTCAAT 1998  
Qy 661 GlnSerLeuAenArgGlnGlyIleThrTyrTyrAenTyrAspGluPheAspLeuAsp 680  
Db 1999 CAGTCATTAATACACAAGGCATAACTTATTATTAATTATGACGAATTTGATGATTAGAT 2058  
Qy 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2059 GAAAGTAGAAGTATATTTCNATAAAAACCGCTCAATATCAAGAAGAGATTGATATCTTA 2118  
Qy 701 LysAspIleLysIleIleGlnAenLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2119 AAAGATATTAAATCATCCAGNATPAAAGATGCCAAATCGCAGTCAGTATTTTTATCCC 2178  
Qy 721 AsnThrLeuAenGlyLeuValLysLysLeuAenAsnIleIleGluTyrAenLysAenIle 740  
Db 2179 AATACATTAACCGCTAGTGAAATAAACTAAACAATATTATTGAATATAATAAAATATA 2238  
Qy 741 PheValIleValLeuHisValAspLysAenHisLeuThrProAspIleLysLysGluIle 760  
Db 2239 TTCGTTATTGTTCTACATGTTGATGAAGATCATCTTACCCAGATATCAAAAAAGAAATA 2298  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAenAspIleSerTyrTyr 780  
Db 2299 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATATGATATCTATATAC 2358  
Qy 781 ThrSerAenArgLeuIleLysThrGluAlaHisLeuSerAenIleAenLysLeuSerGln 800  
Db 2359 ACGAGTAATAGATTAAATAAAACTGAGCGCATTTAAGTAATAATTATAAATTAAGTCAG 2418  
Qy 801 LeuAenLeuAenCysGluTyrIleIlePheAspAenHisAspSerLeuPheValLysAen 820  
Db 2419 TTAATCTAAATTTGTAATACATCATCATTTTGTATATCATGACAGCCTATTTCGTTAAAAAT 2478  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAenPheSerAlaLeuThrHis 840  
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 841 AspTrpIleGluLysIleAenAlaHisProProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2539 GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTAAAAAGCTCATTTAAACATTATTT 2598  
Qy 861 AsnAspAenAspLeuLysSerMetAenValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2599 AATGACAAATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCACAAAGGTATGTTTATGACG 2658  
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAAGTCATCACATCTTGCCAGTCA 2718  
Qy 901 IleAspSerValProGluTyrAenThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2719 ATTGATAGTGGCAGAAATAAACACTGAGGATATTTGGTTCCCAATTTGACATTTTAATC 2778  
Qy 921 LeuGluLysLysThrGlyHisValPheAenLysThrSerThrLeuThrTyrMetProTrp 940  
Db 2779 TTAGAAAAAGAAACCGGCCATGTATTTTAATAAAACATCGACCCCTGACTTATATGCCCTGG 2838  
Qy 941 GluArgLysLeuGlnTrpThrAenGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960

Db 2839 GAACGAAAAATTACAATGGACAAATGAACAAATTTGAAAGTGCACAAAGAGGAGAAATATA 2898  
Qy 961 ProValAsnLysPheIleIleAenSerIleThrLeu 972  
Db 2899 CCTGTTAACAAAGTTTCATTATTATATAGTATAACTCTA 2934  
RESULT 9  
US-10-172-527-9  
; Sequence 9, Application US/10172527  
; Publication No. US20030092118A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Kshama  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: HYALURONAN SYNTHASE GENES AND EXPRESSION THEREOF IN BACILLUS SUBTI  
; FILE REFERENCE: 3554.048  
; CURRENT APPLICATION NUMBER: US/10/172,527  
; CURRENT FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: 60/297,788  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 60/297,744  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 09/469,200  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: pasteurella multocida  
US-10-172-527-9  
Alignment Scores:  
Pred. No.: 0 Length: 2937  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
DB: 5 Gaps: 0  
US-10-642-248-2 (1-972) x US-10-172-527-9 (1-2937)  
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAenSerAenAspTyrGlnLeuAlaLeu 20  
Db 19 ATCAATACATTTATCACAAGCAATAAAAGCATATATAACAGCAATGACTATCAATTAGCACTC 78  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 79 AAATTTATTTGAAAGTCGGCGGAATCTATGGACGGAATAATTTGTTGAATTTCAATTTACC 138  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 139 AAATGCCAAGAAAACTCTCAGCACATCCTTCTGTTAATTCAGCACATCTTCTGTAAAT 198  
Qy 61 LysGluGluLysValAenValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 199 AAAGAAGAAAAAGTCAATGTTTCGGATAGTCCGTAGATATTGCAACACACAACTGTTACTT 258  
Qy 81 SerAenValLysLysLeuValLeuSerAspSerGluLysAenThrLeuLysAenLysTrp 100  
Db 259 TCAACGCTAAAAAATTTAGTACTTTTCTGACTCCGAAAAAACACGTTTAAAAAATAAATGG 318  
Qy 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120  
Db 319 AAATTGCTCACTCAGAAGAAATCTGAAATCGGAGGTAGAGCGGTGCGCCCTTGTACCA 378  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAenAspPheThr 140  
Db 379 AAAGATTTTCCCAAGATCTGTTGTTAGCGCCTTTACCTGATCATGTAAATGATTTTACA 438

141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
142 TGGTACAAAAAGCGAAGAAAGACTTGGCATATAAACTGAAACATCAACATGTTGGTCTT 498  
161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
162 TCTATTATCGTTACAACATTCATCGACAGCAATTTTATCGATTACATTAGCCCTGTTTA 558  
181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
182 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTACAGAA 618  
201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
202 GATCTATCCCGATCATCTCGCAATATGAAATAAATTTGGATATTCGCTACGTACAGACAA 678  
221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
222 AAAGATAACGGTTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT 738  
241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
242 GACTTTATTTGGCTTACTCGCTGATATGCGCCAAATCCATTTATGGGTTCAATCTTAT 798  
261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
262 GTTCAGAGCTATTAGAAGATGATGATTTAAATCATCTGTTCCGAAAGAAATACATCGAT 858  
281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
282 ACACAACATATTGACCCAAAAGACTTCTTAATAACGCGAGTTTCTTGAATCATTAACA 918  
301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
302 GAAAGTGAACCAACAAATAATAGTGTTCGCGAAAAGGGAGGAACAGTTCTCTCGATTGG 978  
321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
322 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTCCGTTTT 1038  
341 PheAlaAlaGlyAsnValAlaPheAlaLysTyrTrpLeuAsnLysSerGlyPheAsp 360  
1039 TTTGCGCGGGTAATGTTGCTTCGCTAAATAATGGCTAAATAAATCCGGTTCTTTGAT 1098  
361 GluGluPheAsnHisTrpGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
1099 GAGGAATTTAATCACTGGGCTGGAGAAGATGTGGAAATTTGGATATTCGCTTATTCGCTTAC 1158  
381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
1159 GGTAGTTCTTTAAACCTATTGATGGCATTATGGCTTACCCTCGATATTATGAGAGAAAG 1218  
401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGlyLys 420  
1219 GAAATGAACCGATCGTGAAGCGGGAATAATATTACCTCGATATTATGAGAGAAAG 1278  
421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1338  
441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCACGTTGCGTAGAT 1398  
461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
1399 AGTGCACTGATCAGACTGTTGTTGATCTCGAGTTTGTATTGTGAACGATGGTCAACA 1458  
481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
1459 GATAATACCTTAGAAGTGTCAATAAGCTTTATGGTAAATACCTTAGGGTACGCATCATG 1518  
501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520

1519 TCTAAACCAATGGCGAATAGCTTCAGCATCAATCGACGCGTTTCTTTTCTTAAGGT 1578  
521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
1579 TATTACATTTGGCAGTTAGATTTCAGATGATTACTTCAGCCTGATGAGTTGAACCTGTGT 1638  
541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
1639 TTTAAAGAAATTTTAAAGATMAAACGCTAGCTGTGTGTATATACCACTAATAGAAACGTC 1698  
561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGlyLys 580  
1699 AATCCGATGATAGCTTAATTCGCTTAATTCGCTTAATTCGCTTAATTCGCTTAATTCGCTTA 1758  
581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
1759 CTCAACAGGCTATGATTGCTCACCATTTAGATGTTTCAGATTTAGAGCTTGGCATTTA 1818  
601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
1819 ACTGATGATTCATCAATGAAATAATGAAATGCGCTAGACTATGACATGTTCTCTCAAACTC 1878  
621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
1879 AGTGAAGTTGGAAATTTAAACATCTTAATAAATCTGCTATAACCGGTGATTACATGCT 1938  
641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
1939 GATAACACATCAATTAAGAAACTTGGCATTCGCAAGAAACCAATTTTGTGTAGTCAAT 1998  
661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
1999 CAGTCATTAATAGACAGGCTAACTATTATTAATATGACGAATTTGATGATTAGAT 2058  
681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluLysLeu 700  
2059 GAAAGTAGAAAGTATATTTTCAATAAACCCTGAAATATCAAGAGAGATTTGATATCTTA 2118  
701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
2119 AAGATATTAATAATCATCCAGATTAAGATGCGCAAAATCGCAGTCAGTATTTTATATCCC 2178  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
2179 AATCATTTAAACGGCTTAGTGAATAAATACTAAACATATTTATTAATAATAATAATAATA 2238  
741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
2239 TTCGTTATTTGTTTACATGTTGATAAGAAATCATCTTACCCAGATATCAAAAAAGAAATA 2298  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
2299 CTAGCTTCTATCATATAACATCAAGTGAATTTTCTACTAATATGATATCTCATATATAC 2358  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
2359 ACGATTAATAGATTAAATAAATACTGAGCGCATTTTAAGTAAATATTAATAATAATAAGTCAG 2418  
801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
2419 TTAATCTAAATTTGTAATATCATCATCTTTTGAATAATCATGACGAGCTATTCGTTAAAAAT 2478  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
2479 GACAGCTATGCTTATATGAAAAAATATGATGCGCATGAAATTTCTCAGCATTAACACAT 2538  
841 AspTyrIleGluLysIleAsnAlaHisProProPheLysLysLeuIleLysThrTyrPhe 860  
2539 GATTGATCGAGAAATCAATCGCATCCACCATTTAAAAAGCTCATTTAAAACTTATTTT 2598  
861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880

Db 2599 AATGACAATGACTTAAAGAGTATGAATGTGAAAGGGGCATCACAGGATGTTTATGACG 2658  
Qy TyrAlaLeuAlaHisGluLeuLeuThrIleIleIysGluValIleThrSerCysGlnSer 900  
Db 2659 TATCGGTAGCGCATGAGCTTCTGACGATTATTAAAGAAAGTCATCACATCTTGCCAGTCA 2718  
Qy IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2719 ATTGATAGTGTCCAGAAATATACACTGAGGATATTGGTTCCAATTTGCATTTTAAATC 2778  
Qy LeuGluIysIysThrGlyHisValPheAsnIysThrSerThrLeuThrTyrMetProTrp 940  
Db 2779 TTAGAAAAGAAAACCGCCATGTTATTAATAAAACATCGACCTGACTTATATGCCCTTGG 2838  
Qy GluArgIysLeuGlnTrpThrAsnGluGlnIleGluSerAlaIysArgGlyGluAsnIle 960  
Db 2839 GAACGAAAATTTACAATGCGACAAATGAACAAATTGAAAAGTGCAAAAGAGGAGGAAAAATATA 2898  
Qy ProValAsnIysPheIleIleAsnSerIleThrLeu 972  
Db 2899 CCTGTTAAACAAGTTCATTAATTAAGTATAACTCTA 2934

## RESULT 10

US-10-309-560-7  
; Sequence 7, Application US/10309560  
; Publication No. US20030235893A1  
; GENERAL INFORMATION: PAUL H  
; APPLICANT: WEIGEL,  
; APPLICANT: KUMARI, KSHANA  
; TITLE OF INVENTION: HYALURONAN SYNTHASES AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 35541.082  
; CURRENT APPLICATION NUMBER: US/10/309,560  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: 60/336,105  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-10-309-560-7

Alignment Scores:  
Pred. No.: 0 Length: 2937  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
DB: 6 Gaps: 0

US-10-642-248-2 (1-972) x US-10-309-560-7 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleIysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 19 ATGATACATTATCACAGCAATTAAGCATATATACAGCAATGACTATCAATTAGCACTC 78  
Qy 21 LysLeuPheGluIysSerAlaGluIleTyrGlyArgIysIleValGluPheGlnIleThr 40  
Db 79 AAATTAATTGAAAAGTCGGCGGAATCTATGACGCGAAAATTGTTGAATTTCAAAATTACC 138  
Qy 41 LysCysIysGluIysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 139 AAATGCCAAGAAAACCTCTCAGCATCCCTCTCTGTTAATTCAGCACATCTTCTGTAAAT 198  
Qy 61 LysGluGluIysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 199 AAAGAAGAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACAACTGTACTT 258  
Qy 81 SerAsnValIysIysLeuValLeuSerAspSerGluIysAsnThrLeuLysAsnLysTrp 100  
Db 259 TCCAACGTAAAAAATAGTACTTCTGACTCGGAAAAAACAAGTAAAAAATAAATGG 318  
Qy 101 LysLeuLeuThrGluIysIysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 319 AAATTGCTCACTGAGAGAAATCTGAAATCGGAGGTAAAGCGGTGCGCCTTGTACCA 378  
Qy 121 LysAspPheProIysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 379 AAAGATTTTCCCAAGATCTGGTTTGTAGCGCCTTACCTGATCATGTTAATGATTTTACA 438  
Qy 141 TrpTyrIysIysArgIysIysArgLeuGlyIleIysProGluHisGlnHisIvalGlyLeu 160  
Db 439 TGGTACAAAAGCGAAGAAAGACCTTGGCATAAAACCTGAAACATCAACATGTGTGCTT 498  
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 499 TCTATTATCGTTACAACATTCATCGACCGCAATTTTATCGATTACATTAGCCTGTTTA 558  
Qy 181 ValAsnGlnIysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 559 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnIysLeuAspIleArgTyrValArgGln 220  
Db 619 GATCTATCACCGATCATTCGCCAATATGAAATTAATTTGGATATTCGCTACGTCAGACAA 678  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 679 AAAGATAACCGTTTTCAAGCAGTCGCTCGGATATGCGATATGCGATTACGTTAGCAAAATAT 738  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
Db 739 GACTTTTGGCTTACTCGAGTGTATATGCGCCAAATCCAATATGGGTTCATCTTAT 798  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgIysTyrIleAsp 280  
Db 799 GTTGCAGAGCTATTAGAAGATGATGATTTAACCAATCATTTGGTCCAGAAAATACATCGAT 858  
Qy 281 ThrGlnHisIleAspProIysAspPheLeuAsnAsnAlaSerLeuLeuGluLeuLeuPro 300  
Db 859 ACAACATATTGACCCCAAAAGACTTCTTAATTAACGCGAGTTTGGTTGANTCATTTACCA 918  
Qy 301 GluValIysThrAsnAsnSerValAlaLysGlyGluGlyThrValSerLeuLeuAspTrp 320  
Db 919 GAAGTGAATAACCAATAATAGTGTTCGCGCAAAAGGGGAGGAAACAGTTTCTCTGGATTGG 978  
Qy 321 ArgLeuGluGlnPheGluIysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGAACAAATTCGAAAAAAGCAGAAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1038  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysIysTrpLeuAsnIysSerGlyPhePheAsp 360  
Db 1039 TTTGCGCGGGTAATGTTGCTTTTCGCTTAAAAAATGCGTAATAATATCCGTTTCTTTGAT 1098  
Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1099 GAGCAATTTAATCACCTGGGTGAGAGAAGATGTGGAATTTGGATATCGCTTATTCCTCGTTAC 1158  
Qy 381 GlySerPhePheIysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1159 GGTAGTTTCTTTAAAACTATTGATGCGCATTTATGCGCTTACCATCAAGAGCACCAGGTAAA 1218  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAATGAAACCGATCGTGAGCGGGGAAAAAATATATACGTCGATATATATGAGNAGAAAG 1278  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAAACCTTTTACCATAATAGAGATTCGCATATCAATAGAGTACCT 1338  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATATCAACCTGCGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480



Db 1399 AGTCACATGATCAGCTGTTGATCTCGAGGTTGTTATTTCTTAACGATGGTTCAACA 1458  
Qy 481 AspAenThrLeuGluValIleAenLysLeuTyrcGlyAenAenProAerGValArgIleMet 500  
Db 1459 GATAATACCTTAGAAGTGATCAATTAAGCTTTATCGTTAATATCTTAGGTCAGCATG 1518  
Qy 501 SerLysProAenGlyGlyIleAerAerAenAlaValSerPheAlaLysGly 520  
Db 1519 TCTAAACCAATGGCGAATAGCTCAGCATCAATGCGAGCGTTCTTTGCTAAAGGT 1578  
Qy 521 TyrtvriileGlyGlnLeuAenSerAerAerLeuGluProAerAerAlaValGluLeuCys 540  
Db 1579 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCGCTGATGCGATTGAACCTGTG 1638  
Qy 541 LeuLysGluPheLeuLysAerPheThrLeuAlaCysValTyrtvriileAerAerAerAerVal 560  
Db 1639 TTTAAAGAAATTTTAAAGATTAACCGCTAGCTTGTGTGTATACCATTAATAGAAACGTC 1698  
Qy 561 AenProAerGlySerLeuIleAaAenGlyTyrtvriileAerAerAerAerAerAerAerAer 580  
Db 1699 AATCCGATGTAGCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTCACGAGAAATA 1758  
Qy 581 LeuThrThrAlaMetIleAaHisPheAerGMetPheThrIleAerAlaTrpHisLeu 600  
Db 1759 CTCACACGGCTATGATTGCTCACCATTTTAGAATGTTACGATTAGAGCTTGGCATTTA 1818  
Qy 601 ThrAerGlyPheAenGluLysIleGluAenAlaValAerPheAerAerAerAerAerAerAer 620  
Db 1819 ACTGATGATTCAATGAAATTAATGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1878  
Qy 621 SerGluValGlyPhePheLysHisLeuAenLysIleCysTyrtvriileAerAerAerAerAer 640  
Db 1879 AGTGAAGTTGGAAATTTTAAACATCTTAATTAATCTCTGATTAACCGTGATTAATCGGT 1938  
Qy 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValAerAer 660  
Db 1939 GATAACATCAATTAAGAACTTGGCATTCAGAAAGAAACCACTTTTGTGTAGTCAAT 1998  
Qy 661 GlnSerLeuAenAerGlnGlyIleThrTyrtvriileAerAerAerAerAerAerAerAer 680  
Db 1999 CAGTCATTAATAGCAAGGCATACTTATTATTAATATGACGAAATTTGATGATTAGAT 2058  
Qy 681 GluSerAerGlyTyrtvriilePheAenLysThrAlaGluTyrcGlnGluLysIleAerPhe 700  
Db 2059 GAAAGTAGAAGATATATTTCATTAATTAACCGCTGAATATCAAGAAAGATTAATCTTA 2118  
Qy 701 LysAerPheIleIleGlnAenLysAerAerAerAerAerAerAerAerAerAerAerAer 720  
Db 2119 AAAGATATTAATCAATCAAGATTAAGATGCAAAATCGCAGTCAGTATTTTATCC 2178  
Qy 721 AenThrLeuAenGlyLeuValLysLysLysAenAenIleIleGluTyrtvriileAerAerAer 740  
Db 2179 AATACATTTAAACGGCTTAGTGAATAAACTTAACAAATATTATTGAATATAATAAATAATA 2238  
Qy 741 PheValIleValLeuHisValAerLysAenHisLeuThrProAerPheLysGluIle 760  
Db 2239 TTCGTTATTGTTCTACATGTTTGAATGAATCACTTTACACGAGATCAAAAGAAATA 2298  
Qy 761 LeuAlaPheTyrtvriileHisGlnValAenIleLeuAenAerAerAerAerAerAerAer 780  
Db 2299 CTAGCGCTTCTATCAATCAATCAAGTGAATATTTTACTAATAATGAATATCTCATATTAC 2358  
Qy 781 ThrSerAerAerGluIleLysThrGluAlaHisLeuSerAerAerAerAerAerAerAerAer 800  
Db 2359 ACGAGTAAATAGATTAATAAACTCAGGCGCATTTTAAGTAAATATTAAATAAATAAGTCAG 2418  
Qy 801 LeuAenLeuAenCysGluTyrtvriilePheAerAerAerAerAerAerAerAerAerAer 820  
Db 2419 TTTAAATCTAAATGTGAATACATCAATTTTGTGAATATCATGACGAGCTTATCGTTAAAT 2478  
Qy 821 AspSerTyrtvriileMetLysLysTyrtvriileValGlyMetAerAerAerAerAerAer 840

Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 841 AspTrpIleGluLysIleAenAlaHisProPheLysLysLeuIleLysThrTyrtvriile 860  
Db 2539 GATTGATCGAAGAAATCAATCGCATCCACCATTTTAAAGGCTCAATTAACATTTATTT 2598  
Qy 861 AenAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAer 880  
Db 2599 AATGACATGACTTAAAGATATGAATGTGAAGGGGCATCACAAGGTATGTTTATGACG 2658  
Qy 881 TyrtvriileAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAer 900  
Db 2659 TATGCGCTAGCGATGAGCTTCTGACATTAATTAAGAAATCATCATCTTGGCAGTCAT 2718  
Qy 901 IleAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAer 920  
Db 2719 ATTGATGATGCGAGATATTAACATGAGATATTTGGTTCCAAATTTGCATTTTAATC 2778  
Qy 921 LeuGluLysLysThrGlyHisValPheAerAerAerAerAerAerAerAerAerAerAer 940  
Db 2779 TTAGAAAGAAACCGGCTATGTTTAAATAAACAATCGACCTGACTTATATGCTTGG 2838  
Qy 941 GluAerGlyLysLeuGlnTyrtvriileAerAerAerAerAerAerAerAerAerAerAer 960  
Db 2839 GAACGAAATTTACAAATGCAAAATGAACAAATGAAAGTGAAGAAAGAGGAGAAATA 2898  
Qy 961 ProValAerLysPheIleIleAerAerAerAerAerAerAerAerAerAerAerAer 972  
Db 2899 CTTGTTAAAGTTCAATTAATTAATGATTAACCTCA 2934  
RESULT 11  
US-09-842-484A-3  
; Sequence 3, Application US/09842484A  
; Publication No. US20030104601A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL L.  
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 4605.003  
; CURRENT APPLICATION NUMBER: US/09/842,484A  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-09-842-484A-3  
Alignment Scores:  
Pred. No.: 0 Length: 2979  
Score: 4502.50 Matches: 845  
Percent Similarity: 93.21% Conservative: 61  
Best Local Similarity: 86.93% Mismatches: 59  
Query Match: 88.15% Indels: 7  
DB: 3 Gaps: 2  
US-10-642-248-2 (1-972) x US-09-842-484A-3 (1-2979)  
Qy 1 MetAenThrLeuSerGlnAlaIleLysAlaTyrtvriileAerAerAerAerAerAerAerAer 20  
Db 61 ATGAATACATTTATCAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 120  
Qy 21 LysLeuPheGluLysSerAerAerAerAerAerAerAerAerAerAerAerAerAerAer 40  
Db 121 AAATTTATTTGAGAGTCTGCTGAAACCTTACCGGCGGAAATTCGTGAAATTCGAAATTC 180  
Qy 41 LysCysLysGluLysLeuSerAerAerAerAerAerAerAerAerAerAerAerAerAer 60  
Db 181 AAATGTAAGAAATCACTC-----TCGACCAATTTCT-----TATGTAAGT 219  
Qy 61 LysGluGluLysValAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAer 80



Db 220 GAAGATAAAAAAACAGCTGTTGGGATAGCTCATTAGATATCGCAACAGCTCTTACTT 279  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
Db 280 TCCAACGTAAAAAATTAACTCTATCCGAATCAGAAAAAACAGCTTTAAAAAATAAATGG 339  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 340 AAATCTATCTACTCGGAAAAAATCGGAGAACCGCAAAATCAGAAGGTGGAACTAGTACCC 399  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 400 AAAGATTTTCTTAAAGATCTTGTTCTCTCCATTCGCAAGATCAATGTTAATGATTTTACA 459  
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
Db 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATAAAGCTGTAAATAAGAAATATCGGTCTT 519  
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 520 TCTATTATTATCTCATCAATTAATCGTAGCCGTATTTTAGATATAACGTTAGCCTGTTTG 579  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 580 GTCAATCAGAAAAACAACTACCCATTTGAAGTCGTTGTCAGATGATGTAGTAGGAA 639  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 640 AACTTACTTACCATTGTCAAAAATACGAACAAAACTTGACATANAAGTATGTAAGACAA 699  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 700 AAAGATTATGGATATCAATTTGTGTCAGTCAGAACTTAGGTTTACGTACAGCAAAAGTAT 759  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
Db 760 GATTTTGTCGATCTAGACTGCGATATGCGACCAACAAATATGCGGTTTCATCTTAT 819  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 820 CTTACAGAACTATTAGAAGACAATGATATTGTTTAAATGGACCTAGAAAAATATGTGGAT 879  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 880 ACTATAATATTACCGCAGAACCAATCTCTTAACGATCCATATTATTAATAGAATCACTACCT 939  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
Db 940 GAAACCCCTACAAATAACAATCCTTCGATTACATCAAAAGAAATATATCGTTGGATGG 999  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 1000 AGATTAGAACAATTTCAAAAAAACCGATAATCTAGCTCTATGTTCTCCGTTTCGTTAT 1059  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPheAsp 360  
Db 1060 TTTAGTTGCGGTAAATGTTGCAATTTCTTAAAGAATGGCTAAATAAAGTAGGTGGTTCGAT 1119  
Qy 361 GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1120 GAAGAATTTAATCAATCGGGGGCGGAAGATGTAGATTTGGTTACAGATTTATGGCCAAA 1179  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1180 GGCTGTTTTTCAGAGTAATGACGGCGGAATGGCATAACCATCAAGAACCCACCTGGTAAA 1239  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGlyLys 420  
Db 1240 GAAAAATGAAACAGACCCCGAAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTGAAAGAAAAG 1299  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440

Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCATAAGAGATTCCACATATTCCATAGATAACCT 1359  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1360 TTAGTTTCTATTATATCCCGCTTATAACTGTGCAAAATATATATTCAAAGATGTGTAGAT 1419  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1420 AGTGCTCTTAAATCAAACTGTGTGCAATCTCGAGGTTTGTTATTGTAAACGATGGTTCAACA 1479  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1480 GATAATACCTTAGAAGTGATCAATAGCTTTATGGTAAATACTCTAGGCTAGGCATCATG 1539  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1540 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAAGCGCTTTCTTTTGTCTAAAGGT 1599  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1600 TATTCAATTTGGGAGTTTAGATTCAAGATGATTTCTTTGAGCCGTATGCAGTTGNACTGTGT 1659  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1660 TTTAAAGAAATTTTAAACGATAAACGCTAGCTTGTTGTTTATACCCTAATAGAAACGTC 1719  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580  
Db 1720 AATCCGGATGGTAGCTTAATCGCTAATGTTTACAATTTGGCCAGAAATTTTCACGAGAAAAA 1779  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrHisLeu 600  
Db 1780 CTCACAAACGGCTATGATGCTCACCATTAGCAATTTAGCAATTTTACGATTAGAGCTTGGCATTTA 1839  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1840 ACGGATGGATTTAACCGAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTC 1899  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1900 AGTGAAGTTGGAATAATTTAAACATCTTAATAAAATCTGCTATAAACCGCGTATTACATGGT 1959  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1960 GATAACACATCCATTAAGAACTCGGCATTTCAAAAGAAACCCATTTTGTGTAGTCAAT 2019  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
Db 2020 CAGTCATTAATAGACAAGGCATCAATTATATAATTATGACAAATTTGATGATTTAGAT 2079  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu 700  
Db 2080 GAAAGTAGAAAGTATATCTTCAATAAAACCGCTGAATATCAAGAGAAATGGATATTTTA 2139  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2140 AAAGATCTTAAATCTTCAATAAAGATGCCAAATCGCAATCGCAGTCAGTATTTTCTATCCC 2199  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2200 NATACATTAACCGCTTAGTGAANAACCTAACAATATTATTGAATATAATAAATAATA 2259  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2260 TTCGTTATTATTCTCATGTGTGATAAGATCATCTTACACCAAGACATCAAAAAGAAATA 2319  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyr 780  
Db 2320 TTGCGCTTTCTATCATGAAGCACCAGGGAATATTTTACTAAATGATGACATCTCATATTAC 2379  
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2380 ACGAGTAAATAGACTAATAAAACTGAGGCACATTTTAAGTAAATATTATAAATTAAGTCAG 2439



Db 880 ACTCATAATATTACCGCAGAACAAATTCCTTAACGATCCATATTTAATAGAATCACTACCT 939  
Qy 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAsePtp 320  
Db 940 GAAACCGCTACAAATAACAATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAsePtpPheAtpPhe 340  
Db 1000 AGATTAGACATTTCAAAAGAACCGATAATCTAGCTCTATGTGATTTCTCCGTTTCGTTAT 1059  
Qy 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPheAseP 360  
Db 1060 TTTAGTTGCGGTAAATGTTGCATTTTCTAAAGATGGCTAAATAAGTAGTGTGTTTCGAT 1119  
Qy 361 GluGluPheAenHisTrpGlyGluAsePValGluPheGlyThrArgLeuPheAtpTrp 380  
Db 1120 GAAGAAATTTAATCATTTGGGGGGGGAAGATGTAGATTTGGTTACAGATTTATTTGCCAAA 1179  
Qy 381 GlySerPhePheLysThrIleAsePglyLeuMetAlaTyRHisGlnGluProProGlyLys 400  
Db 1180 GGCTGTTTTTCAGAGTAATTTGACGGCGGAATGGCATACCATCAAGAACCACTGGTAAA 1239  
Qy 401 GluAenGluThrAsePArgGluAlaGlyAseNileThrLeuAsePilleMetArgGluLys 420  
Db 1240 GAAATCAACACAGACCGGAAGCTGGTAAAGTATTACGCTTAAATTTGTGAAGAAAAG 1299  
Qy 421 ValProTyRileTyRArgLysLeuLeuProIleGluAsePserHisIleAenArgValPro 440  
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCATAAGATAGATTCACATATTTCATAGAATACCT 1359  
Qy 441 LeuValSerIleTyRileProAlaTyRasnCysAlaAenTyRileGlnArgCysValAseP 460  
Db 1360 TTAGTTTCTATTTATATATCCCGCTTATAACTGTGCAATATATATTCAAAGATGTGTAGAT 1419  
Qy 461 SerAlaLeuAenGlnThrValValAsePLeuGluValCysIleCysAenAsePglySerThr 480  
Db 1420 AGTGCTCTTAATCAAACTGTTGCGATCTCGAGGTTGTATTTGTTAAGATGGTTCAACA 1479  
Qy 481 AspAenThrLeuGluValIleAseNlyLeuTyRArgLeuAenProArgValArgIleMet 500  
Db 1480 GATAAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATATCTTAGGTCAGCATCATG 1539  
Qy 501 SerLysProAenGlyGlyIleAlaSerAlaSerAenAlaAlaValSerPheAlaLysGly 520  
Db 1540 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGACCGGTTCTTTTGTCTAAAGGT 1599  
Qy 521 TyRtyRileGlyGlnLeuAsePserAsePtyRLeuGluProAsePAlaValGluLeuCys 540  
Db 1600 TATTACATTGGCAGTTAGATTTCAGATGATTATCTTGAGCTGATGTCAGTTGAACGTGT 1659  
Qy 541 LeuLysGluPheLeuLysAsePlyThrLeuAlaCysValTyRThrAenArgAseNVal 560  
Db 1660 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTATATACCACTAATAGAAACGTC 1719  
Qy 561 AseProAsePglySerLeuIleAlaAseNlyTyRAsnTrpProGluPheSerArgGluLys 580  
Db 1720 AATCCGATGGTACGTTAAATCGCTTAATGGTTACAAATGGCCAGAAATTTTCACGAGAAAA 1779  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1780 CTCACACGGCTATGATGTCTCACATTTTAGATGTTTACGATTAGAGCTTGGCATTTA 1839  
Qy 601 ThrAsePglyPheAenGluLysIleGluAseNAlaValAsePtyRAspMetPheLeuLysLeu 620  
Db 1840 ACGGATGGATTTAACGAAATATTGAAAAACCGCTGGATTATGACATGTTCTTAAACTC 1899  
Qy 621 SerGluValGlyLysPheLysHisLeuAseNlyIleCysTyRAsnArgValLeuHisGly 640  
Db 1900 AGTGAAGTTGGAAATTTAAACATCTTAAATAAAATCTGCTATATAACCCGCTATTACATGGT 1959  
Qy 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValAseN 660  
Db 1960 GATPACACATCCATTAGAAACTCGGCATTCAAAAGAAAGAACCAATTTTGTGTAGTCAAT 2019

Qy 661 GlnSerLeuAseNArgGlnGlyIleThrTyRtyRAsnTyRAspGluPheAsePLeuAseP 680  
Db 2020 CAGTCATTAATAATAGACAGGCATCAATATTATTAATATATGACAAATTTGATGATTTAGAT 2079  
Qy 681 GluSerArgLysTyRilePheAenLysThrAlaGluTyRArgGlnGluGluLysAsePilleLeu 700  
Db 2080 GAAAGTAGAAGATATATCTTCAATAAACCCTGTAATATCAAGAAGAAATGGATATTTTA 2139  
Qy 701 LysAsePilleLysIleGlnAenLysAsePAlaLysIleAlaValSerIlePheTyRPro 720  
Db 2140 AAAGATCTTTAAACTCATTCAAAATAAAGATGCCAAATCGCAGTCAGTATTTTCTATCCC 2199  
Qy 721 AseNThrLeuAseNlyLeuValLysLysLeuAseNileIleGluTyRAsnLysAseNile 740  
Db 2200 AATACATTTAAACCGCTTAGTGAATAAACATAACATATTATTGAAATATAATAAAATATA 2259  
Qy 741 PheValIleValLeuHisValAsePlyAseNHisLeuThrProAsePilleLysLysGluIle 760  
Db 2260 TTCGTTATTATCTACATGTTGATAAGATCATCTTACACAGACATCAAAAAAGAAATA 2319  
Qy 761 LeuAlaPheTyRHisLysHisGlnValAseNileLeuLeuAseNAspIleSerTyRtyR 780  
Db 2320 TTGGCTTTCTATCATTAAGCACCAAGTGAATATTTTACTAAATATGACATCTCATATTAC 2379  
Qy 781 ThrSerAseNArgLeuLysThrGluAlaHisLeuSerAseNileAseNlyLysLeuSerGln 800  
Db 2380 ACAGTAATAGACTAATAAACTGAGGCACATTTAAGTAATATTAATAATTAAGTCAG 2439  
Qy 801 LeuAseNLeuAseNlyLeuTyRilePheAsePAsnHisAsePserLeuPheValLysAseN 820  
Db 2440 TTAATCTAAATGTGATACATCATTTTGTATTAATCATGACAGCTTATTCGTTAAAAAT 2499  
Qy 821 AsePserTyRAlaTyRMetLysLysTyRAspValGlyMetAseNpheSerAlaLeuThrHis 840  
Db 2500 GACAGCTATGCTTATATGAAAAATATGATGTCGCATGAATTTCTCAGCATTAACACAT 2559  
Qy 841 AsePTrpIleGluLysIleAseNAlaHisProPheLysLysLeuLysLysThrTyRphe 860  
Db 2560 GATTTGATCGAGAAATCAATGCGCATCCACCATTTTAAAGCTGATTAACCTATTTT 2619  
Qy 861 AseAsePAsnAsePLeuLysSerMetAseNValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2620 AATGACATGACTTAGAAGTATGAATGGAAGGGGCATCAAGGTATGTTTATGAAG 2679  
Qy 881 TyRAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2680 TATGCGCTACCGCATGAGCTTCTGACGATTTATTAAGAAAGTCATCATCTGCCAATCA 2739  
Qy 901 IleAsePserValProGluTyRAsnThrGluAsePilleTrpPheGlnPheAlaLeuLysIle 920  
Db 2740 ATTGATAGTGTGCCAAGATATAACCTGAGGATATTGTTGGTTCCAAATTTGACATTTTAAATC 2799  
Qy 921 LeuGluLysLysThrGlyHisValPheAseNlyThrSerThrLeuThrTyRMetProTrp 940  
Db 2800 TTAGAAAAGAAACCGGCATGTATTATTAATAAACAATCGNCCCTGACTATATGCTCTGG 2859  
Qy 941 GluArgLysLeuGlnTrpThrAenGluGlnIleGluSerAlaLysArgGlyGluAseNile 960  
Db 2860 GAACGAAATTTACAAATGGACAAATGAACAAATTTCAAAGTCAAAAAAGGCGAAATATC 2919  
Qy 961 ProValAseNlyPheIleIleAseNserIleThrLeu 972  
Db 2920 CCGTTTAAACAAAGTTCAATTATTAATAGTATAACGCTA 2955

## RESULT 13

US-10-197-153-4

; Sequence 4, Application US/10197153

; Publication No. US20050124046A1

; GENERAL INFORMATION:

; APPLICANT: DeAngelis, Paul

; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES

; FILE REFERENCE: 3554.080

;; CURRENT APPLICATION NUMBER: US/10/197,153  
;; CURRENT FILING DATE: 2002-07-16  
;; PRIOR APPLICATION NUMBER: 09/437,277  
;; PRIOR FILING DATE: 1999-11-10

;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: Patent in version 3.1  
;; SEQ ID NO 4

;; LENGTH: 2979  
;; TYPE: DNA  
;; ORGANISM: Pasteurella multocida  
US-10-197-153-4

## Alignment Scores:

Pred. No.:	0	Length:	2979
Score:	4502.50	Matches:	845
Percent Similarity:	93.21%	Conservative:	61
Best Local Similarity:	86.93%	Mismatches:	59
Query Match:	88.15%	Indels:	7
DB:	9	Gaps:	2

US-10-642-248-2 (1-972) x US-10-197-153-4 (1-2979)

Qy	1	MetAenThrLeuSerGlnAlaIleLysAlaTyrAenSerAenApsTyrGlnLeuAlaLeu	20
Db	61	ATGAATACATTTATCACAAGCAATAAAGCATATACAGCAATGACTATGAATTTAGCACTC	120
Qy	21	LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr	40
Db	121	AAATATTATTGAGAAGTCGTCTGCTGAAACCTACGGGGGCAAAATCGTTGAATTTCAAAATTATC	180
Qy	41	LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen	60
Db	181	AAATGTAAGAAACCTC-----TCGACCAATTC-----TATGTAAGT	219
Qy	61	LysGluGluLysValAenValCysApsSerProLeuApsIleAlaThrGlnLeuLeuLeu	80
Db	220	GAAAGATAAAAAACAGTGTTCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT	279
Qy	81	SerAenValLysLeuValLeuSerApsSerGluLysAenThrLeuLysAenLysTrp	100
Db	280	TCCAACGTAAAAAAATTAACCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG	339
Qy	101	LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro	120
Db	340	AAATCTATCACTGGGAAAAAATCGAGAACCGAGAAATCAGAAAGTGGAACTAGTACCC	399
Qy	121	LysApsPheProLysApsLeuValLeuAlaProLeuProApsHisValAenApsPheThr	140
Db	400	AAAGATTTTCTTAAAGATCTTGTCTTCTGCTCCATTCAGATCATGTTAAATGATTTTACA	459
Qy	141	TrpTyrLysLysArgLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu	160
Db	460	TGGTACAAAAATCGAAAAAAGCTTAGGTATAAAGCCCTGTAATAAGAAATATCGGCTT	519
Qy	161	SerIleIleValThrPheAenArgProAlaIleLeuSerIleThrLeuAlaCysLeu	180
Db	520	TCTATTATTCTTACATTTAATCGTACCGCTATTTAGATATAACGTTAGCCCTGTTG	579
Qy	181	ValAenGlnLysThrHisTyrProPheGluValIleValThrApsApsGlySerGlnGlu	200
Db	580	GTCATCAGAAAAACAACTACCCATTTTGAAGTCGTTGTCAGATGATGCTAGTAAGGAA	639
Qy	201	ApsLeuSerProIleLysArgGlnTyrGluAenLysLeuApsIleArgTyrValArgGln	220
Db	640	AACTTACTTACCATTTGTGCAAAATACGAAACAAAACTTGACATAAAGTATGTAGACAA	699
Qy	221	LysApsAenGlyPheGlnAlaSerAlaAlaArgAenMetGlyLeuArgLeuAlaLysTyr	240
Db	700	AAAGATTATTGGATATCAATTTGTGTCAGTGCAGAACTTAGTTAGTTAGTACACAAAGTAT	759
Qy	241	ApsPheIleGlyLeuLeuApsCysApsMetAlaProAenProLeuTrpValHisSerTyr	260
Db	760	GATTTTGTCTGATCTAGACTGCGATATGGCACCACACAAATTTATGGGTTCACTTCTAT	819

Qy	261	ValAlaGluLeuLeuGluApsApsLeuThrIleIleGlyProArgLysTyrIleAps	280
Db	820	CTTACAGAACTATTAGAAGACAATGATGATTTTAAATTTGACCTAGAAAAATATGTGGAT	879
Qy	281	ThrGlnHisIleApsProLysApsPheLeuAenAenAlaSerLeuLeuGluSerLeuPro	300
Db	880	ACTCATAATATTATCCGCAGAACAAATTCCTTAACCATCCATATTTAATAGAATCACTACCT	939
Qy	301	GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuApsTrp	320
Db	940	GAAACCCGCTACAAATAACAATCTCTCGATTACATCAAAAGGAAATATATCTCGATTGG	999
Qy	321	ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerApsSerProPheArgPhe	340
Db	1000	AGATTAGAACAATTTCAAAAAAACCAGATAATCTAGCTCTATGTGATTCTCCGTTTCGTTAT	1059
Qy	341	PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPhePheAps	360
Db	1060	TTTAGTTGCGGTAAATGTTGCATTTTCTAAAGAAATGGCTAAATAAAGTAGGTGGTTCGAT	1119
Qy	361	GluGluPheAenHisTrpGlyGlyValGluApsValGluPheGlyTyrArgLeuPheArgTyr	380
Db	1120	GAAGAAATTAATCATTTGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTATTTGCCAAA	1179
Qy	381	GlySerPhePheLysThrIleApsGlyIleMetAlaTyrHisGlnGluProProGlyLys	400
Db	1180	GGCTGTTTTTTCAGAGTAATTCAGCGGGAATGGCATACCATCAAGAACCACTGGTAAA	1239
Qy	401	GluAenGluThrApsArgGluAlaGlyAenIleThrLeuApsIleMetArgGluLys	420
Db	1240	GAATAATGAACAGACCCGAGCTGGTAAAGTATTACGCTTTAAATTTGTGAGAAAGAAG	1299
Qy	421	ValProTyrIleTyrArgLysLeuLeuProIleGluApsSerHisIleAenArgValPro	440
Db	1300	GTACTTTACATCTATAGAAAGCTTTTACCATAAGAGATTCCATATTTATAGATACT	1359
Qy	441	LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAps	460
Db	1360	TTAGTTTCTATTATATCCCGCTTATAAATGTCMAATATATTTCAAGATGTTGTAGAT	1419
Qy	461	SerAlaLeuAenGlnThrValValApsLeuValCysIleCysAenApsGlySerThr	480
Db	1420	AGTGCTCTTAATCAAACTGTTGTCGATCTCAGGTTGTATTTGTAACGATGTTTCAACA	1479
Qy	481	ApsAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet	500
Db	1480	GATTAATACCTTAGAAGTATCAATAGCTTTATGGTATATATCTTAGGGTACGATCATG	1539
Qy	501	SerLysProAenGlyIleAlaSerAlaSerAenAlaAlaValSerPheAlaLysGly	520
Db	1540	TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCGCTTCTTTTGTAAAGGT	1599
Qy	521	TyrTyrIleGlyGlnLeuApsSerApsApsTyrLeuGluProApsAlaValGluLeuCys	540
Db	1600	TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTTAGCCCTGATGCGAGTTGAT	1659
Qy	541	LeuLysGluPheLeuLysApsLysThrLeuAlaCysValTyrThrAenAenArgAenVal	560
Db	1660	TTAAAGAAATTTTAAAGATAAAACCGCTAGCTGTGTTTATACCACTAATAGAAACGCTC	1719
Qy	561	AenProApsGlySerLeuIleAlaAenGlyTyrAenTrpProGluPheSerArgGluLys	580
Db	1720	AATCCGGATGTTAGCTTAATCGTAAATGTTTACAAATTTGCCAGAAATTTTCCAGAGAAA	1779
Qy	581	LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu	600
Db	1780	CTCAACAGGCTATGATTTGCTCACCAATTTTGAATGTTTACGATTTAGAGCTTTGGCATTTA	1839
Qy	601	ThrApsGlyPheAenGluLysIleGluAenAlaValApsTyrApsMetPheLeuLysLeu	620
Db	1840	ACGGATGATTTTAAAGAAATATTGAAACCGCGGTGGATTATGACATGTTCTCTTAAACTC	1899





640 AACCTACTTACCATTGTGCAAAAATACGAACAAAACTTGACATAAAGTATGTAGACAA 699 Db  
221 LysAspAsnGlyPheGlnAlaSerAlaalaArgAsnMetGlyLeuArgLeuAlaLysTyr 240 Qy  
700 AAAGATTATGATATCAATTTGTGTCAGTCAGAACCTTAGGTTCACGTACAGCAAAAGTAT 759 Db  
241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260 Qy  
760 GATTTCGTCTGATTCCTAGATCGCATATGGCACCACCAACAATATATGGTTCATCTTAT 819 Db  
261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280 Qy  
820 CTTACAGAACTATTAGAAGACAATGATATTTGTTTAAATTGGACCTAGAAAAATATGTGGAT 879 Db  
281 ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300 Qy  
880 ACTCATATATATACCGCAGAACAAATCTCTTACGATCCATATTTATAGATACACTACT 939 Db  
301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320 Qy  
940 GAAACCGCTACAAATACAACTCTTCGATTACATCAAAAGGAATATATCGTTGGATTGG 999 Db  
321 ArgLeuGluGlnPheGlySerThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340 Qy  
1000 AGATTAGAACATTTCAAAAAAACCGATAATCTACGCTATGTGATCTCCGTTTCGTTAT 1059 Db  
341 PheAlaAlaGlyAsnValAlaPheAlaLysTyrLeuAsnLysSerGlyPhePheAsp 360 Qy  
1060 TTTAGTTCGGTAAATGTTGCATTTCTAAAGAAATCGCTAAATAAAGTAGTGGTTGCTGAT 1119 Db  
361 GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380 Qy  
1120 GAAGAAATTTAATCATTTGGGGGGCGAGAGATGTAGAAATTTGGTTACAGATTATTTGCCAAA 1179 Db  
381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400 Qy  
1180 GCCTGTTTTTTCAGAGTAATTCACGGCGGAATGGCATACCATCAAGAACCACTCGTAAA 1239 Db  
401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420 Qy  
1240 GAAATGAAACAGACGCGGAAGCTGGTAAAGTATTTACGCTTAAATTTGTGAAAGAAAG 1299 Db  
421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440 Qy  
1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCATATTCATAGATACCT 1359 Db  
441 LeuValSerIleTyrProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460 Qy  
1360 TTAGTTTCTATTATATCCCGCTTATTAACCTGTGCAATTTATTTCAAGATGTGTAGAT 1419 Db  
461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480 Qy  
1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1479 Db  
481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500 Qy  
1480 GATAATACCTTAGAAGTGATCAATAGCTTTATGTGTAAATCCCTAGGGTAGCATCATG 1539 Db  
501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520 Qy  
1540 TCTAAACCAATGGCGGATAGCTCAGCATCAATGTCAGCGCTTCTTTTGTCTAAAGGT 1599 Db  
521 TyrTyrIleGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540 Qy  
1600 TATTACATTTGGGCAGTTAGATTGATATCTTTGAGCGCTGATGTCAGTTGAACCTGTGT 1659 Db  
541 LeuLysGluPheLeuLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560 Qy  
1660 TTAAGAAATTTTAAAGATATAAACCGCTAGCTTGTGTTTATACCACTAATAGAACGTC 1719 Db  
561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580 Qy  
1720 AATCCGGATGGTAGCTTAATCGCTANTGTTACAAATGGCCAGAAATTTTTCACGAGAAAA 1779 Db

581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrPheIleLeu 600 Qy  
1780 CTCACAAACGGCTATGATTGCTCACCAATTTAGAAATGTTTACGATTAGAGCTTGGCATTTA 1839 Db  
601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620 Qy  
1840 ACGGATGGATTTAACGAAAAATATTGAAACGCCGTGGATATATGACATGTTCTTTAAACTC 1899 Db  
621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640 Qy  
1900 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATTAACCGGTATTACATGGT 1959 Db  
641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660 Qy  
1960 GATAACACATCCATTAAGAACTCGGCATTCAAAAGAAAAAACCATTTTGTGTAGTCAAT 2019 Db  
661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680 Qy  
2020 CAGTCATTTAAATAGACAGGCATCAATTTATTAATATATGACAAATTTTGATGATTTAGAT 2079 Db  
681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700 Qy  
2080 GAAAGTAGAAAGTATATCTTCATTAACCCCTGATATCAAGAAGAAATGGATATTTTA 2139 Db  
701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720 Qy  
2140 AAAGATCTTAACATCAATTTCAAAATAAGATGCCAAAATCGCAGTCAGTATTTCTATGCC 2199 Db  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740 Qy  
2200 AATACATTTAAACGGCTAGTGAATAAACTAAACCAATATTTATGATATAATAAAAAATA 2259 Db  
741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760 Qy  
2260 TTCGTTATTTATCTACATGTTGTAAGAAATCATCTTACCCAGACATCAAAAAAGAAATA 2319 Db  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780 Qy  
2320 TTGGCTTTCTATATAGCACCAAGTGAATATTTTACTAAATATATGACATCTCATATTAC 2379 Db  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800 Qy  
2380 ACGAGTAATAGACATAATAAAACCTGAGGCACATTTTAAGTAAATATTAATAATAGTAC 2439 Db  
801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820 Qy  
2440 TTAATCTAAATTTGTGAATATACATCATTTTGTATATCATGACAGCTATTCGTTAAATAT 2499 Db  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840 Qy  
2500 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAAATTTCTCAGCATTAACACAT 2559 Db  
841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860 Qy  
2560 GATTGGATCGAGAAAAATCAATCGCATCCACCATTTAAAAAGCTGATTAAAAACCTATTTT 2619 Db  
861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880 Qy  
2620 AATGCAATGACTTAAGAAAGTATGAATGTGAAGGGGATCAAGAGTATGTTTATGAAG 2679 Db  
881 TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900 Qy  
2680 TATGGCTACCGCATGAGCTTCTGAGGATTTAAAGAAGTCATCACATCCCTGCCAATCA 2739 Db  
901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920 Qy  
2740 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTTGCACCTTTTAAATC 2799 Db  
921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940 Qy  
2800 TTAGAAAGAAAAACCGGCATGATTTTAAATAAAACATGACCCCTGACCTTATATGCTTGG 2859 Db

```
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2860 GAACGAAATTTACAAATGGACAAATGAAACAAATTCAAAGTGCAGAAAGGCGAAATATC 2919

Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCGTTAAACAGTTTCATTAATAGTATAACGCTA 2955

RESULT 15
US-09-842-484A-1
; Sequence 1, Application US/09842484A
; Publication No. US20030104601A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL L.
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 4605.003
; CURRENT APPLICATION NUMBER: US/09/842.484A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-842-484A-1

Alignment Scores:
Pred. No.: 0 Length: 2979
Score: 4490.50 Matches: 843
Percent Similarity: 93.11% Conservative: 62
Best Local Similarity: 86.73% Mismatches: 60
Query Match: 87.91% Indels: 7
DB: 3 Gaps: 2

US-10-642-248-2 (1-972) x US-09-842-484A-1 (1-2979)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 61 ATGAATACATTTATCACAAGCAATAAAGCATATATACAGCAATGACTATGAATTAGCACTC 120

Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 121 AAATATTGTGAGAAGTCTGTGAAACCTACGGCGGCAAAATCGTTGAATTCCAAATATC 180

Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 181 AAATGTAAAGAAATCTC-----TCGACCAATTCT-----TATGTAAGT 219

Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 220 GAAGATAAAAAACAGTGTGTGCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 279

Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 280 TCCAACGTAAAAAAATTAACCTCTATCCGAATCAGAAAAAAACAGTTTAAAAAAATAATGG 339

Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 340 AAATCTATCACTGGGAAAAAATCGGAGAACCGAGAAATCAGAAAGGTGGAAGTAGTACCC 399

Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 400 AAAGATTTCCTAAAGATCTTGTCTTCTGCTCCATTCGATGAGCTATGTTAATGATTTTACA 459

Qy 141 TrpTyrLysLysArgLysLysArgGlyLysProGluHisGlnHisValGlyLeu 160
Db 460 TGGTACAAAAATCGAAAAAAAGCTTTAGGTATAAGCCTGTAAATAAGAAATATCGGTCTT 519

Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 520 TCTATTATTCTCACAATTTAATCGTAGCCGTATTTAGATATACGTTAGCCTGTTTG 579
```

```
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 580 GTCATCAGAAACAAACATACCATTGGAAGTCGTTGTTGCGATGATGTTAGTAGTAAGAA 639

Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 640 AACTTACTTACCATTGTCGCAAAAATACGAAACAAAACCTTGACATAAAGTATGTAGACAA 699

Qy 221 LysAspAsnGlyPheGlnAlaSerAlaIleArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 700 AAAGATTATGGATATCAATTTGTGTCAGTCAGAAACCTTAGGTTTACGTACAGCAAAAGTAT 759

Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260
Db 760 GATTTTGTTCGATTCCTAGACTCGATATGGCACCACAATATATGGGTTCATTTCTTAT 819

Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 820 CTTACAGAACTATTAGACACAATGATATTGTTTTTAATTGGACCTAGAAAAATATGTGAT 879

Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 880 ACTCATAATATTACCGCAGAACAAATTCCTTAACGATCCATATTTAATAGAAATCACTACCT 939

Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320
Db 940 GAAACCGCTACAAATAACAAATCCTTCGATTACATCAAAAGGAAATATATCTGTTGGATTGG 999

Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 1000 AGATTAGAACATTTCAAAAAACCGGATATCTACGTCATGTGATTCTCGGTTTCGGTAT 1059

Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360
Db 1060 TTTGTTGCGGGTAATGTTCATTTTCTAAAGAAATGGCTAAATAAAGTAGGTTCGTTCCGAT 1119

Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1120 GAAGAATTTAATCATTTGGGGGGCGGAGATGTAGAATTTGGTTACAGATTTATTTGCCAAA 1179

Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1180 GGCTGTTTTTTCAGAGTAATTTGACGCGGAATGCGCCATCCATCAAGAACCCACCTGGTAAA 1239

Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1240 GAAAAATGAACAGAACCGGAAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTGAAGAAAG 1299

Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnAspValPro 440
Db 1300 GTACCTTACATCTATAGAAGCTTTTACCANTAGAAGATTCACATATTTCATAGAAATACCT 1359

Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1360 TTAGTTTCTATTATATCCCGCTTATAACTGTGCAAAATATATATTCAAAAGATGTGTAGAT 1419

Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1420 AGTGCTCTTAATCAAACTGTGTGCGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA 1479

Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1480 GATAATACCTTTAGAAGTGATCAATAGCTTTTATGGTAATAATCTTAGGGTACGCATCATG 1539

Qy 501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 1540 TCTAAACCAATGGCGAATAGCTCCTCAGCATCAATGCACCGCTTTCTTTTGTCTAAAGGT 1599

Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1600 TATTACATTCGGCAGTTAGATTTCAGATGATTATCTTTGAGCCTGTATGCAGTTGAACCTGTGT 1659
```



```
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1660 TTAAGAAGATTTTAAAGATATAAACCCTAGCTTGTGTATATACCACCTAATAGAAACGTC 1719
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580
Db 1720 AATCCGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTCACGAGAAAAA 1779
Qy 581 LeuThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1780 CTCACACGGCTATGATGCTCACCATTTTAAAGATGTTTACGATTAGAGCTTGGCATTTA 1839
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1840 ACGGATGGATTTAACGAAATATTGAAAAACCGCTGGATTATGACATGTTCTTAAACTC 1899
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1900 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAATCTGCTATAAACCGCGTATTACATGGT 1959
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
Db 1960 GATAACACATCCATTAAGAAATCTGGCATTCGCAATCAAAAGAAAAACCAATTTTGTGTAGTCAAT 2019
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 2020 CAGTCATTAATAGACAGGCGATCAATTTATTTATTAATGACAAATTTTGATGATTAGAT 2079
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2080 GAAAGTAGAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTA 2139
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2140 AAAGATCTTAAACTCAATCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTCTATCCC 2199
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 2200 AATACATTAACCGGCTTAGTGAAANAACTAACAATATTTTGAATATTAATAAANAATA 2259
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2260 TTCGTTATTATTCTACATGTTGATAAGAAATCATCTTACACAGACATCAAAAAAGAAATA 2319
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuAsnAsnAspIleSerTyrTyr 780
Db 2320 TTGGCTTTCTATCATAGCACCAGTGAATATTTTACTAAAAATGACATCTCATATTTAC 2379
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2380 ACGAGTAATAGACTAATAAAAACTAGGCACATTTTAAGTAATATTAAATAAATAAGTCAG 2439
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2440 TTAATCTAATTTGTAATACATCATTTTGTATAATCATGACAGCCTATTGCTTAAAAAT 2499
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2500 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2559
Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2560 GATTGGATCGAANAATCAATCGGCATCCACCATTTTAAAGAGCTGATTAAAAACCTATTTT 2619
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2620 AATGACATGACTTAAGAAGTATGAATGTGAAGGGGCATCACAGGTATGTTTATGAAG 2679
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900
Db 2680 TATGCGCTACCGCATGAGCTTCTGACGATTATTAAGAAGTTCATCACATCTCTGCCAATCA 2739
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheAlaLeuLeuIle 920
```

```
Db 2740 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAATTTGCACITTTTATC 2799
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2800 TTAGAAAAAGAAAAACCGGCCCATGTATTATTAATAAACAATCGACCCCTGACTTATATGCTTGG 2859
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2860 GAACGAAAAATTACAATGGACAATGAACAAATTCAAAAGTGCAAAAAAGGCGAAAAATATC 2919
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCGGTTAACCAAGTTTCATTATTATTAAGTATAACGCTA 2955
```

Search completed: January 9, 2006, 02:27:35  
Job time : 1698 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 8, 2006, 16:53:15 ; Search time 7680 Seconds

(without alignments)  
5921.490 Million cell updates/sec

Title: US-10-642-248-2

Perfect score: 5108

Sequence: 1 MNTLSQAIKAYNSNDYQAL.....SAKGENIPVKNFIINSITL 972

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool\_p/US10642248/runat\_06012006\_125010\_26878/app\_query.fasta\_1.1159  
-DB=EST -OPMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10642248 @CGN\_1\_1\_8010 @runat\_06012006\_125010\_26878 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gsa1:\*  
10: gb\_gsa2:\*  
11: gb\_gsa3:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	225	4.4	1223	9	CC799180
C 2	220	4.3	878	10	C2545903
C 3	220	4.3	2110	9	BH770860
C 4	214.5	4.2	807	10	CL696206
5	210.5	4.1	832	10	C2541282
6	207	4.1	773	10	CL673825
C 7	201	3.9	720	10	CL677451

CL652986	PRI0116b_	742	10	CL652986	3.9	201	3.9
CL683612	PRI0137b_	829	10	CL683612	3.9	201	3.9
CZ541577	SRAA-aad3	841	10	CZ541577	3.9	197.5	3.9
AI724383	RH121_34	475	1	AI724383	3.8	195	3.8
BH387189	AG-ND-138	753	9	BH387189	3.7	189.5	3.7
BH861035	312_Liarte	655	9	BH861035	3.7	188	3.7
CJ414912	CJ414912	724	7	CJ414912	3.6	183.5	3.6
CL680585	PRI0129d	468	10	CL680585	3.4	173	3.4
AG948871	Drosophila	662	10	AG948871	3.4	173	3.4
DQ049456	Homo sapi	1500	11	DQ049456	3.3	171	3.3
CJ390966	CJ390966	647	7	CJ390966	3.3	170	3.3
AK028506	Mus muscu	3796	4	AK028506	3.3	169.5	3.3
AK019995	Mus muscu	3683	4	AK019995	3.3	168.5	3.3
BH770718	LLMGTg46	1497	9	BH770718	3.2	162.5	3.2
BH368025	BJ368025	630	3	BJ368025	3.2	161	3.2
CZ534794	SRAA-aac9	846	10	CZ534794	3.2	161	3.2
BJ364255	BJ364255	595	3	BJ364255	3.1	160.5	3.1
BJ393189	BJ393189	541	3	BJ393189	3.1	160	3.1
BJ367215	BJ367215	563	3	BJ367215	3.1	160	3.1
CX892917	JGI_CAAW4	846	8	CX892917	3.1	159.5	3.1
AK049222	Mus muscu	2748	4	AK049222	3.1	159.5	3.1
AG936607	Drosophila	297	10	AG936607	3.1	158	3.1
CR857560	Pongo pyg	6021	4	CR857560	3.0	154.5	3.0
BH382993	AG-ND-162	777	9	BH382993	3.0	152.5	3.0
BZ576465	msb2_4946	1330	9	BZ576465	3.0	152	3.0
CN230043	WLBO08001	507	8	CN230043	3.0	151	3.0
DR846253	JGI_CABE1	897	8	DR846253	3.0	151	3.0
BU365467	BU365467	783	5	BU365467	2.9	150.5	2.9
CK187525	EST776840	849	7	CK187525	2.9	150.5	2.9
CK187848	EST777163	929	7	CK187848	2.9	150.5	2.9
BZ573948	msb2_3438	853	9	BZ573948	2.9	150	2.9
BH771023	LLMGTg74	9664	9	BH771023	2.9	150	2.9
BN820362	Arabidops	1863	4	CNS0A8M6	2.9	149.5	2.9
BJ368787	BJ368787	603	3	BJ368787	2.9	148.5	2.9
BH395862	AG-ND-119	662	9	BH395862	2.9	148.5	2.9
CK235970	AGENCOURT	812	7	CK235970	2.9	147.5	2.9
AY403817	Mus muscu	1737	10	AY403817	2.9	147.5	2.9
AK033494	Mus muscu	2607	4	AK033494	2.9	147.5	2.9

ALIGNMENTS

RESULT 1  
CC799180/c  
LOCUS CC799180 1223 bp DNA linear GSS 03-SEP-2004  
DEFINITION CC799180 Rumen metagenome subtractive hybridization library  
uncloned organism genomic clone HHX01C01, genomic survey  
sequence.

ACCESSION CC799180.1 GI:40539296  
VERSION CC799180  
KEYWORDS GSS  
SOURCE uncloned organism  
ORGANISM uncloned organism  
REFERENCE unclassified sequences; environmental samples.  
1 (bases 1 to 1223)  
AUTHORS Galbraith, E.A., Antonopoulos, D.A. and White, B.A.  
TITLE Suppressive subtractive hybridization as a tool for identifying genetic diversity in an environmental metagenome: the rumen as a model

JOURNAL Environ. Microbiol. 6 (9), 928-937 (2004)  
PUBMED 15305918  
COMMENT Contact: Galbraith EA  
Department of Animal Sciences  
University of Illinois  
1207 W. Gregory Dr., Urbana, IL 61801, USA  
Tel.: 217 244 4305  
Fax: 217 333 8804  
Email: galbraith@uiuc.edu  
Insert Length: 1223 Std Error: 0.00  
Class: PCR-based subtractive hybridization.  
Location/Qualifiers  
1..1223  
/organism="uncultured organism"

FEATURES

source



```

Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 286 CGAANAACAAACGGCGGTTTCATCCGCGGTATGAAGTATTAAGCGGCTCCGGA 227
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAlaValGluLeuCys 540
Db 226 TGCTATATCTGCTTCTTGGACAGCGATGACACTTATGAACGGGACTTTATCCGACACTG 167
Qy 541 LeuLysGluPheLeuLysAsp 547
Db 166 GTGAGTAAAGTCACACAGGAT 146

RESULT 3
BH770860/c 2110 bp DNA linear GSS 01-MAY-2002
LOCUS BH770860 2110 bp DNA linear GSS 01-MAY-2002
DEFINITION LLMGTg598 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
ACCESSION BH770860
VERSION BH770860.1 GI:20373817
KEYWORDS GSS.
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
REFERENCE 1. (bases 1 to 2110)
AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is rge (56%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 2082.
Location/Qualifiers
1..2110
/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/sub_species="Cremoris"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site 1: SmaI; Library of
chromosomal fragments of L. lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."

ORIGIN
Alignment Scores:
Pred. No.: 2,53e-13 Length: 2110
Score: 220.00 Matches: 136
Percent Similarity: 38.81% Conservative: 112
Best local Similarity: 21.28% Mismatches: 206
Query Match: 4.31% Indels: 186
DB: 9 Gaps: 30

US-10-642-248-2 (1-972) x BH770860 (1-2110)
Qy 411 AsnIleThrLeuAspIleMetArgGluLysValProTyrIleTyrArgLysLeuLeuPro 430
Db 1793 AATTTGAGTGTACAATGCTCAGATCT-----TACCATTACAACCTCCG 1749
Qy 431 IleGluAsp-----SerHisIle-AsnArgValProLeu----- 441
Db 1748 ATGGATGAATATCGTTTCAGGAATAGAACATATTATCTTTTAAGTAGGTGAATATGACAA 1689
Qy 442 ----ValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAs 460
Db 1688 AAAAGTATCAGTCGTAGTGACATGCTACATCAACGAAAAATTTATGAAGATGCTTACG 1629

```

```

Qy 460 pSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerTh 480
Db 1628 TAGCATTTTTCGCGCAAACTCATCAGAAACATTGAACCTTCTAGTTTAAATAGTGGTCGAC 1569
Qy 480 rAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnPro-----ArgValAr 498
Db 1568 AGATGATCTTGGTCGACGATAAATTTCAAAAGTGTGAAGAATCACCATTGCTGCTGAAACTCA 1509
Qy 498 gIleMetSerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAl 518
Db 1508 TTATTTTTCAGGAGAAATAGAGGCTAGCTTTTGTACGAAATGATGCTTTAAGTAAGAG 1449
Qy 518 aLysGlyTyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAlaValG 538
Db 1448 CACAGCGGATTTTCTACTTTTGTAGTAGTGAATATTTCTTAATGCTGACCATATTTGA 1389
Qy 538 uLeuCysLeuLysGluPheLeu----LysAspLysThrLeuAlaCysValTyrThrAs 557
Db 1388 AAAGTTACTGACAGAGCTGTTAGCAACAGATTCAGATATTGCGCTATTGTCAGCTATGGGA 1329
Qy 557 nArgAsn-----ValAsnProAspGlySerLeuIleAlaAsnGlyTyrAs 572
Db 1328 TTTTAATGCTCAAAAAGACCTTCTTCGCCAGAT----- 1295
Qy 572 nTrpProGluPheSerArgGluLysLeuThrThrAlaMetIleAlaHisPheArgMe 592
Db 1294 ----TTAGATATAGCTTTTAAAAAACAACTAGAGGGAATCTGATTGCTGCTCATTT 1239
Qy 592 tPheThrIleArgAlaTrpHisLeuThrAsp---GlyPheAsnGluLysIleGluAsnAl 611
Db 1238 G-----GTTAGGACCTCAAAAATTTGTCGACATAAAATTTGATGAATCTTTAAATAATAA 1185
Qy 611 aVal-----AspTyrAspMetPheLeuLysLeuSerGluValGlyLysPheLysHisLe 629
Db 1184 AACACTTGAAGATTATGATTTTGGTTAGGATTAATC----- 1148
Qy 629 uAsnLysIleCysTyrAsnArgValLeuHisGlyAspAsnThrSerIleLysLysLeuGl 649
Db 1147 -----ATTAATAATGAGCAAAACCTATTTT 1122
Qy 649 yIleGlnLys---LysAsnHisPheValValValAsnGlnSerLeuAsnArgGlnGlyI 668
Db 1121 TGTTTCAAAATACAAAATTGAATTCGAGTTTTAGAACAACTCTTGAGTCAAGAGGA-- 1064
Qy 668 eThrTyrTyrAsnTyr----- 673
Db 1063 -AATTGGGAAAACCTATTATCAATCGTATTTTATATACCAATAGTACAGTAAAAAAT 1005
Qy 674 -----AspGluPheAs 677
Db 1004 TCCGTCAGAACTGATAGAGCGCTCCAAAACAACTTACTACTTTGGGTAGATATAATATCA 945
Qy 677 pAspLeuAspGluSerArg---LysTyrIlePheAsnLysThrAlaGluTyrGlnGluGl 696
Db 944 AAACCTTACAAATTCATAGACAGACAGCAACTTGTGATAAAGCTCAAGAGTATCTTGAACA 885
Qy 696 uIleAspIleLeuLysAspIleIleIleGlnAsnLysAspAlaLysIleAlaValIse 716
Db 884 AGAAGAACGCGATGAAA-----AAAACAATAGCTGCACAAAGATATCCCATATTGCT----- 836
Qy 716 rIlePheTyrProAsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyr 736
Db 835 -----AATCAAGAAAGTGAATTTCTGAAATTAATACTAATTTCTTTTGCATA 792
Qy 736 r-----AsnLysAsnIlePheVa 742
Db 791 TCGGCTAATAATAAGTGATACATCCCTTAGGAAAAGAGGATGAACAATAAATTTATTCCT 732
Qy 742 lIleValLeuHisValAspLysAsnHisLeuThrPro----- 754
Db 731 ATACGTA-----CATTTAACCGAAAATACCGAGTTTGAGTCCACGCTT 590

```

```

Qy 755 -----AspileLysLysGluLeuAlaPheThyRHisLysHisGlnValAs 770
Db 689 ATTTACCAATTGAACCAATACCGACAAATTTGATGNAAGTTTCTTCATTTCAAATAGT 630
Qy 770 nileLeuLeuAsnAspIleSerTyRThrSerAsnArgLeuIleLysThrGluAl 790
Db 629 -TTAATGGATGAAATGCCITAGCTACACTGACAGCGCAAAATCTCATT-----GACGG 577
Qy 790 aHisLeuSerAsnIleAsnLys-----LeuSerGlnLeuAsnLeuAs 804
Db 576 TTTTATGCAACGCTGAAATAAAGGCTATGACTTTGTTGCTTGCTGACAGCGATGAACA 517
Qy 804 nCysGluTyRleIlePheAspAsnHisAspSerLeuPheValLysAsnAspSer----- 822
Db 516 TTATGGATTTGAAAAAATCTGCATCCTATGATTCGGTGACAAATATGATGATCTGTTT 457
Qy 823 -----TyrAlaTyRMetLysLysTyRAspValGlyMe 833
Db 456 TGGACCAAGTTTACGATTTTGAAGGAATTTTCTTAAGCTTTAATAA---GATTCAAATGT 400
Qy 833 tAsnPheSerAlaLeuThrHisAspTrpIleGluLysIleAsnAlaHisProPheLys 853
Db 399 TGATTTCTGGGAATTACTAATAACCGAAGTCATAAAGTAAAGTAAACCATGGAAGCCCGTGA 340
Qy 853 sLysLeu-----IleLysThrTyRAsnAspAsnAspLeuLysSerMe 868
Db 339 AGCAATTTGTTTACCAGATCATATTCAAGTTATTTTGTAAATTACAAACAAAATAATGT 280
Qy 868 tAsnValLysGlyAlaSerGlnGlyMetPheMetThrTyrAlaLeuAlaHisGluLeuLe 888
Db 279 AAAAAGTAAGCT-----TTTGAAGATTTTGGCAAAATATTGAAGTTT 235
Qy 888 uThrIleLysGluValleThrSerCysGlnSerIleAspSerValProGluTyRAs 908
Db 234 AGATGATGTTGTGAAGTCATTTGAAAATATGAACA-----GCAATGACGAATAT-- 183
Qy 908 nThrGluAspIleTrpPheGlnPheAlaLeuLeuIleLeuGluLysLysThrGlyHisVa 928
Db 182 -TTTGAAGATGCTGGCTTT-----AAATCAGAGATTAAT 151
Qy 928 lPheAsnLysThrSerThrLeuThrTyRMetProTrpGluArgLysLeuGlnTrp 946
Db 150 TTTTGAC-----ACAGTAAAGAGAGTGG 126

RESULT 4
LOCUS CL696206
DEFINITION CL696206.1 GI:50218114
ACCESSION CL696206
VERSION 1
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 807)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7

```

```

FEATURES
    source
    Class: fosmid ends
    Location/Qualifiers
        1..807
            /organism="Pristionchus pacificus"
            /mol_type="genomic DNA"
            /strain="California"
            /db_xref="taxon:54126"
            /clone_lib="Mixed stage fosmid library of P. pacificus
            var. California"
            /notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 2,25e-13 Length: 807
Score: 214.50 Matches: 63
Percent Similarity: 41.54% Conservative: 50
Best Local Similarity: 23.16% Mismatches: 118
Query Match: 4.20% Indels: 41
DB: 7 Gaps: 7

US-10-642-248-2 (1-972) x CL696206 (1-807)
Qy 436 IleAsnArgValProLeuValSerIleTyRleProAlaTyRAsnCysAlaAsnTyRle 455
Db 19 ATGAACAGCACCAATAAACTTAGCCTTTTATTCCTTATATAATCGGGCGATGTTTC 78
Qy 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475
Db 79 CGCACTTGATGGAATCTTAATTACGCAAAACCTGCACTGCTCGGAAATCATATTATT 138
Qy 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyRGlYAsnAsnPro 495
Db 139 AACGATGGTTCAACGGATAATTCTGTGAAATGACAAAGATTATTCGCAAGAAATCTAC 198
Qy 496 ArgValArgIleMetSerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaVal 515
Db 199 CAGTTTCGTTTGTGCATCAGCGAATGCTGGCGCATCGTGGCGGTAATCGTGGGATT 258
Qy 516 SerPheAlaLysGlyTyRTrIleGlyGlnLeuAspSerAspTyRLeuGluProAsp 535
Db 259 GAAGTGGCAACGGCAATATGTCGCTTTTGTGATGCTGACGATGAAGTCTATCCACC 318
Qy 536 AlaValGluLeuCysLeuLysGluPheLeuLysAsp-----LysThrLeuAlaCysVal 553
Db 319 ATGTACGAACGCTGATGTTTTTGGCGTTAGAGCAGCACCTGCACGTCGGCGAGTGC-- 375
Qy 554 TyrThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyRAsnTrp 573
Db 376 -----AACGCTGACTGCTGTTTTCGTGAAACGGAGAAACCTGG 414
Qy 574 ProGluPheSerArgGluLysLeuThrAla----- 584
Db 415 CAATCCATCCCAACCGATCGCTTCCTCAACGGCGCTCTTAACGGCCCGGACTGGCTG 474
Qy 585 MetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPhe 604
Db 475 CGGATGGGGCTTCTTCGGCGCGTGGACTCAGCTTGTCTGGATGGGGTTTATCCCGCT 534
Qy 605 AsnGluLysIleGluAsnAlaValAspTyRAspMetPheLeuLysLeuSerGluValGly 624
Db 535 GATGTTATTTGTTAAAAATAACATTAATTTATTCGGGATTATCATCATCAGGATATTGTC 594
Qy 625 -----LysPheLysHisLeuAsnLysIleCysTyR 634
Db 595 TGGACAACAGAAATTCATGTTTAAACGGCTGCTGCGCGATATACCGAGCAATCATATAT 654
Qy 635 AsnArgValLeuHisGlyAspAsnThrSerIleLysLysLeu----- 648
Db 655 AATATATATCTGCAT-----AATACGTGAGTGTCGGTTGCATAGACACAGGAATAAA 708
Qy 649 GlyIleGlnLysLysAsnHisPheValValAsnGlnSerLeuAsnArgGlnGlyIle 668
Db 709 AACCTTAATTATCAACGTCACATATATAAGATTACCGCGCTGCTGGAGAAATTAATCGA 768

```

```

Qy 669 ThrTyrTyrAsn-----TyrAspGluPhe 676
Db 769 AATTATCGGACAAAATTATGATTATCCGGAATTI 804

RESULT 5
CZ541282 832 bp DNA linear GSS 13-MAY-2005
LOCUS SRRA-aad37b05.g1 Strongyloides ratti whole genome shotgun library
DEFINITION (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloidea; Strongyloides.
1 (bases 1 to 832)
Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,
Ritter,E., Martin,J., Wylie,T., Dante,M., Waterston,R.H.,
Clifton,S.W. and Wilson,R.
Genome Survey sequences from the rat parasitic nematode
Strongyloides ratti
Unpublished (2005)
Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristol.ac.uk) and Mark Viney
(Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,
UK.
Class: shotgun.
FEATURES
source
Location/Qualifiers
1..832
/organism="Strongyloides ratti"
/mol_type="genomic DNA"
/strain="Isolated female line ED321 heterogenic"
/db_xref="taxon:34506"
/dev_stage="infective larval stage (iL3)"
/lab_host="GS10"
/clone_lib="Strongyloides ratti whole genome shotgun
library (SRAAGSS 004)"
/note="Vector: pOTW13; Site 1: BstX1; Site 2: BstX1;
Strongyloides ratti genomic DNA was randomly sheared,
end-repaired and size fractionated to enrich for 2-4 kb
fragments. Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristol.ac.uk) and Mark Viney
(Mark.Viney@bristol.ac.uk) at the University of Bristol,
Bristol, UK. Sequencing by Washington University Genome
Sequencing Center, St. Louis, MO."
ORIGIN
Alignment Scores:
Pred. No.: 6,89e-13 Length: 832
Score: 210.50 Matches: 67
Percent Similarity: 49.34% Conservative: 45
Best Local Similarity: 29.52% Mismatches: 60
Query Match: 4.12% Indels: 56
DB: 10 Gaps: 10
US-10-642-248-2 (1-972) x CZ541282 (1-832)

Qy 423 TyrIleTyrArgLysLeuLeuProleuVal 442
Db 179 TATATTGTAAAAATAC-----CAATGCTGAAGTT 211

Qy 443 SerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSerAla 462
Db 212 TCCATCATTCACCTCGTACAAATCTTCAAAATTTCTGGAGAACCAATAGCGTCTGTA 271

Qy 463 LeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThrAspAsn 482
Db 272 CAAAACCAGACTTTTACAGATTGGGAATGGCTGATTACAGATGACAGATCTTACAGACAAT 331

Qy 483 ThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValAlaGlle---MetSer 501
Db 332 TCTGTAGAAATGATTGAGAAATA-----AACGATCCGAGAAATAAAACCTTACTGTTGCA 385

Qy 502 LysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGlyTyr 521
Db 386 GAAAAAACCGAGGAGGAGCAGCAGCATGCAAGAAATATTTTCAATAAAAAATGCTACAGGAAGA 445

Qy 522 TyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCysLeu 541
Db 446 TTTATCACCTTTCTGGATGAGATGATTTTGGGAACCAAGAAATTTCTTCAGGAA---ATG 502

Qy 542 LysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThr-----Asn 557
Db 503 ACTGCTTTTATGAAAAATNAACACGCAGAAATTCCTTACTTCTTATGCAAGATGTGAT 562

Qy 558 ArgAsnValAsnPro-----AspGly 564
Db 563 GAAATTTAAAGCTTAAATTTGAAGACTTCAACAGCAGATAAAGAGTTACTTTTCGATAAT 622

Qy 565 -----SerLeuIleAlaAsnGlyTyrAsn----- 572
Db 623 TTATTAAAAACCTGCCGCTCTCTTTTATTATCTTCTATGATGATCTTAAAGAGATGGGT 682

Qy 573 -----TrpProGluPheSerArgGlu-LysLeu----- 581
Db 683 ATAGATATATTTCCCGGAAGGAAGTAAACGTAAGATCATGTAATGTGGCTCAATTTGCTC 742

Qy 582 -ThrThrAlaMetIleAlaHisPheArgMetPheThr---IleArgAlaTrpHisLe 600
Db 743 AAAAAATTTCCCGGTGGGAACCACTTCCGAACGATGACAAATATACAGGA-ATGCACGC 801

Qy 600 uThrAspGlyPheAsnGlu 606
Db 802 AACAAAGTGGTTTCCAGAA 820

RESULT 6
LOCUS CL673825 773 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0110C C05.2 - PRI0110C.BR (773) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL673825
VERSION CL673825.1 GI:50176112
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 773)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: 17
Class: fosmid ends.
Location/Qualifiers
1..773
source

```



```
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 1.55e-12 Length: 773
Score: 207.00 Matches: 65
Percent Similarity: 39.34% Conservative: 42
Best Local Similarity: 23.90% Mismatches: 111
Query Match: 4.05% Indels: 54
DB: 10 Gaps: 7

US-10-642-248-2 (1-972) x CL673825 (1-773)
QY 436 IleAsnArgValProLeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIle 455
Db 18 ATGAACAGCAGCAATAAATAGTTAGTTATATCCGTTATATATCGCGCGATGATTC 77
QY 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475
Db 78 CGCACTTGATGGAATCTTAAATACGCAACCTGGACTGCTCTGGAAATCATATATT 137
QY 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnPro 495
Db 138 AACGATGGTTCAACGGGATAATCTGTTGAATAGCAAAATGATTACGCGAGAAACTATCCG 197
QY 496 ArgValArgIleMetSerLysProAsnGlyIleAlaSerAlaSerAlaAlaVal 515
Db 198 CACGTTGCTTGTGTCATCAGGCGAATGCTGGCGCATCGGTGCGGTAAATCGTGGGATT 257
QY 516 SerPheAlaLysGlyTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAsp 535
Db 258 GAAGTGGCAACGGCAATATGCTTTGTCGATGCTGACGATGAGTCTATCCACC 317
QY 536 AlaValGluLeuCysLeuLysGluPheLeuLysAsp-----LysThrLeuAlaCysVal 553
Db 318 ATGTACGAAACGCTGATGACCATGGCGTTAGAGGACGACCTCGACGTGGCGCAGTGC--- 374
QY 554 TyrThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyr 573
Db 375 -----AACGTCAGCTGCTGTTTCGTGAAACGGGAGAAACCTGG 413
QY 574 ProGluPheSerArgGluLysLeuThrAla----- 584
Db 414 CAATCCATCCCGACCGATCGCTCGCTCAACGGCGCTTAAACGGCGCGACTGGCTG 473
QY 585 MetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPhe 604
Db 474 CGGATGGGGCTTCTTCGCGCGGTGGACTCACGTTGCTGGATGGGGGTTTATCGCGT 533
QY 605 AsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeuSerGluValGly 624
Db 534 GATGTTATTCTTAAAAATAACATTAAATTTATTGCCGGATTACATCATAGGATATTGTC 593
QY 625 -----LysPheLysHisLeuAsnLysIleCysTyr 634
Db 594 TGGACAACAGAAATTCATGTTTAACGGCTGCGTGGCGATATACCGGCAATCATATAT 653
QY 635 AsnArgValLeuHisGlyAspAsnThrSerIleLysLysLeuGlyIleGlnLysAsn 654
Db 654 AAATATTATTCGCAAT-----AATACGTCAGTCAGTCG----- 686
QY 655 HisPheValValAsnGlnSerLeuAsnArgGlnIleThrTyrTyrAsnTyrAsp 674
Db 687 -----TTGCATAGACAAAGGGAATAAAAAACCTTAAATAT--- 719
QY 675 GluPheAspAspLeuAspGluSerArgLysTyrIle 686
Db 719 -----
```

```
Db 720 -----CAACGTCACATATATT 734

RESULT 7
CL677451/c
LOCUS
DEFINITION
CL677451 720 bp DNA linear GSS 09-JUL-2004
PRI0120b.D10.2 - PRI0120b.BR (720) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
VERSION CL677451.1 GI:50183459
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 720)
Srinivasan,J., Otto,G.W., Kahlow,U., Geigler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
JOURNAL
PUBMED
14681447
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..720
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

FEATURES
source
1..720
ORIGIN
Alignment Scores:
Pred. No.: 6.87e-12 Length: 720
Score: 201.00 Matches: 45
Percent Similarity: 47.30% Conservative: 25
Best Local Similarity: 30.41% Mismatches: 68
Query Match: 3.94% Indels: 10
DB: 10 Gaps: 2

US-10-642-248-2 (1-972) x CL677451 (1-720)
QY 436 IleAsnArgValProLeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIle 455
Db 509 ATGAACAGCAGCAATAAATAGTTAGTTATATCCGTTATATATCGCGCGATGATTC 450
QY 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475
Db 449 CGCACTTGATGGAATCTTAAATACGCAACCTGGACTGCTCGGAAATCATATATT 390
QY 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnPro 495
Db 389 AACGATGGTTCAACGGGATAATCTGTTGAATAGCAAAAGTATTACCGAGAAACTATCCG 330
QY 496 ArgValArgIleMetSerLysProAsnGlyIleAlaSerAlaSerAlaAlaVal 515
Db 329 CACGTTCTGTTGTCATCAGCGCATCGTGGCGCATCGTGGCGGTAATCGTGGGATT 270
QY 516 SerPheAlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAsp 535
Db 269 GAAGTGGCAACGGCAATATGTCGCTTTTGTGATGCTGACGATGAAAGTCTATCCACC 210
```

```

Qy 536 AlavalGluLeuCysLeuLeuValPheLeuLeuAsp-----LysThrLeuAlaCysVal 553
Db 209 ATGTACGAACGCTGATGACCATGCGCTTAGAGCAGACCTCGAGCGGCGCAGTGC--- 153
Qy 554 TyrThrThrAsnArgAsnValAsnProAspGlySerLeuLeuAlaAsnGlyTyrAsnTrp 573
Db 152 -----AACGCTGACTGCTGTTTTCGTGAAACGGGAGAAACCTGG 114
Qy 574 ProGluPheSerArgGluLeuLeu 581
Db 113 CAATCCATCCCCACCGATCGCCTT 90

RESULT 8
CL652986 742 bp DNA linear GSS 09-JUL-2004
LOCUS PRI0116b.D06 - PRI0116b.B21 (742) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL652986 GI:50131764
VERSION 1
KEYWORDS Pristionchus pacificus
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 742)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppAD8: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
Location/Qualifiers
source
1..742
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 7,228-12 Length: 742
Score: 201.00 Matches: 45
Percent Similarity: 47.30% Conservative: 25
Best Local Similarity: 30.41% Mismatches: 68
Query Match: 3.94% Indels: 10
DB: 10 Gaps: 2

US-10-642-248-2 (1-972) x CL652986 (1-742)

Qy 436 IleAsnArgValProLeuValSerIleTyrProAlaTyrAsnCysAlaAsnTyrIle 455
Db 145 ATGACAGCAGCAACAACTAGTGTATTATTCGTTATATGCGGCGCATGATTC 204
Qy 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475
Db 205 CGCACTTGTATGAACTCTTAAATAGCAACCTGGACTGCTCTGGAATCATATTATT 264
Qy 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnPro 495

```

```

Db 265 AACGATGGTTCAACGGATAATTCTGTGAAATAGCAAGATTATTACGAGAAAATATCCG 324
Qy 496 ArgValArgIleMetSerLysProAsnGlyGlyIleAlaSerAlaSerAlaVal 515
Db 325 CAGTTTCGTTTGTGTCATCAGCGAATGCTGGCGCATCGGTGCGGTAATCGTGGGATT 384
Qy 516 SerPheAlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAsp 535
Db 385 GAAGTGGCAACGGCAAAATATGTCGCTTTTGTGATGCTGACGATGAAGTCTATCCACC 444
Qy 536 AlavalGluLeuCysLeuLeuValPheLeuLeuAsp-----LysThrLeuAlaCysVal 553
Db 445 ATGTACGAACGCTGATGACCATGCGCTTAGAGCAGACCTCGAGCGGCGCAGTGC--- 501
Qy 554 TyrThrThrAsnArgAsnValAsnProAspGlySerLeuLeuAlaAsnGlyTyrAsnTrp 573
Db 502 -----AACGCTGACTGCTGTTTTCGTGAAACGGGAGAAACCTGG 540
Qy 574 ProGluPheSerArgGluLeuLeu 581
Db 541 CAATCCATCCCCACCGATCGCCTT 564

RESULT 9
CL683612/c 829 bp DNA linear GSS 09-JUL-2004
LOCUS PRI0137b.E11.2 - PRI0137b.BR (829) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL683612 GI:50191365
VERSION 1
KEYWORDS Pristionchus pacificus
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 829)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppAD8: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
Location/Qualifiers
source
1..829
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 8,678-12 Length: 829
Score: 201.00 Matches: 45
Percent Similarity: 47.30% Conservative: 25
Best Local Similarity: 30.41% Mismatches: 68
Query Match: 3.94% Indels: 10
DB: 10 Gaps: 2

US-10-642-248-2 (1-972) x CL683612 (1-829)

```

```
Qy 436 IleAsnArgValProLeuValSerIleTyrIleProAlaIleTyrAsnCysAlaAsnTyrIle 455
Db 564 ATGACAGCACCATAAATAGTGTATTATTCGTTATATATATGCGGGCGATGATTC 505
Qy 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475
Db 504 CGCAGTTGTATGGAATCTTTAATTACGCAACCTGGAGCTCTCTGGAATCATTTATT 445
Qy 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnPro 495
Db 444 AACGATGTTCAACGGATAATCTTGTGTAATAGCAAAAGTATTACGCGAGAAACTATCCG 385
Qy 496 ArgValArgIleMetSerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaVal 515
Db 384 CAGCTTGTTGTGATCAGCGAATGCTGCGCCATCGGTGGCGCTAATCGTGGGATT 325
Qy 516 SerPheAlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAsp 535
Db 324 GAAGTGGCAACGGGCAATATGTCCTTTGTCGATGCTGACGATGAAGTCTATCCACC 265
Qy 536 AlaValGluLeuLysLeuLysGluPheLeuLysAsp-----LysThrLeuAlaCysVal 553
Db 264 ATGTACGAAACGCTGATGACCATGCGCTTAGAGACGACCTCGACGTGGCGCAGTGC--- 208
Qy 554 TyrThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyr 573
Db 207 -----AACGCTGATGGTGTGTTTTCGTGAAACGGGAGAAACCTGG 169
Qy 574 ProGluPheSerArgGluLysLeu 581
Db 168 CAATCCATCCCCCGATCGCCTT 145
```

```
RESULT 10
CZ541577 841 bp DNA linear GSS 13-MAY-2005
LOCUS SRAA-aad39b05.g1 Strongyloides ratti whole genome shotgun library
DEFINITION (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.
ACCESSION CZ541577
VERSION CZ541577.1 GI:64667882
KEYWORDS GSS.
```

```
ORGANISM Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloidea; Strongyloides.
```

```
REFERENCE 1. (bases 1 to 841)
Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,
Ritter,E., Martin,J., Wylie,T., Dante,M., Waterston,R.H.,
Clifton,S.W. and Wilson,R.
```

```
TITLE Genome Survey sequences from the rat parasitic nematode
Strongyloides ratti
```

```
JOURNAL Unpublished (2005)
COMMENT Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
```

```
Email: nematode@watson.wustl.edu
Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristol.ac.uk) and Mark Viney
(Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,
UK.
```

```
FEATURES
source Location/Qualifiers
1. 841
/organism="Strongyloides ratti"
/mol_type="genomic DNA"
/strain="Isotemale line ED321 heterogonic"
/db_xref="taxon:34506"
/dev_stage="infective larval stage (L3)"
/lab_host="GS10"
/clone_lib="Strongyloides ratti whole genome shotgun
library (SRAAGSS 004)"
```

```
/note="Vector: pOTW13; Site 1: BatX1; Site 2: BatX1;
Strongyloides ratti genomic DNA was randomly sheared,
end-repaired and size fractionated to enrich for 2-4 kb
fragments. Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristol.ac.uk) and Mark Viney
(Mark.Viney@bristol.ac.uk) at the University of Bristol,
Bristol, UK. Sequencing by Washington University Genome
Sequencing Center, St. Louis, MO."
```

## ORIGIN

```
Alignment Scores: 2,26e-11 Length: 841
Pred. No.: 197,50 Matches: 48
Score: 56,55% Conservative: 34
Percent Similarity: 56,55% Mismatches: 46
Best Local Similarity: 33,10% Indels: 17
Query Match: 3,87% Gaps: 5
DB: 10
```

US-10-642-248-2 (1-972) x CZ541577 (1-841)

```
Qy 423 TyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValProLeuVal 442
Db 179 TATATTGTAATAAATAC-----CAAAATGCGCTGAAGTT 211
Qy 443 SerIleTyrIleProAlaIleTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSerAla 462
Db 212 TCCATCATTTACCCCTGCTACAATTTCTCACAATTTCTGGAATAACAATAAGCTCGTA 271
Qy 463 LeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThrAspAsn 482
Db 272 CTAAACCAACTTTTACAGATTGGGAATGCGTCAATACAGATCAGATCTACAGACAAT 331
Qy 483 ThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIle---MetSer 501
Db 332 TCTGTGTAAATGATGAAAAATA-----AACGATCCGAGATAAAACTTACTGTTGCA 385
Qy 502 LysProAsnGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGlyTyr 521
Db 386 GAAAAAACGGAGGAGGAGGACATGCAAGAAATATTTTCATTAATAATGCTACAGGAAGA 445
Qy 522 TyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCysLeu 541
Db 446 TTTATCACCTTTCTGGATGCGAGATGATTTTGGGAACCAAGATTTCTTCAAGAA---ATG 502
Qy 542 LysGluPheLeuLysAspLysThrLeuAlaCysValTyrThr-----Asn 557
Db 503 ACTGCTTTTATGAAAAATCAAAACGCGAGAAATTCCTACTTCTTACTTATGCAAGATGTGAT 562
Qy 558 ArgAsnValAsnPro 562
Db 563 GAAAAATTTCAAGCCT 577
```

## RESULT 11

```
LOCUS RHIZ1_34_H11.Y2_A001 Rhizome1 (RHIZ1) Sorghum halepense cDNA, mRNA
DEFINITION sequence.
AI724383 475 bp mRNA linear EST 19-JUL-2000
AI724383.1 GI:5043235
```

```
ACCESSION AI724383
VERSION AI724383.1
KEYWORDS EST.
```

```
SOURCE Sorghum halepense
ORGANISM Sorghum halepense
```

```
REFERENCE 1. (bases 1 to 475)
Cordonnier-Pratt,M.-M., Gingle,A., Pratt,L.H. and Paterson,A.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
```

```
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Pratt,L.H. and Paterson,A.
TITLE An EST database from Sorghum: Sorghum halepense rhizomes
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
```

Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: T7

High quality sequence start: 16

High quality sequence stop: 475

POLYA=No.

#### FEATURES

source

1. .475

/organism="Sorghum halepense"

/mol\_type="mRNA"

/db\_xref="taxon:4560"

/clone\_lib="Rhizome1 (RHIZ1)"

/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II.

Clones to be sequenced were prepared by mass excision."

#### ORIGIN

Alignment Scores:  
Pred. No.: 1.72e-11 Length: 475  
Score: 195.00 Matches: 44  
Percent Similarity: 46.62% Conservative: 25  
Best Local Similarity: 29.73% Mismatches: 69  
Query Match: 3.82% Indels: 10  
DB: 1 Gaps: 2

US-10-642-248-2 (1-972) x A1724383 (1-475)

QY 436 IleAsnArgValProLeuValSerIleTyrlleProAlaTyraAsnCysAlaAsnTyrlle 455  
Db 33 ATGAACAGCACCACCAATAAACTTAGTCTATTATTTCGTTATATATATGCGGCGATATTC 92  
QY 456 GlnArgCysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCys 475  
Db 93 CGCATTTGTATGGAAATCTTAAATACGCAAACTCGACTGCTCTCGAATATCATATTATT 152  
QY 476 AsnAspGlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrlleGlyAsnAsnPro 495  
Db 153 AACGATGGTTCACCGGATTAATCTCTGTAATAGCAAAAGTATTACGACAGAACTATCCG 212  
QY 496 ArgValArgIleMetSerLysProAsnGlyIleAlaSerAlaSerAsnAlaVal 515  
Db 213 CACGTTCTGTTTGTGATCAGCGCAATGCTGCGCATCGTGGCGCGTAATCGTGGATT 272  
QY 516 SerPheAlaLysGlyTyrlleGlyGlnLeuAspSerAspAspTyrlleGluProAsp 535  
Db 273 GAAGTGGCAACGGCAATATGCTGTTTGTGATGCTGACGATGAAGTCTATCCACC 332  
QY 536 AlaValGluLeuCysLeuLysGluPheLeuLysAsp-----LysThrLeuAlaCysVal 553  
Db 333 ATGTACGAACCGCTGATGACCATGGCTTGTAGAGGACGACCTCGACGTGCGCAGTGC--- 389  
QY 554 TyrThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrlle 573  
Db 390 -----AACGCTGACTGCTGTTTTCGTGAAACGGGAGAAACCTGG 428  
QY 574 ProGluPheSerArgGluLysLeu 581  
Db 429 CAATCCATCCACCGCATGCGCTT 452

#### RESULT 12

BH387189/c

LOCUS

DEFINITION

AG-ND-138J10.7F ND-TAM Anopheles gambiae genomic clone

AG-ND-138J10, genomic survey sequence.

ACCESSION

BH387189

VERSION

BH387189.1 GI:17333331

KEYWORDS

GSS

SOURCE

BH387189 753 bp DNA linear GSS 10-DEC-2001  
AG-ND-138J10.7F ND-TAM Anopheles gambiae genomic clone  
AG-ND-138J10, genomic survey sequence.  
BH387189  
BH387189.1 GI:17333331  
GSS  
Anopheles gambiae (African malaria mosquito)

#### ORGANISM

Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;  
Culicidae; Anophelinae; Anopheles.

#### REFERENCE

AUTHORS

1 (bases 1 to 753)  
Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,  
Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B.,  
Gardner,M.J. and Collins,F.H.

#### TITLE

Construction of a BAC library and generation of BAC end  
sequence-tagged connectors for genome sequencing of the African  
malaria mosquito Anopheles gambiae

#### JOURNAL

PUBMED

COMMENT

Mol. Genet. Genomics 268 (6), 720-728 (2003)  
1265398

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjloftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by  
F.H. Collins and sequenced by The Institute for Genomic Research  
(TIGR). The BAC library was generated from A. gambiae PEST strain  
DNA. All DNA was extracted from newly hatched first instar larvae  
to minimize the inclusion of DNA from microorganisms that inhabit  
the gut. The DNA is derived from mixed sexes of larvae. The BAC  
library was constructed at Texas A&M University BAC Center  
University, College Station, Texas 77843-2123, USA using a HindIII  
partial digest.  
Seq primer: M13 For  
Class: BAC ends.

#### FEATURES

source

1. .753

/organism="Anopheles gambiae"

/mol\_type="genomic DNA"

/strain="PEST"

/db\_xref="taxon:7165"

/clones="AG-ND-138J10"

/clone\_lib="ND-TAM"

/note="Vector: pECBAC1; Site\_1: HindIII"

#### ORIGIN

Alignment Scores:  
Pred. No.: 1.6e-10 Length: 753  
Score: 189.50 Matches: 47  
Percent Similarity: 48.53% Conservative: 19  
Best Local Similarity: 34.56% Mismatches: 51  
Query Match: 3.71% Indels: 19  
DB: 9 Gaps: 4

US-10-642-248-2 (1-972) x BH387189 (1-753)

QY 440 ProLeuValSerIleTyrlleProAlaTyraAsnCysAlaAsnTyrlleGlnArgCysVal 459  
Db 482 CCGTTAGTCAGCATCATTAATACCATGCTATATGCTTCATATATATAAAGAGTTCTT 423  
QY 460 AspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySer 479  
Db 422 GAAAGTGTCATCAACAACTTACCAGAAATGAAATGATTTATTTATCAATCATGAACG 363  
QY 480 ThrAspAsnThrLeuGluValIleAsnLysLeuTyrlleGlyAsnAsnProArgValArgIle 499  
Db 362 ACAGATACCTACATTAGATATTATACGAATTTT-----AAAAATCTCATTTTCATATT 309  
QY 500 MetSerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLys 519  
Db 308 TACAGTCAGGAAACAAAGGGCTTTCTGATACCAGAAATTTTGGATTAGAAAAGCATCTT 249  
QY 520 GlyTyrlleGlyGlnLeuAspSerAspTyrlleGluProAspAlaValGluLeu 539  
Db 248 GGTGATTTTGTTCTTTTTCGACAGTACGATATTCTTCCTGCTACTACTATAGAA--- 192  
QY 540 CysLeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrlleThrThrAsnArgAsn 559



Db338ATGCCCAATCCATAGAACTCAATGAAGCTGCTTTGGATCCGCTAGCAATCTATT397

Qy553ValTyrThrThrAsnArgAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrAsn572

Db398ATTGGCACA-----AAGGTTTATCGT418

Qy573TrpProGluPheSerArgGluLysLeuThr-----582

Db419GAACCCGCAACTCAACACGATACACAAATGGATCAACACACTAACCTGCACAA478

Qy583-----ThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu600

Db479CTATACACACAAATGTACACTTCATCGGACCCTGAGTCCGCAACTTGGTTTATG538

Qy601ThrAspGlyPheAsnGluLysIleGluAsnAlaVal-----612

Db539-----CATAAAAATGTGTACAAATGAAGTTGCTGCAATTTCTGAAGCTGGAAAG586

Qy613-----AspTyrAspMetPheLeuLysLeuSerGluValGly-----624

Db587GGAACACCGGAAGACTATATCTCTTTTAAATCAATTTAAACTTTGGTGGAAACCTACAT646

Qy625-----LysPheLysHisLeuAsnLysIleCysTyrAsnArgVal637

Db647AGAGTANACCATGTTTACTAAGTATCGACAT-----679

Qy638LeuHisGlyAspAsnThrSerIle645

Db680---CATGGCAACGCTACTAGTCTA700

RESULT 15

CL680585/c

LOCUS

DEFINITION

PR10129d.B07.2 - PR10129d.BR (468) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1. .468

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"

/note="Vector: pEpifos-5 Fosmid vector"

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

5.99e-09

173.00

46.27%

29.85%

3.39%

10

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

468

40

22

62

10

2

US-10-642-248-2 (1-972) x CL680585 (1-468)

Qy450AsnCysAlaAsnTyrIleGlnAcgCysValAspSerAlaLeuAsnGlnThrValValAsp469

Db467AATCCGGAGATGATTTCGCCACTTGTATGGAATCTTTAATAGCAAACTTGGACTGCT408

Qy470LeuGluValCysIleCysAsnAspGlySerThrAspAsnThrLeuGluValIleAsnLys489

Db407CTGGAATCATTAATTATTAAAGATGTTCAACGGATAATCTGTTGAAATAGCAAGTAA348

Qy490LeuTyrGlyAsnAsnProArgValArgIleMetSerLysProAsnGlyGlyIleAlaSer509

Db347TACGCAGAAAATATATCCGCACGTTCTGTTTGTGCATCAGGCGAATGCTGGCGCATCGGTG288

Qy510AlaSerAsnAlaAlaValSerPheAlaLysGlyTyrTyrIleGlyGlnLeuAspSerAsp529

Db287GCGCGTAATCGTGGATTTGAAGTGGCAACGGGCAAAATATGTCGCTTTTGTGATGCTGAC228

Qy530AspTyrLeuGluProAspAlaValGluLeuLysGlyLeuLysGluPheLeuLysAsp-----547

Db227GATGAGTCTATCCACCATGTACGAAACGCTGATGACCATGGCGTTAGAGGACGACCTA168

Qy548LysThrLeuAlaCysValTyrThrAsnArgAsnValAsnProAspGlySerLeuIle567

Db167GACGTGGCGCAGTGC-----AACGCTGACTGGTGTTCGT132

Qy568AlaAsnGlyTyrAsnTyrProGluPheSerArgGluLysLeu581

Db131GAAACGGAGAAACCTGGCAATCCATCCCAACCATGCGCTT90

Search completed: January 8, 2006, 23:00:07

Job time : 7697 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 8, 2006, 13:05:42 ; Search time 1191 Seconds

(without alignments)  
5439.195 Million cell updates/sec

Title: US-10-642-248-2

Perfect score: 5108

Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAKRGENIPVKNFIINSITL 972

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool.p/US10642248/runat\_06012006\_125009\_26862/app\_query.fasta\_1.1159  
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -ENDS=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10642248 @CGN 1.1.1096 @runat\_06012006\_125009\_26862 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq\_21.\*  
1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5104	99.9	2916	9 ABT44090	Abt44090 Pasteurel
2	5104	99.9	2937	2 AAX58857	Aax58857 Pasteurel
3	5104	99.9	2937	3 AAZ35589	Aaz35589 P. multoc
4	5104	99.9	2937	10 ADC77478	Adc77478 Pasteurel

5	5104	99.9	2937	10	ADD93325	Add93325 Pasteurel
6	4502.5	88.1	2979	6	ABA05098	Aba05098 Pasteurel
7	4502.5	88.1	2979	11	ADP75650	Adp75650 Pasteurel
8	4502.5	88.1	2979	14	AEA04966	Aea04966 Chondroit
9	4490.5	87.9	2979	3	AAA27449	Aaa27449 P. multoc
10	4490.5	87.9	2979	6	ABA05097	Aba05097 Pasteurel
11	4490.5	87.9	2979	11	ADP75648	Adp75648 Pasteurel
12	3964	77.6	2271	11	ADP75667	Adp75667 Pasteurel
13	3705	72.5	2136	11	ADP75698	Adp75698 Pasteurel
14	3697	72.4	2112	14	AEA04964	Aea04964 Hyaluron
15	3693	72.3	2112	3	AAA27448	Aaa27448 P. multoc
16	3693	72.3	2112	11	ADP75718	Adp75718 Pasteurel
17	3690	72.2	2112	11	ADP75692	Adp75692 Pasteurel
18	3690	72.2	2112	11	ADP75693	Adp75693 Pasteurel
19	3689	72.2	2112	11	ADP75665	Adp75665 Pasteurel
20	3689	72.2	2112	11	ADP75695	Adp75695 Pasteurel
21	3689	72.2	2112	11	ADP75680	Adp75680 Pasteurel
22	3689	72.2	2112	11	ADP75689	Adp75689 Pasteurel
23	3689	72.2	2112	11	ADP75663	Adp75663 Pasteurel
24	3689	72.2	2112	11	ADP75687	Adp75687 Pasteurel
25	3689	72.2	2112	11	ADP75683	Adp75683 Pasteurel
26	3688	72.2	2112	11	ADP75658	Adp75658 Pasteurel
27	3688	72.2	2112	11	ADP75681	Adp75681 Pasteurel
28	3688	72.2	2112	11	ADP75686	Adp75686 Pasteurel
29	3688	72.2	2112	11	ADP75694	Adp75694 Pasteurel
30	3688	72.2	2112	11	ADP75696	Adp75696 Pasteurel
31	3688	72.2	2112	11	ADP75690	Adp75690 Pasteurel
32	3688	72.2	2112	11	ADP75659	Adp75659 Pasteurel
33	3688	72.2	2112	11	ADP75659	Adp75659 Pasteurel
34	3686	72.2	2112	11	ADP75664	Adp75664 Pasteurel
35	3686	72.2	2112	11	ADP75682	Adp75682 Pasteurel
36	3686	72.2	2112	11	ADP75688	Adp75688 Pasteurel
37	3686	72.2	2112	11	ADP75666	Adp75666 Pasteurel
38	3686	72.2	2112	11	ADP75691	Adp75691 Pasteurel
39	3686	72.2	2112	11	ADP75697	Adp75697 Pasteurel
40	3684	72.1	2112	11	ADP75685	Adp75685 Pasteurel
41	3607	70.6	2061	11	ADP75679	Adp75679 Pasteurel
42	3506	68.6	2007	11	ADP75678	Adp75678 Pasteurel
43	3471	68.0	1980	11	ADP75674	Adp75674 Pasteurel
44	3414	66.8	1953	11	ADP75657	Adp75657 Pasteurel
45	3336	65.3	1902	11	ADP75675	Adp75675 Pasteurel

#### ALIGNMENTS

RESULT 1  
ABT44090  
ID ABT44090 standard; DNA; 2916 BP.  
XX  
XX  
AC ABT44090;  
XX  
XX  
DT 17-OCT-2003 (first entry)  
XX  
XX  
DE Pasteurella multocida hyaluronan synthase DNA.  
KW Hyaluronic acid; glycosaminoglycan; hyaluronan synthase; antirheumatic;  
KW UDP-glucose 6-dehydrogenase; UDP-glucose pyrophosphorylase; orthopaedic;  
KW UDP-N-acetylglucosamine; ophthalmological; dermatological; joint surgery;  
KW eye; rheumatology; dermatology; adhesion; development; cell motility;  
KW cancer; angiogenesis; wound healing; ds; gene.  
XX  
XX  
OS Pasteurella multocida.  
XX  
XX  
PN WO2003054163-A2.  
XX  
XX  
PD 03-JUL-2003.  
XX  
XX  
PF 20-DEC-2002; 2002WO-US041067.  
XX  
XX  
PR 21-DEC-2001; 2001US-0342644P.  
XX  
XX  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
XX

PI Sloma A, Behr R, Widner W, Tang M, Sternberg D, Brown S;  
 XX WPI; 2003-559139/52.  
 DR P-PSDB; ABJ72189.  
 XX  
 PT Producing a hyaluronic acid (e.g. for use in eye and joint surgery,  
 PT orthopedics, rheumatology or dermatology) comprises cultivating a  
 PT Bacillus host cell and recovering the hyaluronic acid from the  
 PT cultivation medium.  
 XX  
 XX Claim 132; Page 186-190; 218pp; English.  
 XX  
 CC The invention relates to a novel method which comprises producing a  
 CC hyaluronic acid via cultivating a Bacillus host cell under conditions  
 CC suitable for production of the hyaluronic acid and subsequently  
 CC recovering the hyaluronic acid from the cultivation medium. The most  
 CC abundant heteropolysaccharides of the body are the glycosaminoglycans, of  
 CC which hyaluronic acid is an example. A number of enzymes are involved in  
 CC the biosynthesis of hyaluronic acid including hyaluronan synthase, UDP-  
 CC glucose 6-dehydrogenase, UDP-glucose pyrophosphorylase and UDP-N-  
 CC acetylglucosamine. The molecules of the invention demonstrate  
 CC ophthalmological, antirheumatic and dermatological activities, whilst the  
 CC method itself may be useful for producing a hyaluronan in a recombinant  
 CC host cell. The hyaluronan generated may be used in eye and joint surgery,  
 CC orthopaedics, rheumatology or dermatology and may exhibit further uses  
 CC within the fields of adhesion, development, cell motility, cancer,  
 CC angiogenesis and wound healing. The current sequence is that of the DNA  
 CC of the invention which encodes a protein that plays a role in the  
 CC synthesis of hyaluronic acid  
 XX  
 SQ Sequence 2916 BP; 1067 A; 481 C; 506 G; 862 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 0 Length: 2916  
 Score: 5104.00 Matches: 971  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.90% Mismatches: 0  
 Query Match: 99.92% Indels: 0  
 DB: 9 Gaps: 0

US-10-642-248-2 (1-972) x ABT44090 (1-2916)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrrAsnSerAsnAspTyrrGlnLeuAlaLeu 20  
 Db 1 ATGAATACATTTATCACAAGCAATTAAGACATATTAACAGCAATGATGATCAATATGACACT 60  
 Qy 21 LysLeuPheGluLysSerAlaGluIleTyrrGlyArgLysIleValGluPheGlnIleThr 40  
 Db 61 AAATATTTGAAAAGTTCGGCGGAATCTATGGACGGAAATTTGTTGAATTTCAATTTACC 120  
 Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
 Db 121 AAATGCCAAGAAAGAACTCTCAGCACATCTTCTGTTAAATTCAGCACATCTTCTGTAAT 180  
 Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
 Db 181 AAAGAAGAAAAGTCAATGTTTGGCGATAGTCGTTAGATATTGCAACACACACTGTTACTT 240  
 Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
 Db 241 TCCACGCTAAATAAATTTAGTACTTCTTCGACTCGGAAATAAACAACGTTTAAATAATATGG 300  
 Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaArgAlaValAlaLeuValPro 120  
 Db 301 AAATGTCTACTGAGAGAAATCTGAAATTCGGAGAGGTAGAGCGTCGCGCTTGTACCA 360  
 Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
 Db 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTACCTGATCATGTGTAATGATTTTACA 420  
 Qy 141 TrpTyrrLysLysArgLysValArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
 Db 421 TGGTACAAAAGCGAAGAAAGACTTGGCAATAAACCCTGAAATCAACATGTTGGTCTT 480

Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrIleuAlaCysLeu 180  
 Db 481 TCTATTATCGTTTACAACATTCATCACCAGCAATTTTATCGGATTTACATTAGCTGTGTTA 540  
 Qy 181 ValAsnGlnLysThrHisTyrrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
 Db 541 GTAAACCAAAAACACATTCACCGTTTGAAGTTATCGTGCACAGATGATGTTAGTACAGAA 600  
 Qy 201 AspLeuSerProIleIleArgGlnTyrrGluAsnLysLeuAspIleArgTyrrValArgGln 220  
 Db 601 GATCTATCACCGATCATTCGCCAATATGAAATAAATTTGGATATTCGCTACGTCAGCAACA 660  
 Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyrr 240  
 Db 661 AAAGATAACCGTTTCAAGCCAGTCGCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 720  
 Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyrr 260  
 Db 721 GACTTTATGGCTTACTCGACTGTGATATGGCCCAATCCATATATGGGTTCAATCTTAT 780  
 Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrrIleAsp 280  
 Db 781 GTTGCAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAAGAAAATACATCGAT 840  
 Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
 Db 841 ACACAACATATTGACCCAAAAGACTTCTTAAATTAACGCGAGTTTGTCTGTAATCATTTACA 900  
 Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
 Db 901 GAAGTGAACCAACCAATTAATGTTGCGCAAAAGGGAGGAACAGTTTCTCTGGATTGG 960  
 Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
 Db 961 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCTTCCGTTTT 1020  
 Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrrLeuAsnLysSerGlyPhePheAsp 360  
 Db 1021 TTTGCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATCCCGTTCTTTGAT 1080  
 Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrrArgLeuPheArgTyrr 380  
 Db 1081 GAGAAATTTAATCCTGGGGTGGAGAGATGAGAAATTTGGATATCGCTTATTTCCGTTAC 1140  
 Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrrHisGlnGluProProGlyLys 400  
 Db 1141 GGTAGTTTCTTTAAACTATTGATGCAATTTATGGCTTACCATTCAAGAGCCACCAGGTAAA 1200  
 Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
 Db 1201 GAAAAATGAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260  
 Qy 421 ValProTyrrIleTyrrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
 Db 1261 GTCCCTTATATCTATAGAAACCTTTTACCANTAGAGATTCGCATATCAATAGATGACT 1320  
 Qy 441 LeuValSerIleTyrrIleProAlaTyrrAsnCysAlaAsnTyrrIleGlnArgCysValAsp 460  
 Db 1321 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACCTTGGTAGAT 1380  
 Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
 Db 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAACTGGTTCAACA 1440  
 Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrrGlyAsnAsnProArgValArgIleMet 500  
 Db 1441 GATAATACCTTTAGAAGTGATCAATAGCTTTATGGTAATAATCTTAGGGTAGCGATCATG 1500  
 Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
 Db 1501 TCTAACCAAAATGCGGAATAGCTTCAGCATCAATGACCGCTTCTTCTTGTAAAGGT 1560

QY 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValAluLeuCys 540  
DB 1561 TATTACATTGGCGCAGTTAGATTTCAGATGATTATCTTTGAGCCTGATGCGAGTTGAACCTGTGT 1620  
QY 541 LeuIysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
DB 1621 TTTAAAGAAATTTTAAAGAGATAAAACGCTAGCTGTGTGTATACCACTAAATAGAAAACGTC 1680  
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580  
DB 1681 AATCCGATGAGTGTAAATCGCTAATGTTTACAAATGGCCAGAAATTTTCACGAGAAAA 1740  
QY 581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
DB 1741 CTCACACGGCTATGATTGCTCACCACCTTAGAATGTTTACAGATTTAGAGCTTGGCATTTA 1800  
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
DB 1801 ACTGATGGAATTCATATGAAAAAATTTGAAAAATGCGTAGACTATGACATGTTCTCTCAAACTC 1860  
QY 621 SerGluValGlyPhePheIysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
DB 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTCTATAACCGTGTATTACATGCT 1920  
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
DB 1921 GATAACACATCAATTAAGAACTTGGCATTCAAAAGAAAACCACTTTTGTGTAGTCAAT 1980  
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
DB 1981 CAGTCATTAATAGACAAGGCATACTTATTATATAATTATGACGAATTTGATGATTTAGAT 2040  
QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluLysIleAspIleLeu 700  
DB 2041 GAAAGTAGAAGTATATTTCATTAATAAACCGCTGAATATCAAGAGAGATGATATCTTA 2100  
QY 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
DB 2101 AAAGATATTAAATCATCCAGAAATAAGATGCCAAATCGCAGTCAGTATTTTATCC 2160  
QY 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
DB 2161 AATACATTAAACGGCTTAGTAAAAAACTAAACAATATTATTGAATATAATAAAAAATATA 2220  
QY 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
DB 2221 TTTCGTTATTGTTCTCATGTTGATGAATCATCTTTACACCGATATCAAAAAAGAAATA 2280  
QY 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
DB 2281 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAATAATAGATATCTCATATTAC 2340  
QY 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
DB 2341 ACGAGTAATAGATTAATAAAAACTGAGGCGCATTTAAGTAATATTAAATAAATAAGTCAG 2400  
QY 801 LeuAsnLeuAsnCysGluTyrIleLysPheAspAsnHisAspSerLeuPheValLysAsn 820  
DB 2401 TTTAAATCTAAATTTGTGAATACATCATTTTTTGTAAATCATGACGCGCTATTCGTTAAAAAT 2460  
QY 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
DB 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAAATTTCTCAGCATTACACAT 2520  
QY 841 AspTrpIleGluLysIleAsnAlaHisProProPheLysLeuLeuIleLysThrTyrPhe 860  
DB 2521 GATTGATCGAGAAATCAATGGCATCCACCATTTAAAAAGCTCATTTAAAACTTATTTT 2580  
QY 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
DB 2581 AATGACAAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTATGAGC 2640  
QY 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900

DB 2641 TATCGCTAGCGCATGAGCTTCTGACCATTTATAAAGAGTCATCACATCTTGCAGTCA 2700  
QY 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
DB 2701 ATTGATAGTGTGCAGCAATATAACACTGAGGATATTTGGTTCCAATTTGCACATTTAATC 2760  
QY 921 LeuGluLysIysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
DB 2761 TTAGAAAAAGAAAACCGCCCATGTATTTAATAAAAAACATCGACCTGACTTATATGCTTTGG 2820  
QY 941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
DB 2821 GAACGNAATTTACAAATGGACAAATGAACAAATTTGAAAGTGCNAAGAGGAGAAATATA 2880  
QY 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
DB 2881 CCTGTTAAAGTTTCATTTATTAATAGTATACTCTA 2916  
RESULT 2  
AAX58857  
ID AAX58857 standard; DNA; 2937 BP.  
XX AAX58857;  
AC AAX58857;  
XX 16-AUG-1999 (first entry)  
DT  
DE Pasteurella multocida hyaluronate synthase pmHAS DNA.  
XX  
KW Hyaluronate synthase; pmHAS; hyaluronic acid; hyaluronan; ss.  
XX  
OS Pasteurella multocida.  
XX  
FH Key Location/Qualifiers  
FT CDS 19..2937  
FT /\*tag= a  
XX  
XX WO9923227-A2.  
XX  
XX 14-MAY-1999.  
XX  
XX 30-OCT-1998; 98WO-US023153.  
XX  
XX 31-OCT-1997; 97US-0064435P.  
XX 26-OCT-1998; 98US-00178851.  
XX (OKLA ) UNIV OKLAHOMA STATE.  
XX  
XX Weigel PH, Kumari K, Deangelis P;  
XX  
XX WPI: 1999-337486/28.  
XX P-PSDB; AAY06212.  
XX  
XX Nucleic acid encoding hyaluronate synthase for production of hyaluronic acid with controlled molecular weight and targeting specificity.  
XX  
XX Disclosure; Page 123-125; 125pp; English.  
XX  
XX This DNA sequence codes for the hyaluronate synthase (pmHAS, see AAY06212) of Pasteurella multocida Carter type A. The pmHAS enzyme has different kinetic optima with respect to pH and metal ion dependence, and different Km values compared with the HAS enzymes of Streptococcus equisimilis (see AAY06206) and Streptococcus pyogenes. Km values are about 2- to 3-fold higher. The invention provides recombinant vectors containing hyaluronate synthase DNA, especially S. equisimilis hyaluronate synthase DNA (see AAX58841), and prokaryotic or eukaryotic host cells which produce the enzyme and its hyaluronic acid product, particularly a product with modified structure or molecular size. The hyaluronic acid produced this way is purer than that produced by conventional methods  
XX  
XX Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

## Alignment Scores:

```
Pred. No.: 0 Length: 2937
Score: 5104.00 Matches: 971
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatch: 0
Query Match: 99.92% Indels: 0
DB: 2 Gaps: 0

US-10-642-248-2 (1-972) x AAX58857 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 19 ATGAATACATTATCAACAGCAATAAAGCAATATAACAGCAATGACTATCAATTAGCACTC 78
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATTATTGAAAGTCGGCGGAATCTATGGACGAAATTTGTTGAATTTCAAAATPACC 138
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 139 AAATGCCAGAAAACCTCTCAGCAATCCCTCTCTGTTAAATTCAGCAATCTCTTCGTAAAT 198
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 199 AAAGAAGAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 258
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db 259 TCCAAACGTAAAAAATTAGTACTTTCTGACTTCGGAAAAAACAACGTTTAAAAAATAAATGG 318
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 319 AAATGTCTCACTGAGAGAAATCTGAAATTCGGAGGTAAGCGGTCGCTTGTACCA 378
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 379 AAAGATTTTCCAAAGATCTGGTTTATAGGCTTTTACCTGATCATGTTTAAATGATTTTACA 438
Qy 141 TrpTyrLysLysArgLysLysArgGluGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 439 TGGTACAAAAAGCGAAAGAAAGACTTGGCATATAAAACCTGAACATCAACATGTTGGTCTT 498
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 499 TCTATTATCGTTACAAACATTCATCGACCACAAATTTTATCGATTACATTAGCCTGTTTA 558
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 559 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATTCGTGACAGATGATGGTAGTCAGGAA 618
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 619 GATCTATCACCGATCATTCGCAATATGAAATAAATTTGGAATATTCGCTACGTCAGACAA 678
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 679 AAAGTAAACGGTTCCTCAAGCCAGTCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 738
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260
Db 739 GACTTTATTGGCTTACTCGACTGTGATATGCGGCCAAATCCATTATGGGTTCAITCTTAT 798
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 799 GTTCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGTCCTCAAGAAAAATACATCAT 858
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 859 ACAACAACATATTGACCCAAAAGACTTCTTAAATACCGGAGTTGCTTGAATCATTACCA 918
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320
Db 919 GAAGTGAAACCAATAATAGTTGTTGCCGCAAAAGGGGAAGCAAGTTTCTCTGGAATTGG 978
```

```
Qy 321 AtgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 979 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCTTTCCGTTT 1038
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp 360
Db 1039 TTTGCGCGGGTAATGTTGCTTTTCCGCTAAAAAATGCTAAATATAATCCGCTTTCTTTGAT 1098
Qy 361 GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1099 GAGGAAATTTAAATCACTCGGGTGGAGAGATGCGAAATTTGGATATCGCTTATTTCCGTTAC 1158
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1159 GGTAGTTCCTTTTAAAACTATTGATGGCATATGCGCTACCATCAAGAGCCACCGGTAAA 1218
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1219 GAAAAATGAAACCGATCGTGAGCGGGAAAAAATATTTACGCTCGATATATTAGAGAAAAAG 1278
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT 1338
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1339 TTAGTTTCAATTTATATCCAGCTTATTAATCTGTGCAACATATATTTCAACGTTGCGTAGAT 1398
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1399 AGTGCACTGATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAACGATGTTCAACA 1458
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1459 GATAATACCTTTAGAGTGATCAATAAGCTTTATGGTAATAATCTTAGGGTACGCATCATG 1518
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 1519 TCTAAACCAAAATGGCGAATAGCCTCAGCATCAATTCGACCCGCTTTCTTTTGTCTAAAGGT 1578
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1579 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCTTGATGTCAGTTGAACGTGT 1638
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560
Db 1639 TTAAGAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1698
Qy 561 AspProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580
Db 1699 AATCCGAGTGGTAGCTTAATCGCTAATGTTTACATTTGGCCAGAAATTTTCCAGAGAAAAA 1758
Qy 581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1759 CTCAACCGCTATGATGCTCACCCTTTAGAAATGTTACAGATTAGAGCTTGGCAATTA 1818
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1819 ACTGATGATTTCAATGAAAAAATGAAAAATGCGGTAGCATATGACATGTTTCTCCCAACTC 1878
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1879 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT 1938
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660
Db 1939 GATAACACATCAATTAAGAACTTGGCAATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1998
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 1999 CAGTCATTAAATAGCAAGGCATACTTATATAATTTATGACGAATTTGTAGATTTAGAT 2058
```

```
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2059 GAAAGTAGAAGTATATTTTCAATAAAACCCCTGAATATCAAGAAGAGATTGATATCTTA 2118
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2119 AAAGATATTAAATCATCCAGATAAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 2178
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 2179 AATACATTAAACGGCTTAGTGAAAACTAAACAAATATTATTGAAATATAATAAAATATA 2238
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2239 TTCGTTATGTTCTACATGTTGATPAAGATCATCTTACACAGATATCAAAAAAGAAATA 2298
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2359 ACGAGTAATAGATTAAATAAACTGAGCGCATTTTAAGTAATATTAAATAATTAACTCAG 2418
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2419 TTAATCTTAATTTGTAATACATCATCTTTTGTATATCATGACAGCTATTCGTTAAAAAT 2478
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2479 GACAGCTATGCTTATATGAAAAATATGATGTGCGCATGAAATTTCTCAGCATTAACACAT 2538
Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2539 GATTGGATCGAGAAATCAATCGCATCCACCATTTAAAGAGCTCATTAAGAACTTATTTT 2598
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2599 AATGCAATGACTTAAAGATGATGATGTGAAGGGCATCACAGGTATGTTTATGAGC 2658
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900
Db 2659 TATCGCTAGCGCATGAGCTTCTGACGATTATTAAGAGAGTCATCACATCTTGGCAGTCA 2718
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2719 ATTGATAGTGTCCAGATATATACACTGAGGATATTGTTGCCAATTTGCACTTTTAATC 2778
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2779 TTAGAAAAAGAAACCGCCCATGTATTTTAATAAACAATCATGCCCTGACTTATATGCTTGG 2838
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2839 GAACGAAATTAACAATGGACAAATGAACAAATTTGAAGGTGCAAAAGAGAGAGAAATATA 2898
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2899 CCTGTTAAACAAGTTCAATTATTATATAGTATAACTCTA 2934

RESULT 3
AAZ35589
ID AAZ35589 standard; DNA; 2937 BP.
XX
AC AAZ35589;
XX
DT 06-AUG-2003 (revised)
DT 01-FEB-2000 (first entry)
XX
P. multocida hyaluronate synthase (PmHAS) nucleotide sequence.
XX
KW Hyaluronate synthase; PmHAS; hyaluronan; hyaluronic acid; HA; cosmetic;
KW drug delivery; angiogenesis; wound healing; capsule synthesis;
```

```
KW fowl cholera; shipping fever; ss.
XX
OS Pasteurella multocida.
XX
PH Key Location/Qualifiers
FT CDS 19..2937
FT /*tag= a
FT /product= "PmHAS"
FT /note= "Hyaluronate synthase"
```

W09951265-A1.

14-OCT-1999.

01-APR-1999; 99WO-US007289.

02-APR-1998; 98US-0080414P.

26-OCT-1998; 98US-00178851.

(OKLA ) UNIV OKLAHOMA.

Deangelis P;

WPI; 2000-013032/01.

P-PSDB; AAY43099.

New isolated hyaluronate synthase nucleic acids, used for the production of hyaluronic acid, for developing antibiotics and vaccines and for diagnostic applications.

Claim 3; Page 113-114; 121pp; English.

This is the Pasteurella multocida hyaluronate synthase (PmHAS) nucleic acid sequence. Hyaluronic acid (HA) or hyaluronan, is a polysaccharide that serves both structural and recognition roles in higher animals. Bacteria produce extracellular capsules of HA which mimic their host HA and aid escape from a host immune response. The invention includes a vector containing the PmHAS nucleotide sequence which can be used to express PmHAS in a foreign host. The HS nucleic acids can be used for the production of HA. Also, specific changes to the HS coding sequence can result in the production of HA having a modified size distribution or structural configuration and functional properties. The HA products can be used in e.g. drug delivery, angiogenesis and wound healing. The HS nucleic acid stabilisation of recombinant proteins and in cosmetics. The HS nucleic acids can also be used to develop agents to block capsule synthesis by pathogens and act as antibiotics. The avirulent P. multocida strains can be used as vaccines for fowl cholera or shipping fever. (Updated on 06-AUG-2003 to correct OS field.)

Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 2937  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservatives: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
DB: 3 Gaps: 0

US-10-642-248-2 (1-972) x AAZ35589 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 19 ATGATATACATTATCACAGCAATAAAAGCATATAACAGCAATGACTATCATATTAGCACATC 78  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 79 AAATTATTTGAAAAAGTCGCGGAAATCTATGGACGGAAAAATTTGTTGAATTTCAATATACC 138  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 139 AAATGCCAAGAAAAAACTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTAAAT 198

Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeu 80  
Db 199 AAGAGAGAAAAGTCAATGTTTGGATAGTCGCTAGATATTTGCAACACAACTGTTACTT 258  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 259 TCCAACGTAAAAAATTAGTACTTTCTGACTCGCGAAAAAACACGTTTAAAAAATAAATGG 318  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 319 AAATTGCTCACTGAGAGAGAAATCTGAAATCGCGAGGTAAGAGCGCTCGCCCTTGTACCA 378  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 379 AAGATTTTCCCAAGATCTGCGTTTATGCGGCTTTTACCTGATCATGTTTAATGATTTTACA 438  
Qy 141 TrpTrpLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
Db 439 TGGTACAAAAAGCGAAGAAAAGACTTGGCATAAAACTGAACATCAACATGTTGGTCTT 498  
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 499 TCTATTATCGTTACAACATTCATCGACCAACAAATTTTATCGATTACATTAGCCCTGTTA 558  
Qy 181 ValAsnGlnLysThrHisTrpProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
Qy 201 AspLeuSerProIleIleArgGlnTrpGluAsnLysLeuAspIleArgTrpValArgGln 220  
Db 619 GATCTATCACCGATCATTCGCCATATGAAATTAATTTGGATATTCGCTACGTCAGACAA 678  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTrp 240  
Db 679 AAAGATAACGGTTTTCAGGCAGTGCCTCGGAATATGGGATTTACGCTTACGCAAAATAT 738  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTrp 260  
Db 739 GACTTTTATGGCTTACTCGCATGTGATATGGCGCAAAATCCATTTATGGGTTTCATCTTAT 798  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTrpIleAsp 280  
Db 799 GTTGCAGAGCTATTAGAAGATGATGATTAACATCATTTGGTCCCAAGAAATACATCGAT 858  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 859 ACAACAATATTGACCCCAAAAGACTTCTTAAATAACCGCAGTTTGGCTTGAATCATTTACCA 918  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 919 GAAGTGAACCAATAATAGTGTGGCCGCAAAAGGGGAAGGAAACAGTTTCTCTGGATTGG 978  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGACAAATTCGAAAAACAGAAAATCTCGCTTATCCGATTCCGCTTCCGTTT 1038  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPheAsp 360  
Db 1039 TTTCCGCGGGTAATGTTGCTTTCGCTAAAAAATGGCTAAATAATCCGGTTTCTTTGAT 1098  
Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTrpArgLeuPheArgTrp 380  
Db 1099 GAGGAAATTAATCTACTCGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGTTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTrpHisGlnGluProProGlyLys 400  
Db 1159 GGTAGTTTCTTTAAAACTATTGATGGCATATATGCGCTTACCATCAAGGCCACCAAGTAAA 1218  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAATGAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG 1278  
Qy 421 ValProTrpIleTrpArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440

Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCBAATAGAGATTCGCATATCAATAGATACCT 1338  
Qy 441 LeuValSerIleTrpIleProAlaTrpAsnCysAlaAsnTrpIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAGAACTATATTTCAACCGTTCGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1399 AGTGCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTACCGATGGTTCAACA 1458  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTrpGlyAsnAsnProArgValArgIleMet 500  
Db 1459 GATAATACCTTAGAAGTGATCAATAGCTTTATGGTAATAATCTTAGGGTAGCATCATG 1518  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1519 TCTAAACCAAAATGGCGAATAGCTCAGCATCAAAATGAGCCGCTTTCTTTTGTAAAGGT 1578  
Qy 521 TrpTrpIleGlyGlnLeuAspSerAspAspTrpLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTTGGGCGAGTTAGATTCCAGATGATTTATCTTGAGCCTGATGCAGTTGAACGTGT 1638  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTrpThrThrAsnArgAsnVal 560  
Db 1639 TTAAGAAGATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCTACTAATAGAAAGTC 1698  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTrpAsnTrpProGluPheSerArgGluLys 580  
Db 1699 AATCCGAGTGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTCCAGAGAAAA 1758  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1759 CTCACAACCGCTATGATGCTCACCACTTTAGAAATGTTACAGATTAGAGCTGGCATTTA 1818  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTrpAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCAATGAAAAAATTTGAATTCGCGTAGACTATGACATGTTCTCTCAAACTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTrpAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGGAATAATTAACATCTTAATAAAATCTGCTATTAACCGTGTATTACATGGT 1938  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660  
Db 1939 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1998  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTrpTrpAsnTrpAspGluPheAspAspLeuAsp 680  
Db 1999 CAGTCATTAAATAGACAGGCATACTTATTATAATATGACGAAATTTGATGATTTAGAT 2058  
Qy 681 GluSerArgLysTrpIlePheAsnLysThrAlaGluTrpGlnGluGluIleAspIleLeu 700  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAAGAGATTGATATCTTA 2118  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTrpPro 720  
Db 2119 AAAGATATTAAAAATCATCCAGAAATAAAGATGCCAAATCCGACGTAGTATTTTATATCCC 2178  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTrpAsnLysAsnIle 740  
Db 2179 AATACATTAACCGCTTAGTGAATAAACTAAACAAATATTATTGAAATATAATAAATATA 2238  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2239 TTCGTTATTTCTTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298  
Qy 761 LeuAlaPheTrpHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTrpTrp 780  
Db 2299 CTAGCTTCTTATCATAAACATCAAGTGAATTTTACTAAATTAATGATATCTCATATTAC 2358  
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800



Db 2359 ACGAGTAATAGATTAAATAAAACCTGAGCGCATTTTAAGTAATATTAATAAAATTAAGTCAG 2418  
QY 801 LeuAsnLeuAenCysGluTyrIlePheAspAsnHisAspSerLeuPheValIysAen 820  
Db 2419 TTAATCTAAATTTGTAATACATCATTTTGTATATCATGACAGCTATTCTGTAAATAAT 2478  
QY 821 AspSerTyrAlaTyrMetIlysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2479 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAAATTTCTCAGCATTAACACAT 2538  
QY 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2539 GATTGGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAAAGCTCATTTAAATTTT 2598  
QY 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2599 AATGCAATGACTTAAAGATGATGAATGTGAAGGGGCATCAAGGATGTTTATGACG 2658  
QY 881 TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900  
Db 2659 TATGGCTAGCGCATGAGCTTCTGACGATTTAAGAAGTCATCACATCTTGCCAGTCA 2718  
QY 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuLe 920  
Db 2719 ATTGATAGTGTCCAGAAATATAACACTGAGGATATTTGGTTCCAATTTGCACTTTTAATC 2778  
QY 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
Db 2779 TTAGAAAAAGAAACCGGCATCTGATTTTATAAARACATCGACCTGACTTATATGCTTGG 2838  
QY 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Db 2839 GAACGAAATTAACATGGCAATATGACAAATTTGAAGTGCATAAAGAGGAGAAATATA 2898  
QY 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2899 CCTGTTAAACAAGTTTCAATTATTAATAGTATAACTCTA 2934  
RESULT 4  
ID ADC77478  
ID ADC77478 standard; DNA; 2937 BP.  
AC ADC77478;  
XX  
XX 01-JAN-2004 (first entry)  
XX  
DE Pasteurella multocida hyaluronate synthase (HAS) gene sequence.  
XX  
XX hyaluronate synthase; HAS; streptococcal infection;  
XX streptococcal bacteria; phagocytic cell; foreign microorganism;  
XX polysaccharide capsule; hyaluronic acid capsule; HA capsule;  
XX antibacterial compound; bacterial infection; gene; ds.  
XX  
OS Pasteurella multocida.  
XX  
XX Key Location/Qualifiers  
FH 19..2937  
FT CDS /\*tag= a  
FT /product= "Pasteurella multocida hyaluronate synthase"  
XX  
XX US2003092118-A1.  
XX  
XX 15-MAY-2003.  
XX  
XX 13-JUN-2002; 2002US-00172527.  
XX  
XX 31-OCT-1997; 97US-0064435P.  
XX 26-OCT-1998; 98US-00178851.  
XX 21-DEC-1999; 99US-00469200.  
XX 13-JUN-2001; 2001US-0297744P.  
XX 13-JUN-2001; 2001US-0297788P.  
XX  
XX (DEAN/) DEANGELIS P L.

PA (WEIG/) WEIGEL P H.  
PA (KUMARI/) KUMARI K.  
XX  
XX Deangelis PL, Weigel PH, Kumari K;  
XX  
XX WPI; 2003-755179/71.  
DR P-PSDB; ADC77479.  
XX  
XX Recombinant host cell is a Bacillus cell comprising a recombinant vector  
PT having purified nucleic acid segment with a coding region encoding  
PT enzymatically active hyaluronan synthase.  
XX  
XX Claim 106; SEQ ID NO 9; 79pp; English.  
XX  
XX This invention relates to a recombinant Bacillus host cell containing a  
XX recombinant vector including a nucleic acid segment with a coding region  
XX encoding enzymatically active hyaluronate synthase (HAS), where the  
XX coding region is under control of a promoter. The incidence of  
XX streptococcal infections is a major health and economic problem  
XX worldwide. Streptococcal bacteria can grow undetected by the body's  
XX phagocytic cells which are responsible for recognising and engulfing  
XX foreign microorganisms. One way the bacteria evades these cells is by  
XX coating themselves with polysaccharide capsules, such as a hyaluronic  
XX acid (HA) capsule. As HA is non-immunogenic, the encapsulated bacteria do  
XX not illicit an immune response. The present invention provides a means of  
XX preparing HA which may prove useful for the identification of novel  
XX antibacterial compounds for the treatment of bacterial infection. The  
XX present sequence is the DNA sequence which encodes the hyaluronate  
XX synthase (HAS) of Pasteurella multocida, used in the method of the  
XX invention.  
XX  
SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 0 Length: 2937  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
DB: 10 Gaps: 0

US-10-642-248-2 (1-972) x ADC77478 (1-2937)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 19 ATGATACATTATCACAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 78  
QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 79 AAATTTATTTGAAAAGTCGCGGAAATCTATGGACGGAAATTTGTTGAAATTTCAAAATTACC 138  
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 139 AAATGCCAAGAAAAAACTCTCAGACATCTCTCTGTTAATTCAGCACATCTTTCTGTAAT 198  
QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 199 AAAGAAGAAAAAGTCAATGTTTGGCATAGTCGCTTAGATATTGCAACACAACTGTACTTT 258  
QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrIleLysAsnLysTyr 100  
Db 259 TCCAACGTAATAAAAAATTAGTACTTCTTGACTCGGAAAAAACAACGTTAAAAATAAATGG 318  
QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 319 AAATTTGCTCAGAGAGAAATCTGAAAAATGGAGAGTGAAGACGGTCCGCCCTTTGATCCA 378  
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 379 AAAGATTTTCCCAAGATCTGGTTTATGAGCGCTTTTACCTGATCATGCTTAATGATTTTACA 438  
QY 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160



Db 439 TGGTACAAAAGCGAAAGAAAGACTTTGGCATATAAAACCTGGAACATCAACATGTTGGTCTT 498  
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysIleu 180  
Db 499 TCTATTATCGTTACAACATCAATTCGACCGACCAATTTTATCGATTACATTAGCCCTGTTTA 558  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 559 GTAAACCAAAAACACATTTACCCGTTTGAAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 619 GATCTATCACCGATCATTCGCCATATGAAATGAAATTTGGATATTCGCTACGTCAGACAA 678  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 679 AAAGATAACGGTTTTCAGCCAGTCGCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 738  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
Db 739 GACTTTATGGCTTACTCGACTGTGATATGGCGCAATCCATTTATGGGTTTCATTCCTAT 798  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 799 GTTCAGAGCTATTAGAAGATGATGATTTAAACATCATTTGGTCCCAAGAAAATACATCGAT 858  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 859 ACACAACATATTGACCCAAAGACTTCTTAAATAACCGAGTTTGGCTTGAATCATTTACCA 918  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
Db 919 GAAGTGAACCAATAATAGTGTGGCCGCAAAAGGGGAAGAACAGTTTCTCGGATGG 978  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGAACAAATTCGAAAAACAGAAATCTCGCTTATCCGATTCGCCTTTCCGTTT 1038  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPheAsp 360  
Db 1039 TTTGCGCGGGTAATGTTGCTTTCGCTAAAAAATGGCTTAATAAATCCGGTTTCTTTGAT 1098  
Qy 361 GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1099 GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1159 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCAGGTAAA 1218  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAATGAAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG 1278  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1338  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAACATATATTCAACGTTGCGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1399 AGTCACCTGAATCAGACTGTTGTGATCTCGAGGTTTGTATTGTTGTAACGATGGTCAACA 1458  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1459 GATTAATACCTTAGAAGTGAATCAATAGCTTTATGGTAAATATCTTAGGGTACGCATCATG 1518  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1519 TCTAAACCAATGCGGAATAGCCTCAGCATCAAAATGCGCGGTTCTTTTGCTAAAGGT 1578

Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTTGGGAGTTAGATTAGATTATCTTGAGCCTGATGCGTTGAAGTGTGT 1638  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560  
Db 1639 TTTAAAGAAATTTTAAAGAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1698  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580  
Db 1699 AATCCGAGTGGTAGCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCACGAGAAAA 1758  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrHisLeu 600  
Db 1759 CTCAACCGGCTATGATTTGCTCACCACTTTAGAAATGTTTCAGATTAGAGCTTGGCATTTA 1818  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCAAACTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTTGGAAAAATTTAAACATCTTAATAAAAAATCTGCTATAAACCGTGTATTACATGGT 1938  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1939 GATAACACATCAATTAAGAAACTTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1998  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 1999 CAGTCATTAATAGACAGCGCATTAATTTAATTAATGACGAAATTTGATGATTTAGAT 2058  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluLysIleAspIleLeu 700  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAAGAGATTGATATCTTA 2118  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2119 AAAGATATTAAATTCATCCAGATAAAGATGCCAAAATCCGAGTCAGTATTTTTTATCCCC 2178  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2179 AATACATTAAACCGCTTAGTGAAAAAATCAACAAATATTATTGAATATAATAAAATATA 2238  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2239 TTCGTTATTGTTCTACATGTTGATAAGAATCATCTTACACAGATATCAAAAAAGAAATA 2298  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAspIleSerTyrTyr 780  
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358  
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2359 ACAGTAAATAGATTATAAAAACTGAGCGCATTTAAGTAAATATTATAAATTAAGTCAG 2418  
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2419 TTTAAATCTAAATTTGTGAATACATCAATTTTGTATAATCATGCAGCCTTATTCGTTAAAAAT 2478  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2479 GACAGCTATCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2539 GATTGGATCGAGAAATCAATGCGCATCCACATTTAAAAAGCTCAATTAACATTTATTT 2598  
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2599 AATGACAAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCACAAAGGTATGTTTATGACG 2658

Qy	881	TyrAlaLeuAlaHisGluLeuLeuThrIleIleIysGluValIleThrSerCysGlnSer	900
Db	2659	TATCGCTAGCGCATGAGCTTCTGACGATTATTAAAGAAGTCATCATCTTGCCAGTCA	2718
Qy	901	IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle	920
Db	2719	ATTGATTAGTGTGCCAGAAATATAACACTGAGGATATTGGTTCCAAATTTCACITTTAAATC	2778
Qy	921	LeuGluIlystIysThrGlyHisValPheAsnIysThrSerThrLeuThrTyrMetProTrp	940
Db	2779	TTAGAAAGAGAAACCGGCCATGTATTTAATAAACAATCGACCCCTGACTTATATGCGCTGG	2838
Qy	941	GluArgIlyIysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysAspGlyGluAsnIle	960
Db	2839	GAACGAAAAATTACATGTCAGCAAAATGACAAATTGGAAGTGCAGAAAAGAGGAGAAATATA	2898
Qy	961	ProValAsnIysPheIleIleAsnSerIleThrLeu	972
Db	2899	CCTGTTAAACAAGTTTCATTATTAAATAGTATAACTCTA	2934

RESULT 5	
ADD93925	
ID	ADD93925 standard; DNA; 2937 BP.
XX	
XX	
AC	ADD93925;
XX	
DT	29-JAN-2004 (first entry)
XX	
XX	
DE	Pasteurella multocida hyaluronan synthase gene.
XX	
KW	hyaluronan synthase; HAS; Streptococcal infection;
KW	Streptococcal bacterium; phagocytic cell; macrophage;
KW	polymorphonuclear cell; PMN; polysaccharide capsule; hyaluronic acid;
KW	HA capsule; vaccine; gene; ds.
XX	
OS	Pasteurella multocida.

XX SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other:

Alignment Scores:  
 Pred. No.: 0 Length: 2937  
 Score: 5104.00 Matches: 971  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.90% Mismatches: 0  
 Query Match: 99.92% Indels: 0  
 DB: 10 Gaps: 0

US-10-642-248-2 (1-972) x ADD93925 (1-2937)

Qy	1	MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu	20
Db	19	ATGAATACATTATCACAGCAAGCAATAAAGCATATATACAGCAATGACTATCAATTAGCAGCTC	78
Qy	21	LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr	40
Db	79	AAATATTTCGAAAGTCGCGGAATCTATGGACGGAAATTTGTTGAATTTCAAATTAACC	138
Qy	41	LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn	60
Db	139	AAATGCGCAAGAAAACCTCTCAGCACATCTCTCTGTTAATTACAGCACATCTTTCTGTAAAT	198
Qy	61	LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu	80
Db	199	AAAGAAGAAAAGTCAATGTTTGGCATAGTCGGTTAGATATTGCAACACACACTGTTACTT	258
Qy	81	SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp	100
Db	259	TCCAACTGTAATAAATAATTAGTACTTTCTGACTCGGAAAAACACGTTAAAAAATAAATGG	318
Qy	101	LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro	120
Db	319	AAATTGCTCACTGAGAGAAATCTGAAATGCGAGGTAAAGCGGTGCGCCCTTGATACA	378
Qy	121	LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr	140
Db	379	AAAGATTTTCCAAAGATCTGGTTTTAGCGCCTTTACTGATCATGTTAATGATTTTACA	438
Qy	141	TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu	160
Db	439	TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAACATCAACATGTTGGTCTT	498
Qy	161	SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu	180
Db	499	TCTATTATCGTTACAACATTCAAATCGACCAGCAATTTTATCGATTACATTAGCCCTGTTA	558
Qy	181	ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu	200
Db	559	GTAACCCAAAACACATATCCCGTTTGGAGTTATCGTGACAGATGATGGTAGTCAGAA	618
Qy	201	AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln	220
Db	619	GATCTATCACCGATCATTCGCGCAATATGAAATAAATTTGGATATTTCGCTACGCTCAGAA	678
Qy	221	LysAspAsnGlyPheGlnAlaSerAlaIlaArgAsnMetGlyLeuArgLeuAlaLysTyr	240
Db	679	AAAGATAACCGTTTTTCAAGCCAGTGCCTCGGAATATGGGAATACGCTTAGCAAAATAT	738
Qy	241	AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr	260
Db	739	GACTTTATTTGGCTTACTCGACTGTGATATGGCGCCAAATCCCATTTATGGGTTTCATCTTAT	798
Qy	261	ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp	280
Db	799	GTTCAGAGCTATTAGAAAGATGATGATTAAACAATCATTTGGTCCAAAGAAAAATACATCGAT	858
Qy	281	ThrGlnHisIleAspProLysAspPheIleuAsnAsnAlaSerLeuLeuGluSerLeuPro	300
Db	859	ACACAACATATTGACCCAAAAGACTTCTTAAATAACGGAGTTTGCTTGATCATTAACCA	918

Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
Db 919 GAAGTGAACCAATAATAGTGTGGCCGAAAGGGGAAGAACAGTTCTCTGGATTGG 978  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGAACAAATTCGAAAAACACAGAAAAATCTCCGCTTATCCGATTCGCTTCCTCCGTTTT 1038  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPheAsp 360  
Db 1039 TTTGCGCGGGTAAATGTGTCTTCGCTAAAAAATGGCTAAATAATCCGGTTCTTTTGAT 1098  
Qy 361 GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheAspTyr 380  
Db 1099 GAGGAATTTAATCACTGGGGTGGAGAAGATGTGAATTTGGATATCGCTTATTCGGTTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1159 GGTAGTTCCTTTAAACACTATTGATGGCATTATGGCCTACCATCAAGAGCCACCAGGTAAA 1218  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAAAATGAAACCGCATCGTGAAGCGGGAATAATATTACGCTCGATATTATGACAGAAAAAG 1278  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAACCTTTTACCAATAGAAATTCGCATATCAATAGAGTACCT 1338  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAATTTATATCCCGAGCTTATACTGTGCAAACTATATTCAACGTTGGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1399 AGTGCACATGAATCAGACTGTGTGTGATCTCGAGTTTGTATTTGTAAACGATGGTTCAACA 1458  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1459 GATAAATACCTTAGAAGTGAATCAATAGCTTTATCGTAAATATCTTAGGTCAGCATCATG 1518  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1519 TCTAAACCAATGGCGGAATAGCTCAGCATCAATGCACGCGTTCTTTGTCTAAAGGT 1578  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCAAGTTGAACCTGTG 1638  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1639 TTAAGAAGATTTTAAAGATAAACGCTAGCTTGTGTGTATACCACTAATAGAAACGTC 1698  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580  
Db 1699 AATCCGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTCACGAGAAAA 1758  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrPheIleLeu 600  
Db 1759 CTCACACGGCTATGATGCTCACCACCTTTAGAATGTTCACGATTAGAGCTTGGCATTTA 1818  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCAATGAAAAAATTTGAAATGCCGTAGCATATGACATGTTCCTCAAACTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGGAAAAATTAACACATCTTAATAAATCTGCTATAACCGGTGATTACATGGT 1938  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1939 GATAACACATCAATTAAGAACTTGGCATTTCAAAAGAAAAAACCATTTTGTGTAGTCAAT 1998  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680

Db 1999 CAGTCATTAATAGACAGGCATACTTATTATAATTATGACCAATTTGATGATTTAGAT 2058  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluLeuAspIleLeu 700  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTGATATCTTA 2118  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2119 AAAGATATTAAATATCATCCAGATAAAGATGCCAAATGCGAGTCAGTATTTTTTATCTCC 2178  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2179 AATACATTAACCGCTTAGTGAATAAACTAAACAATATTATTTCATATATAATAAATA 2238  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspLysLysGluIle 760  
Db 2239 TTCGTTATTGTTCTCATGATGTGATAAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2298  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358  
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2359 ACAGTAAATAGATTAAATAAACTGAGCGCATTTAAGTAATATTAAATAAATTAAGTCAG 2418  
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2419 TTAATCTAAATTTGTAATACATCATTTTGTGAATATCATGACAGCCTATTTCGTTAAAAAT 2478  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 841 AspTyrIleGluLysIleAsnAlaHisProProPheLysLysLeuIleLysThrTyrPhe 860  
Db 2539 GATTGATCGAGAAATCAATGCGCATCCACATTTAAAAAGCTCATTAATACTTATTTT 2598  
Qy 861 AspAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 2599 AATGACAAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGACG 2658  
Qy 881 TyrAlaIleAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTATTAAAGAAGTCATCACTCTTGCCAGTCA 2718  
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920  
Db 2719 ATTGATAGTGTGCAGAAATATAACATGAGGATATTGTTGCCAATTTGCACITTTAATC 2778  
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940  
Db 2779 TTAGAAAAAGAAAAACCGCCATGTATTATAATAAACATCGACCTGACTTATATGCTTGG 2838  
Qy 941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Db 2839 GAACGAAAAATTACAATGGACAAATGAACAAATTTGAAAGTGCAAAAAGAGGAGAAATA 2898  
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2899 CCTGTTAACAAAGTTCAATTATTATAGTATAACTCTA 2934  
RESULT 6  
ABA05098  
ID ABA05098 standard; DNA; 2979 BP.  
XX  
AC ABA05098;  
XX 22-FEB-2002 (first entry)  
DT  
XX  
DE Pasteurella multocida chondroitin synthase gene #2.  
XX

KW Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer;  
 KW eye application; joint application; moisturiser; drug delivery;  
 KW wound dressing; biocompatible film; ds.

XX Paesteurella multocida.

XX Key Location/Qualifiers  
 XX 61..2958  
 FT CDS /tag= a  
 FT /product= "chondroitin synthase"

XX WO200180810-A2.

XX 01-NOV-2001.

XX 25-APR-2001; 2001WO-US013395.

XX 25-APR-2000; 2000US-0199538P.

XX (DANG/) DE ANGELIS P L.

XX De Angelis PL;

XX WPI; 2002-049237/06.

XX P-PSDB; AAM47336.

XX New chondroitin synthase gene obtained from Pasteurella multocida, useful  
 PT as hyaluronan polysaccharide substitute in medical or cosmetic  
 PT applications, e.g. for eye or joint applications, for moisturizer or  
 PT wound dressings.

XX Claim 4; Page 120-121; 125pp; English.

XX The present invention relates to the coding sequence of the Pasteurella  
 CC multocida chondroitin synthase. A chondroitin polysaccharide may be used  
 CC as a hyaluronan polysaccharide substitute in medical or cosmetic  
 CC applications, for example in eye or joint applications, for moisturiser  
 CC or wound dressings. The enzyme may be used in covalently coupling  
 CC specific drugs, proteins or toxins to the structurally modified  
 CC chondroitin for general or targeted drug delivery or radiological  
 CC procedures, covalently cross linking the hyaluronic acid itself or to  
 CC other supports to achieve a gel or other three dimensional biomaterial  
 CC with stronger physical properties, and covalently linking hyaluronic acid  
 CC to a surface to create a biocompatible film or monolayer. The present  
 CC sequence is one version of the coding sequence of the invention

SQ Sequence 2979 BP; 1130 A; 466 C; 495 G; 888 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 0 Length: 2979  
 Score: 4502.50 Matches: 845  
 Percent Similarity: 93.21% Conservative: 61  
 Best Local Similarity: 86.93% Mismatches: 59  
 Query Match: 88.15% Indels: 7  
 DB: 6 Gaps: 2

US-10-642-248-2 (1-972) x ABA05098 (1-2979)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
 DB 61 ATGAATACATTATCAACAGCAATATAAGCATATATAACAGCAATAGCTATGAAATTAGCACTC 120  
 QY 21 LysLeuPheGluLysSerAlaGluLeuTyrGlyArgLysIleValGluPheGlnIleThr 40  
 DB 121 AAATATTATGAGAAGTCTCTGAAACCTACGGCGCGAAAAAATCGTTGAAATTCCAAATATTC 180  
 QY 41 LysCysLysGluLysSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
 DB 181 AAATGTAAAGAAAAAATCT-----TCGACCAATCT-----TATGTAGT 219  
 QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeu 80  
 DB 220 GAAGATAAAAAAACAAGTGTTCGATAGCTCATATAGATATCGCAACACAGCTCTTACTT 279

QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
 DB 280 TCCAACGTAAAAAATAAATTAACCTCTATCGAATCAGAAAAAACAAGCTTTTAAAAAATAAATGG 339  
 QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
 DB 340 AAATCTATCTACTGGGAAAAAATCGGAGAACGAGAACTGAGAAAGGTGGAACTAGTACCC 399  
 QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
 DB 400 AAAGATTTTCTTAAAGATCTTGTCTGCTCCATTGCCAGATCATGTATTAATGATTTTACA 459  
 QY 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
 DB 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATTAAGCCTGTAAATAAAGAATATCGGTCTT 519  
 QY 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
 DB 520 TCTATTATTATTCCTACATTTAATCGTAGCCGTATTTTAGATATAAGCTTAGCTGTG 579  
 QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
 DB 580 GTCATTCAGAAAAAACAATCTACCTTTGAAGTCGTGTTGCAGATGATGGTAGTAAGGAA 639  
 QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
 DB 640 AACTTACTTACCAATGTGCAAAAAATACGACAAAAAATCTGCACATAAAGTAGTTAAGACAA 699  
 QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
 DB 700 AAAGATTATGATATCAATTTGTGTGCAGTCAAGAACTTAGGTTTACGTACAGCAAAAGTAT 759  
 QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
 DB 760 GATTTGTCTCGATTTCTAGCTGCGATATGSCACCAACAATTTATGGTTTCATTTCTTAT 819  
 QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
 DB 820 CTTACAGAACTATTAGAAGACAATGATATTGTTTAAATGGACCTAGAAAAATATGTGGAT 879  
 QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
 DB 880 ACTCATATATTATAGCGCAGAACAAATTCCTTAACCATCCATATTTAATAAGATACACTACT 939  
 QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
 DB 940 GAAACCGCTACAATATACAACTCTCGATTACATCAAAAGGAATATATATCGTTGGATTGG 999  
 QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
 DB 1000 AGATTAGAACATTTCAAAAAAACCAGATAATCTACGCTCTATGTGATTCCTCCGTTTCGTTAT 1059  
 QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
 DB 1060 TTTAGTTGCGGTAAATGTTGCATTTTCTAAAGAAATGGCTTAAATAAAGTAGTGGTTCCGAT 1119  
 QY 361 GluGluPheAsnHisTrpGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
 DB 1120 GAAGAAATTTAATCATTTGGGGGGCGGAGATGTAGATTTGTTTACAGATATTATTCGCAAA 1179  
 QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
 DB 1180 GGCTGTTTTTTCAGAGTAATTTGACGGCGGAATGGCATACCATCAAGAACCACTCGGTAAA 1239  
 QY 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
 DB 1240 GAAATGAAACAGACCGCGAAGCTGTGTAAAGATTTAGCTTAAATAATTTGTGAAAGAAAAG 1299  
 QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
 DB 1300 GTACCTTATCTATAGAAAGCTTTTACCAATAGAAGATTTCATATTTCATAGATACCT 1359

441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaSerTyrIleGlnArgCysValAsp 460  
1360 TTAGTTTCTATTATATCCCGCGTTATAACTGTGCAAAATATATTTCAAAGATGTTAGAT 1419  
461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTGTATTGTTAAGATGGTTCAACA 1479  
481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
1480 GATAAATACCTTAGAAGTGATCAATAAGCTTTATGCTAATAATCTTAGGTCACGCATCATG 1539  
501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly 520  
1540 TCTAAACCAATGCGGAAGTAGCTCAGCATCAAACTGAGCCGTTCTTTTGTCTAAAGGT 1599  
521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
1600 TATTACATTGGCGAGTTAGATTCAAGATGATTATCTTGAGCCTGATGCAGTTGAAGTGT 1659  
541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
1660 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1719  
561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnThrProGluPheSerArgGluLys 580  
1720 AATCCGATGATGCTTAATCGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTA 1779  
581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrPheLeu 600  
1780 CTCAACAGCGCTATGATGCTCACCATTTTAGATGTTTACGATTTAGAGCTTGCATTTA 1839  
601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
1840 ACGGATGGATTAAACGAAATATTGAAACCGCCGCGGATATGACATGTTCTTAAACCTC 1899  
621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
1900 AGTGAAGTTGGAAATTTAAACATCTTAATAAATCTGCTATAACCGCGTATTACATGGT 1959  
641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
1960 GATTAACATCCATTAGAACTCGGCATTCAAAGAAACCAATTTGTTGTAGTCAAT 2019  
661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
2020 CAGTCATTAAATAGACAAGGCATCAATTTATTAATTTATGACAAATTTGATGATTTAGAT 2079  
681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
2080 GAAAGTAGAAAGTATATCTTCAATAAACCCTGAATATCAAGAAAGAAATGGATATTTTA 2139  
701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
2140 AAAGATCTTAACATCAATCAAAATTAAGATGCCAAATCGCAGTCAGTATTTTCTATCCC 2199  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
2200 AATACATTAACCGCTAGTGAATAAATACTAAACCAATATTTTGAATATAATAAATAATA 2259  
741 PheValIleValLeuHisValAspLysAsnHisIleThrProAspIleLysLysGluIle 760  
2260 TTCGTTATATTCTACATGTTGTAAGAATCATCTTACACGACATCAAAAAAGAAATA 2319  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
2320 TTGGCTTTCTATCATAGACACCAAGTGAATTTTACTAAATATGACATCTCATATTAC 2379  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
2380 ACGAGTAATAGACTAATAAATACTGAGGCACATTTAAGTAATATTAATAAATTAAGTCAG 2439  
801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820

2440 TTTAAATCTAAATTTGTGAATACATCATTTTGTATAATCATGACAGCCTATTCGTTAAAAAT 2499  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
2500 GACAGCTATGCTTATATGAAAAATATGATGTCGCGATGAATTTCTCAGCATTAACACAT 2559  
841 AspTyrIleGluLysIleAsnAlaHisProPheIysLysLeuIleLysThrTyrPhe 860  
2560 GATTGGATCGAGAAATCAATGCGCATCCACCATTTTAAAAAGCTGATTTAAACCTATTTT 2619  
861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyValAsnSerGlnGlyMetPheMetThr 880  
2620 AATGACATGACTTAGAAGTATGATGTAAGAGGGGCATCACAAGGTATGTTTATGAAG 2679  
881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
2680 TATGCGCTACCGCATGAGCTTCTGCGATTTATTAAGAGAGTCATCATCTCGCAATCA 2739  
901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920  
2740 ATTGATAGTGTGCCGAATATAACCTGAGGATATTGTTGCCAATTTGCACATTTTAATC 2799  
921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940  
2800 TTAGAAAAAGAAACCGCCCATGTTATTAATAAACAATCGACCTGACTTATATGCTTGG 2859  
941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
2860 GAACGAAATTTACAAATGGACAAATGAACAAATTTCAAAGTCGAAAAAAGCGCAATATC 2919  
961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
2920 CCCGTTAAACAAGTTCATTATTAATAGTATAACGCTA 2955  
RESULT 7  
ADP75650  
ID ADP75650 standard; DNA; 2979 BP.  
XX  
AC ADP75650;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Pasteurella multocida chondroitin synthase coding sequence #1.  
XX  
KW polymer production; hyaluronic acid polymer; chondroitin polymer;  
KW chondroitin synthase; gene; ds; enzyme.  
XX  
OS Pasteurella multocida.  
XX  
PN WO2003029261-A2.  
XX  
PD 10-APR-2003.  
XX  
PF 12-JUL-2002; 2002WO-US022386.  
XX  
PR 13-JUL-2001; 2001US-0305263P.  
PR 22-JAN-2002; 2002US-0350642P.  
PR 08-MAY-2002; 2002US-00142143.  
XX  
PA (DEAN/) DEANGELIS P L.  
XX  
PI Deangelis PL;  
XX  
DR WPI; 2003-532558/50.  
XX  
DR P-PSDB; ADP75651.  
XX  
PT Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by  
PT providing a functional acceptor, a synthase capable of elongating the  
PT acceptor and sugars such that that synthase elongates the acceptor to provide  
XX polymer.  
XX  
PS Claim 86; SEQ ID NO 3; 538pp; English.

XX The invention comprises a method for producing a polymer, especially a  
 CC hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than  
 CC 150 sugars. The method involves providing a functional acceptor,  
 CC providing a synthase capable of elongating the functional acceptor, and  
 CC providing sugars such that the synthase elongates the functional acceptor  
 CC to provide the polymer. The method of the invention is useful for  
 CC producing a hyaluronic acid or chondroitin polymer composed of 1-150  
 CC sugars. The present DNA sequence encodes a Pasteurella multocida  
 CC chondroitin synthase of the invention.

XX SQ Sequence 2979 BP; 1130 A; 466 C; 495 G; 888 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 0 Length: 2979  
 Score: 4502.50 Matches: 845  
 Percent Similarity: 93.21% Conservative: 61  
 Best Local Similarity: 86.93% Mismatches: 59  
 Query Match: 88.15% Indels: 7  
 DB: 11 Gaps: 2

US-10-642-248-2 (1-972) x ADP75650 (1-2979)

Qy 1 MetAenThrLeuSerGlnAlaIleLysAlaTyrAenSerAenAspTyrGlnLeuAlaLeu 20  
 Db 61 ATGAATACATTTATCACAAGCAATAAAGCATATAACAGCAATGACTATGAATAGCACCTC 120  
 Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
 Db 121 AAATTTATTGAGAGTCTGCTGAAACCTACGGCGCAAAAATCGTTGAATTCCAATATATC 180  
 Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen 60  
 Db 181 AAATGTAAGAAAACCTC-----TCGACCAATCT-----TATGTAAGT 219  
 Qy 61 LysGluGluLysValAenValCysAspSerProLeuAspIleAlaThrGlnLeuLeu 80  
 Db 220 GAAGATAAATAAACAAGTGTTCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 279  
 Qy 81 SerAenValLysLysLeuValLeuSerAspSerGluLysAenThrLeuLysAenLysTrp 100  
 Db 280 TCCACGCTAAATAAATAAATTAACCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 339  
 Qy 101 LysLeuLeuThrGluLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120  
 Db 340 AAATCTATCATCTGGGAAAAAATCGGAGAACCGAGAAATCAGAAAGCTGGAACTAGTACCC 399  
 Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAenAspPheThr 140  
 Db 400 AAAGATTTCTTAAGATCTTGCTTCTCCATTCGACGATCATGTTAATGATTTTACA 459  
 Qy 141 TrpTyrLysLysArgLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
 Db 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATAAAGCCTGTAAGATTAAGATATCGGTCTT 519  
 Qy 161 SerIleIleValThrThrPheAenArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
 Db 520 TCTATTATTATCTTACATTTAATCGTAGCCGATATTTAGATATTAACGTTAGCCCTGTTG 579  
 Qy 181 ValAenGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
 Db 580 GTCAATCAGAAAAACAATACCTCCATTCGAGTCGTTGTTGCAGATGATGTTAGTAAAGAA 639  
 Qy 201 AspLeuSerProIleIleArgGlnTyrGluAenLysLeuAspIleArgTyrValArgGln 220  
 Db 640 AACTTACTTACCATTGTGCAAAAATACGAAACAAACCTTGACATTAAGTATGTAGACAA 699  
 Qy 221 LysAspAenGlyPheGlnAlaSerAlaAlaArgAenMetGlyLeuArgLeuAlaLysTyr 240  
 Db 700 AAAGATTATGGATATCAATTTGTGTCAGTCAGAAACTTAGGTTTACGTACGACAAAGTAT 759  
 Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAenProLeuTrpValHisSerTyr 260

Db 760 GATTTGTCGATTCTAGACTCGGATATGGCACCACACAAATATTGGGTTTCATCTTAT 819  
 Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
 Db 820 CTTACAGAACTATTAGAAGACAATGATATGTTTAAATTCGACCTAGAAAAATATGTCAT 879  
 Qy 281 ThrGlnHisIleAspProLysAspPheLeuAenAenAlaSerLeuLeuGluSerLeuPro 300  
 Db 880 ACTCATAAATATTACCCAGAACAAATTCCTTAAAGCATCCATATTAAATAGAAATCACTACT 939  
 Qy 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
 Db 940 GAAACCCCTACAAATACAAATCTTCGATTACATCAAAAGGAATAATATCGTTGGATTGG 999  
 Qy 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe 340  
 Db 1000 AGATTAGAACATTTCAAAAAAACCAGATAATCTAGCTCTATGTGATTCCTCGTTTCGTAT 1059  
 Qy 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPhePheAsp 360  
 Db 1060 TTTAGTTGCGGTAAATGTTGCATTTTCTAAAGAAATGGCTAAATAAAGTAGGTTGGTTCGAT 1119  
 Qy 361 GluGluPheAenHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
 Db 1120 GAAGAAATTTAATCATTGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA 1179  
 Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
 Db 1180 GGCTGTTTTTTCAGAGTAATTCAGCGCGGAATGGCATACCATCAAGAACACCTGGTAAA 1239  
 Qy 401 GluAenGluThrAspArgGluAlaGlyAenIleThrLeuAspIleMetArgGluLys 420  
 Db 1240 GAAAAATCAACAGACCGCGAAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTGAAGAAAG 1299  
 Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAenArgValPro 440  
 Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAATTCACATATTTCATAGAAATAGCT 1359  
 Qy 441 LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAsp 460  
 Db 1360 TTAGTTTCTATTATATCCCGCTTATAACTGTGCAAAATATATTTCAAGATGTGTAGAT 1419  
 Qy 461 SerAlaLeuAenGlnThrValAspLeuGluValCysIleCysAenAspGlySerThr 480  
 Db 1420 AGTCTCTTAATCAACTGTTGTCGATCTCGAGGTTTGTATTGTTAAACGATGGTTCAACA 1479  
 Qy 481 AspAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet 500  
 Db 1480 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTAATAATCTTAGGCTAGGCATCATG 1539  
 Qy 501 SerLysProAenGlyGlyIleAlaSerAenAlaAlaValSerPheAlaLysGly 520  
 Db 1540 TCTAAACCAATAGCGGAATAGCTTCAGCATCAATGCAGCGGTTCTTTTGTCTAAAGGT 1599  
 Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
 Db 1600 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGACGCTGATGCGAGTTGAACGTGT 1659  
 Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAenArgAenVal 560  
 Db 1660 TTAAGAAGAAATTTTAAAGATAAACCGCTAGCTGTGTGTTTATACCACTAAATAGAAACGTC 1719  
 Qy 561 AenProAspGlySerLeuIleAlaAenGlyTyrAenTrpProGluPheSerArgGluLys 580  
 Db 1720 AATCCGATGTTAGTCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTCACGAGAAAA 1779  
 Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
 Db 1780 CTCACACGGCTATGATTTGCTCACCATTTTAAATGTTTACGATTTAGAGCTTGGCATTTA 1839  
 Qy 601 ThrAspGlyPheAenGluLysIleGluAenAlaValAspTyrAspMetPheLeuLysLeu 620  
 Db 1840 ACGGATGGATTTAAACGAAAAATATTGAAACCGCGGATTTATGACATGTTCTTAAACCTC 1899



```
QY 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1900 AGTGAAGTTGGAAATTTAAACATCTTTAAATAAATCTGCTATTAACCCGCGTATTACATGGT 1959
QY 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660
Db 1960 GATAACACATCCATTAGAATCTCGGCATTCNAAAGAAACCCTTTTGTGTAGTCAT 2019
QY 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680
Db 2020 CAGTCATTAATAGACAAGGCATCAATATTATATAATTATGACAAATTTGATGATTAGAT 2079
QY 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2080 GAAAGTAGAAGTATATCTTTCAATAAAACCGCTGAATATCAAGAAAGAAATGGATATTTTA 2139
QY 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2140 AAGATCTTAACATCATTCANATTAAGATGCCNAATCGCAGTCAGTATTCTTATCCC 2199
QY 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 2200 AATACATTAACCGCTTAGTGMAAAACTAAACAATATTATTGAATATAATAAAATATA 2259
QY 741 PheValIleValLeuHisValAspLysAsnHisIleuThrProAspIleLysLysGluIle 760
Db 2260 TTGCTATTATTCTACATGTGTGAATGATCATCTTTACACGACATCAAAAAAGAAATA 2319
QY 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
Db 2320 TTGGCTTTCTATCATAGCACCAGTGAATATTTTACTAATAATGACATCTCATATTAC 2379
QY 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2380 ACCAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAATATTATAATAAATTAAGTCAG 2439
QY 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2440 TTAATCTAAATTTGTGAATACATCATCTTTTGTATATCATGACAGCCCTATTTCGTAAATAAT 2499
QY 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAAATTTCTCAGCATTAACACAT 2559
QY 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2560 GATTGGATCGAGAAATCAATGCGCATCCACCATTATAAAAGCTGATTAACACCTATTTT 2619
QY 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyValaSerGlnGlyMetPheMetThr 880
Db 2620 AATGACAACTGACTTAAGAGTATGAATGTGAAGGGGCATCACAGGTATGTTTATGAAG 2679
QY 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2680 TATGCGCTACCGCATGAGCTTCTGACGATTTATTAAGAGTCATCACATCCTGCCATCA 2739
QY 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2740 ATTGATAGTGTCCAGAAATATACACTGAGGATATTTGGTTCCCAATTTGCACCTTTAATC 2799
QY 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2800 TTAGAAAAGAAAACCGGCCATGTATTTAATAAAACATCGACCCCTGATATATGCTCTGG 2859
QY 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysAtsGlyGluAsnIle 960
Db 2860 GAACGAAAATTACATGACACAAATGAACAAATTCAAAGTGCATAAAAGGCGGAAATATC 2919
QY 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCGGTTAACAAGTTTCATTATTATTAATAGTATAACGCTA 2955
```

## RESULT 8

AEA04966

ID AEA04966 standard; DNA; 2979 BP.

XX

AC AEA04966;

XX

DT 11-AUG-2005 (first entry)

XX

DE Chondroitin synthase, PmCS, coding sequence, SEQ ID 4.

XX

KW Chondroitin synthase; polysaccharide; gene; ds.

XX

OS Pasteurella multocida.

XX

FH Key Location/Qualifiers

FT CDS 61..2958

FT /\*tag= a

FT /product= "PmCS"

XX

PN US2005124046-A1.

XX

PD 09-JUN-2005.

XX

PF 16-JUL-2002; 2002US-00197153.

XX

PR 10-NOV-1999; 99US-00437277.

XX

PA (DEAN/) DEANGELIS P L.

XX

PI Deangelis PL;

XX

WPI; 2005-417007/42.

DR P-PSDB; AEA04965.

DR GENBANK; AF195517.

XX

Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin), useful in polysaccharide polymer grafting, comprises providing hyaluronic acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the functional acceptor.

XX Disclosure; SEQ ID NO 4; 4lpp; English.

The present invention relates to a method for elongating a functional acceptor. The method comprises providing a hyaluronic acid (HA) synthase (PmHAS; AEA04963) capable of elongating the functional acceptor and providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid synthase elongates the functional acceptor. PmHAS adds sugars to the nonreducing end of a growing polymer chain. The PmHAS sequence is significantly different from the other known HA synthases: there appears to be only two short potential sequence motifs (AEA04967 and AEA04968) in common between PmHAS and the other HA synthases. The method is useful in polysaccharide polymer grafting, which may be utilized in the development of biotechnological medical improvements. These may be used for producing hybrid polysaccharides or for forming polysaccharide coatings. Also disclosed is chondroitin synthase (PmCS; AEA04965) and its coding sequence (AEA04966) from Pasteurella multocida. Type A. P. multocida produces a HA capsule [GlcUA-GlcNAc repeats] and possesses the PmHAS enzyme. On the other hand, Type F. P. multocida produce a chondroitin or chondroitin-like polymer capsule [GlcUA-GalNAc repeats] using PmCS. Either HA or chondroitin chains can serve as acceptors for PmCS as both acceptors serve well for PmHAS.

XX Sequence 2979 BP; 1130 A; 466 C; 495 G; 888 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	0	Length:	2979
Score:	4502.50	Matches:	845
Percent Similarity:	93.21%	Conservative:	61
Best Local Similarity:	86.93%	Mismatches:	59
Query Match:	88.15%	Indels:	7
DB:	14	Gaps:	2

US-10-642-248-2 (1-972) x AEA04966 (1-2979)



Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 61 ATGAATACATATACAAAGCAATAAAGCAATATAACAGCAATGACATATGAATAGCACTC 120  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 121 AAATTAATTCAGAAAGTCGCTGAAACCTACGGCGCAAAATCGTTGAATTCCAAATATATC 180  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 181 AAATGTAAGAAACATC-----TCGACCAATCTCT-----TATGTAAAT 219  
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 220 GAAGATAAATAAACAAGCTGTTGCGATAGCTCATAGATATCGCAACACAGCTCTTACTT 279  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
Db 280 TCCAACGTAAATAAATACTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 339  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 340 AAATCTATCACTCGGCAAAAAATCGGAGAACGAGAAATCAGAAAGGTGGAACCTAGTACCC 399  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 400 AAAGATTTCCTAAGATCTTGTCTTCCTCCATGCCAGATCATGTTAATGATTTTACA 459  
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
Db 460 TGGTCAAAAAATCGAAAAAAGCTTAGGTATAAAGCTGTAAATAGAAATATCGGTCTT 519  
Qy 161 SerIleLeuValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 520 TCTATTATTCTCTACATTAATCTGAGCGGTATTTTAGATATAACGTTTAGCTGTGTTG 579  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 580 GTCAATCAGAAAAACAATACCCATTTGNAAGTCGTGTTGCAGATGATGGTAGTAAGNA 639  
Qy 201 AspLeuSerProIleLeuArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 640 AACTTACTTACCATGTGCAAAATACGAAACAATACTTGACATAAAGTATGTAAAGACA 699  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 700 AAAGATTATGATATCAATTGTGTGCTGAGTCAAGAACTTAGGTTTACGTACAGCAAAAGTAT 759  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
Db 760 GATTTGTCTCGATTCTAGATGCGATATGGCACCACAACTAATTAATGAGTTCACTCTAT 819  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 820 CTTACAGAACTATTAGAGACATGATATTTGTTTAAATGGACCTAGAAAATAATGTGGAT 879  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 880 ACTCATATAATTACCGCAGAAACAATCTCTTAACGATCCATATTTAATAGAATCACTACCT 939  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 940 GAAACCGCTACAAAATAACAACTCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 1000 AGATTAGAACATTTCAAAAAACCAGTAATCTACGCTCTATGTGATCTCCGTTTCGTTAT 1059  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysTyrTrpLeuAsnLysSerGlyPhePheAsp 360  
Db 1060 TTTAGTTGCGGTAAATGTTGCAATTTCTTAAAGAAATGGCTAAATAAAGTAGGTGGTTCCGAT 1119

Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1120 GAAGAAATTTAATCATTTGGGGGGCGAAGATGTAGAATTTGGTTACAGATTTATTTGCCAAA 1179  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1180 GGCTGTTTTTTCAGAGTAATTGACGGCGGATGCGCATACCATCAAGNACCACCTGGTAAA 1239  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1240 GAAAAAGAAACAGACCCGGAAGCTGGTAAAAGTATTACGCTTAAAAATTTGTGAAGAAAAG 1299  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCCAATAGAAGATTACATATTTCAATAGTAACCT 1359  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1360 TTAGTTTCTATTATATCCCGCTTATACTGTGCAAAATTTATTTCAAGAGATGTTAGAT 1419  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1420 AGTCTCTTAATCAAACTGTTGTCGATCTCGAGTTTGTATTGTAAACGATGGTTCAACA 1479  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1480 GATAAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATAATCTTAGGGTACGCATCATG 1539  
Qy 501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1540 TCTAAACCAATGCGGAATAGCCTCAGCATCAATGCGACCGCTTCTTTTGTCTAAGGT 1599  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1600 TATTACATTGGCAGTTAGATTTCAGATGATTATCTTCAGCCTGATGCAGTTGAACCTGTGT 1659  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560  
Db 1660 TTAAGAAGATTTTAAAGATATAAACGCTAGCTAGTTGTGTATTATACCACTTAATAGAAACGTC 1719  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1720 AATCCGATGTTAGCTTAATCGCTTAATGGTTTACAAATTTGGCCAGAAATTTTCACGAGAAAA 1779  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1780 CTCACACGGCTATGATGTTGCTCACCATTTTAGATGTTTACGATTAGAGCTTGGCATTTA 1839  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1840 ACGGATGGATTTAACGAAAAATATTGAAAAACCGCTGGATTATGACATGTTCTTTAAACCTC 1899  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysValTyrAsnArgValLeuHisGly 640  
Db 1900 AGTGAAGTTGGAAAATTTAAACATCTTAATAAATCTGCTATATAACCGCGTATTACATGGT 1959  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1960 GATTAACATCCATTAGAAAATCTCGCATTCAAAAGAAAACCAATTTTGTGTAGTCAAT 2019  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 2020 CAGTCATTTAAATAGACAAGGCATCAATTTATTAATATATATGACAAATTTGTGTAGTATTAGAT 2079  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu 700  
Db 2080 GAAAGTAGAAAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAAGAAATGGATATTITA 2139  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2140 AAAGATCTTAACTCATTTCAAAATTAAGATGCGCAAAATGCGCAGTCAGTATTTTCTATCCC 2199  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740



```
Db 460 TGGTACAAAAATCGAAAAAAGGCTTAGGTATAAAGCCCTGTAATAAAGAAATATCGGTCTT 519
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 520 TCTATATTATTCTTACATTTAACTCGTAGCCGTATTTTAGATATAACGTTAGCCGTGTTG 579
Qy 181 ValAsnGlnIleThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 580 GTCAATCAGAAAAACAACCTACCCATTTGAAAGTCGTGTTGTCAGATGATGGTAGTAAGGAA 639
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnIleLeuAspIleArgTyrValArgGln 220
Db 640 AACTTACTTACCATTTGTCAAAAATACCAACAAAACTTGACATAAAGTATGTAAAGCAA 699
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaIleTyr 240
Db 700 AAAGATTATGATATCAATTTGTGTCAGCTCAGAACTTAGGTTTACGTACAGCAAAAGTAT 759
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db 760 GATTTGTCTCGATTCAGATCGCATATGGCATATGCACCAACAATATATGGTTCATCTTAT 819
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgIleTyrIleAsp 280
Db 820 CTTACAGAACTATTAGAAGACAATCATATATGTTTAAATGGACCTAGAAAAATATGTGGAT 879
Qy 281 ThrGlnHisIleAspProIleAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300
Db 880 ACTCATATATATACCGCAGAAACAATTCCTTTACGATTCATATTTAATAGAATCACTACT 939
Qy 301 GluValIleThrAsnAsnSerValAlaAlaIleGlyGluGlyThrValSerLeuAspTyr 320
Db 940 GAAACCGCTCACAATAACAAATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999
Qy 321 ArgLeuGluGlnPheGluIleThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 1000 AGATTAGAACATTTCAAAAAACCATAATCTACGCTCTATGTGATTCCTCGGTTTCGTTAT 1059
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaIleAlaIleTyrLeuAsnIleSerGlyPhePheAsp 360
Db 1060 TTTGTGCGGGTAATGTTGCATTTCTAAAGAAATGGCTAAATAAAGTAGGTGGTTCGAT 1119
Qy 361 GluGluPheAsnHisTyrGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1120 GAAGAAATTAATCATTTGGGGGGCGAGATGTAGAAATTTGGTTACAGATTATTTCCCAA 1179
Qy 381 GlySerPhePheIleThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1180 GCCTGTTTTTCAGAGTAATTCACGGCGGAATGGCCATCCATCAAGAACCACTCGTAAA 1239
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1240 GAAATGAAACAGAACCGCAAGCTGGTAAAGATTTACGCTTTAAATTTGTGAAAGAAAG 1299
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1300 GTACCTTACATCTATAGAAGCTTTTACCATAGAGAATTCACATATTCATAGATACCT 1359
Qy 441 LeuValSerIleTyrProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1360 TTAGTTTCTATTATATCCCCGCTTATAACTGTGCAAAATTAATTTCAAAAGATGTGTAGAT 1419
Qy 461 SerAlaLeuAsnGlnThrValIleAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1420 AGTGCTCTTAAATCAAACTGTTGTCGATCTCGAGGTTGTATTGTAACCATGGTTCAACA 1479
Qy 481 AspAsnThrGluValIleAsnIleLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1480 GATAATACCTTGAAGTGTATCAATAGCTTTATGGTAAATATCTTAGGGTAGCATCATG 1539
Qy 501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaIleGly 520
Db 1540 TCTNAACCAAAATGGCGGAATAGCCTCAGCATCAATGACGACCGTTCTTTTGTCTAAAGGT 1599
```



880 ACTCATAATATTACCGCAGAACAAATTCCTTAACGATCCATATTTAATAGAAATCACTACCT 939  
Db  
301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Qy  
940 GAAACCGCTACAAATAACAAATTCCTTCGATTAATCATCAAAAGGAATAATATCTGTAATGG 999  
Db  
321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Qy  
1000 AGATTAGAACATTTCAAAAACCAACCGATTAATCTACGCTCTATGATTCCTCCGTTTCGTTAT 1059  
Db  
341 PheAlaAlaGlyAsnValAlaPheAlaLysIleValLysThrLeuAsnLysSerGlyPhePheAsp 360  
Qy  
1060 TTTGTTCGGGTAAATGTTGCATTTTCTAAAGAAATGGCTAAATAAAGTAGGTGGTTTCGAT 1119  
Db  
361 GluGluPheAsnHisTrpGlyGluAspValGluPheGlyValArgLeuPheArgTyr 380  
Qy  
1120 GAAGAATTTAATCATTTGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTATTTGCCAAA 1179  
Db  
381 GlySerPhePheThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Qy  
1180 GGCTGTTTTTCAGAGTAATTCACCGCGGAATGGCCATCCATCAAGAACCACTGGTAAA 1239  
Db  
401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Qy  
1240 GAAATGAACAGAACGCGAGCTGGTAAAGTATTACGCTTAAATTTGTGAAGAAAAG 1299  
Db  
421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Qy  
1300 GTACCTTACATCATAGAAAGCTTTTACCCAATAGAGATTTCATATTCATAGAAATACCT 1359  
Db  
441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Qy  
1360 TTAGTTTCTATTATATCCCGCTTATAACTGTGCMAATATTATTCMAAGATGTGTAGAT 1419  
Db  
461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Qy  
1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGTTGTGATTGTAAACGATGGTTCAACA 1479  
Db  
481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Qy  
1480 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATTAATCCCTAGGGTAGCGATCATG 1539  
Db  
501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Qy  
1540 TCTAAACCAAAATGGCGGAATACCTCAGCATCAATGCGAGCGTTCTTTCTGCTAAAGT 1599  
Db  
521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
Qy  
1600 TATTACATTTGGCAGTTAGATTACAGATGATTATCTTGAGCCTGATGTCAGTTGAACCTGTGT 1659  
Db  
541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Qy  
1660 TTTAAAGAAATTTTAAAGATAAAACGATGCTGTGTTTATACCACTAATAGAAACGTC 1719  
Db  
561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Qy  
1720 AATCCGGATGGTAGCTTAATCGCTAATGGTTACATITGGCCAGAAITTTTACAGAGAAA 1779  
Db  
581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Qy  
1780 CTCACAAACGGCTATGATGCTCACCATTTTAGAATGTTTACGATTAGAGCTTGGCATTTA 1839  
Db  
601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Qy  
1840 ACGGATGGATTTAACGAAATAATTTGAAACCGCGGTGATTAATGACATGTTCTCTTAAACTC 1899  
Db  
621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Qy  
1900 AGTGAAGTTGCAAAATTTTAAACATCTTAATAAAATCTGCTATTAACCGCGTATTACATGGT 1959  
Db  
641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660  
Qy  
1960 GATAACACATCCATTAAAGAACTCGGCATTCAAAAGAAAACCAATTTTGTGTAGTCAAT 2019  
Db

661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Qy  
2020 CAGTCATTAAATACACAAGGCATCAATATTATTAATATGACAAATTTTGATGATTAGAT 2079  
Db  
681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Qy  
2080 GAAAGTAGAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGATATGTTA 2139  
Db  
701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Qy  
2140 AAAAGTCTTAAACTCATTTCAAAATAAGATGCCAAATCGCAGTCAGTATTTCTATCCC 2199  
Db  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Qy  
2200 AATACATTTAAACGGCTAGTGAATAAACTAAGCAATATATTGAATATAATAAATAATA 2259  
Db  
741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Qy  
2260 TTCGTTATTATTCTACATGTTGATAAGAAATCATCTTACCCAGACATCAAAAAGAAATA 2319  
Db  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
Qy  
2320 TTGCTTTCTATCATAGCACCAAGTGNATATTTTACTAATAATGACATCTCATATTAC 2379  
Db  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Qy  
2380 ACGAGTAAATGACATAATAAACTGAGGCACATTTAAGTAATATTAAATAATTAAGTCAG 2439  
Db  
801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Qy  
2440 TTAATCTAAATTTGTGAATACATCATTTTTCATATCATGACGCTATTCGTTAAAAAT 2499  
Db  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Qy  
2500 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAACACAT 2559  
Db  
841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Qy  
2560 GATTGATCGAGAAAATCAATCGCATCCACCATTTAAAAAGCTGATTAAAAACCTATTTT 2619  
Db  
861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Qy  
2620 AATGACAATGACTTAAGAAGTATGAATGTGAAGGGGCATCAAGGTAATGTTTATGAAG 2679  
Db  
881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Qy  
2680 TATGCGCTACCGCATGAGCTTCTGACGATTATTAAGAAGTCATCACATCTCTGCCAATCA 2739  
Db  
901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Qy  
2740 ATTGATAGTGTGCCAGAAATATAACACTGAGGATAATTTGGTCCAAATTTGCACCTTTTAAATC 2799  
Db  
921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
Qy  
2800 TTAGAAAAAGAAACCGGCCATGTTATTATAAATAACATCGACCTGACTTATATGCTTTGG 2859  
Db  
941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Qy  
2860 GAACGAAATTTACAATGGACAATGAACAAATTTCAAGTGCANAAAAAGCGGAAATAATC 2919  
Db  
961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Qy  
2920 CCGCTTAAACAGTTTCATTATTATTAATAGTATAACGCTA 2955  
Db

## RESULT 11

ADP75648

ID ADP75648 standard; DNA; 2979 BP.

XX ADP75648;

AC ADP75648;

XX 12-AUG-2004 (first entry)

DT

XX





|||||  
1420 AGTCTCTTAATCAAACTGTTGTCGATCTCGAGGTGTTGTTAATGCTTAACGATGGTTCAACA 1479  
Qy AspAenThrLeuGluValIleAenLysLeuTyrglyAenAenProArgValArgIleMet 500  
Db GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTAATAATCTCCTAGGGTACGCATCATG 1539  
Qy SerLysProAenGlyGlyIleAlaSerAlaSerAenAlaValSerPheAlaLysGly 520  
Db TCTAAACCAATGGCGGAATAGCCTCAGCATCAATGCGAGCGGTTCTTTTCTTAAGGT 1599  
Qy TyrTyrlleGlyGlnLeuApsSerApsPheLeuGluProApsAlaValGluLeuCys 540  
Db TATTACATGGCGAGTTAGATTTCAGATGATTCTTGAGCGCTGATGCAAGTTGAACGTGT 1659  
Qy LeuLysGluPheLeuLysApsLysThrLeuAlaCysValTyThrAenAenAenVal 560  
Db TTAAGAAGAAATTTAAAGATAAAACGCTAGCTGTGTGTTTATACCACTAAATAGAAACGTC 1719  
Qy AenProApsGlySerLeuIleAlaAenGlyTyraenTTPProGluPheSerArgGluLys 580  
Db AATCGGATGGTAGCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTCACGAGAAAA 1779  
Qy LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db CTCACACGGCTATGATTGCTCACCACTTTTGAATGTTTACGATTTAGAGCTTGGCATTTA 1839  
Qy ThrApsGlyPheAenGluLysIleGluAenAlaValApsTyraenPheLeuLysLeu 620  
Db ACGGATGGATTAAACGAAATATTGAAACCGCGTGATTTATGACATGCTTCTTAAACGTC 1899  
Qy SerGluValGlyLysPheLysHisLeuAenLysIleCysTyraenAenValLeuHisGly 640  
Db AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGCGTATTACATGCT 1959  
Qy ApsAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValValAen 660  
Db GATAACACATCCATTAAAGAACTCGCATTCAAAAGAAACCACTTTTGTGTAGTCAAT 2019  
Qy GlnSerLeuAenArgGlnGlyIleThrTyraenTyraenApsGluPheApsApsLeuAps 680  
Db CAGTCATTAAATAGACAGGCATCAATTTATATAATTTATGACAAATTTTGATGATTTAGAT 2079  
Qy GluSerArgLysTyrllePheAenLysThrAlaGluTyraenGlnGluLysIleApsIleLeu 700  
Db GAAAGTAGAAGATATATCTTCAATAAAACCGCTGAATATCAAGAGAAATGGATATGTTA 2139  
Qy LysApsIleLysIleIleGlnAenLysApsAlaLysIleAlaValSerIlePheTyraenPro 720  
Db AAAGATCTTAACCTCATTCAAATAAAGATGCGAAATCGCAGTCAGTATTTCTATCCC 2199  
Qy AenThrLeuAenGlyLeuValLysLysLeuAenAenIleIleGluTyraenLysAenIle 740  
Db AATACATTAACCGCTTAGTGAATAAACTTAAACAATTTATTTGAATATAATAAAAAATA 2259  
Qy PheValIleValLeuHisValApsLysAenHisLeuThrProApsIleLysLysGluIle 760  
Db TTCTGTTATTATTCTCATCTGATGAAGATCATCTTTACACCGACATCAAAAAAGAAATA 2319  
Qy LeuAlaPheTyraenHisLysHisGlnValAenIleLeuAenAenApsIleSerTyraen 780  
Db TTGGCTTTCTATCATAGACCAAGTAATATTTTACTAATAATAGACATCTCATATTAC 2379  
Qy ThrSerAenArgLeuIleLysThrGluAlaHisLeuSerAenIleAenLysLeuSerGln 800  
Db ACGAGTAAATAGACTAATAAAACCTGAGGCACATTTAAGTAATATTAAATAATTAAGTCAG 2439  
Qy LeuAenLeuAenCysGluTyrlleIlePheApsAenHisSerLeuPheValLysAen 820  
Db TTAATCTAAATTTGTTGAATACATCATCTTTTGAATATCATGACAGCGCTATTCGTTAAAAAT 2499  
Qy AspSerTyraenAlaTyraenMetLysLysTyraenValGlyMetApsPheSerAlaLeuThrHis 840

Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2559  
Qy AspTrpIleGluLysIleAenAlaHisProPheLysLysLeuIleLysThrTyraenPhe 860  
Db GATTGGATCCAGAAATCAATCGCATCCACCATTTAAAAAGCTGATTTAAACCTATTTT 2619  
Qy AsnApsAenApsLeuLysSerMetAenValLysGlyAlaSerGlnGlnGlyMetPheMetThr 880  
Db AATGACATGACTTAAAGAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGAAG 2679  
Qy TyraenAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900  
Db TATCGCTACCGCATGAGCTTCTGACGATTTAATAAGAGTCATCACAATCTCGCAATCA 2739  
Qy IleApsSerValProGluTyraenThrGluApsIleTrpPheGlnPheAlaLeuLeuIle 920  
Db ATTGATAGTGTCCAGAAATATACACTGAGGATATTGGTTCCAATTTGCACCTTTTAATC 2799  
Qy LeuGluLysLysThrGlyHisValPheAenLysThrSerThrLeuThrTyraenMetProTrp 940  
Db TTGAAAAAGAAACCGGCCATGTATTTAATAAAAAACATCGACCTGACTTATATGCTTTGG 2859  
Qy GluArgLysLeuGlnTTPThrAenGluGlnIleGluSerAlaLysArgGlyGluAenIle 960  
Db GAACGAAATTTACAAATGGACAAATGAACAAATTCAAAGTGCAAAAAGGCGAAATATC 2919  
Qy ProValAenLysPheIleIleAenSerIleThrLeu 972  
Db CCGGTTAAACAGTTCAATTTATATAGTATAACGCTA 2955  
RESULT 12  
ADP75667  
ID ADP75667 standard; DNA; 2271 BP.  
AC ADP75667;  
XX 12-AUG-2004 (first entry)  
XX Pasteurella multocida truncated hyaluronidase gene #11.  
XX polymer production; hyaluronidase gene; chondroitin polymer;  
KW hyaluronidase gene; db; enzyme.  
XX Pasteurella multocida.  
OS  
XX  
XX WO2003029261-A2.  
XX  
XX 10-APR-2003.  
XX  
XX 12-JUL-2002; 2002WO-US022386.  
XX  
XX 13-JUL-2001; 2001US-0305263P.  
PR 22-JAN-2002; 2002US-030642P.  
PR 08-MAY-2002; 2002US-00142143.  
XX  
XX (DEAN/) DEANGELIS P L.  
XX  
XX Deangelis PL;  
XX  
XX WPI; 2003-532559/50.  
XX  
XX Producing polymer, e.g. hyaluronidase or chondroitin polymer, by  
PT providing a functional acceptor, a synthase capable of elongating the  
PT acceptor and sugars such that synthase elongates the acceptor to provide  
PT polymer.  
XX  
XX Disclosure; SEQ ID NO 20; 538pp; English.  
PS  
XX The invention comprises a method for producing a polymer, especially a  
CC hyaluronidase (HA) or chondroitin (CD) polymer composed of less than  
CC 150 sugars. The method involves providing a functional acceptor,  
CC providing a synthase capable of elongating the functional acceptor, and  
CC providing sugars such that the synthase elongates the functional acceptor



CC to provide the polymer. The method of the invention is useful for  
CC producing a hyaluronic acid or chondroitin polymer composed of 1-150  
CC sugars. The present DNA sequence encodes a truncated Pasteurella  
CC multocida hyaluronic acid synthase of the invention.

XX  
SQ Sequence 2271 BP; 812 A; 384 C; 404 G; 671 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 0 Length: 2271  
Score: 3964.00 Matches: 755  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.87% Mismatches: 0  
Query Match: 77.60% Indels: 0  
DB: 11 Gaps: 0

US-10-642-248-2 (1-972) x ADP75667 (1-2271)

```
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 1 ATGNATACATTATCACAGCGAATTAAGCATATTAACAGCAATGATCTATCAATTAGCACTC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTATTGAAAGTCCGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAAATTACC 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AAATGCCAAGAAAACTCTCAGCACATCTCTCTGTTAAATTCAGCACATCTCTCTGTAAT 180
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAAGAAGAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACAACTGTTACTT 240
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db 241 TCCAACTGAAATAAATAGTACTTCTGACTCGGAAATAAACACGTTTAAAAAATAAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTGTCTCATGAGAGAAATCTGAAATTCGGAGGTAGAGCGGTCCGCTTTGTACCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAAGATTTTCCAAAGATCTGGTTTTAGCGCTTTTACTGATCAATGATTAATGATTTACA 420
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160
Db 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATATAAACTGAAACATCAACATGTTGGTCTT 480
Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTACAAACATTCAAATCGACCACAAATTTTATCGATTACATTAGCCCTGTTA 540
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAACACATTACCCTTTGAAGTTATCGTGACAGATGATGTTAGTCAGGAA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 601 GATCTATCACCGATCATTCGCCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 660
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 661 AAAGATAACGGTTTTCAGCGCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 720
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db 721 GACTTTATGGCTTACTCGACTGTGATATGGCGCAATTCATTTATGGTTTCATCTTAT 780
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 781 GTTCAGAGCTATTAGAAGATGATGATTTAAACATCATTTGTTCCAGAAATAATACATCAT 840
```

```
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 841 ACAACATATTGACCCAAAGACTTCTTAATTAACGCGAGTTTGCTTGAATCATTACCA 900
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGlyThrValSerLeuAspTyr 320
Db 901 GAAGTGAAACCAATAATAGTGTTCGCGCAAAAGGGAAGGAACAGTTCTCTGGATTGG 960
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 961 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTT 1020
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp 360
Db 1021 TTTGCGCGGGTAATGTTGCTTTCCGCTAAATAATGGCTAATAATCCGGTTTCTTTGAT 1080
Qy 361 GluGluPheAsnHisTyrGlyGlyAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1081 GAGGAATTTAATCACTGGGTGGAGAGATGCGAATTTGGATATCGCTTATTTCCGTTAC 1140
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1141 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCAGGTAAA 1200
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1201 GAAAAAGAAACCCGATCGTGANGCGGGAATAATATTACGCTCGATATTATGAGAGAAAG 1260
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGATGACCT 1320
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1321 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTCGCTAGAT 1380
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAACAGATGGTTCAACA 1440
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1441 GATAATACCTTTAGAGTGATCAATAAGCTTTATGGTAAATAATCTTAGGGTACGCATCATG 1500
Qy 501 SerLysProAsnGlyLysIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAAAATGGCGAATAGCTCAGCATCAAAATGCAGCCGTTTCTTTTGTCTAAAGGT 1560
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1561 TATTACATTTGGCGATTAGATTGAGATGATTATCTTGAGCTGATCGAGTTGAACTGTGT 1620
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCCTAATAAGAAACGTC 1680
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580
Db 1681 AATCCGATGGTAGCTTAATCGCTAATGGTTACAAATTTGGCCAGAAATTTTCCAGGAGAAAA 1740
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrHisLeu 600
Db 1741 CTCAACACGGCTATGATTGCTCACCCTTTAGAAATGTTACAGATTAGAGCTTGGCATTTA 1800
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1801 ACTGATGGAATCAATGAAAAAATTTGAAATTTGAAATTTGAAATTTTCCCAAACTC 1860
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1861 AGTGAAGTTGGAATAATTAACATCTTAATAAAAAATCTGCTATAACCGTGTATTACATGGT 1920
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
```

Db 1921 GATAACACATCAATTAAGAAACTTGGCATTCACAAAGAAACCAATTTTGTGTAGTCAAT 1980  
Qy 661 GlnSerLeuAenArgGlnGlyLeuThrTyrrAsnTyrrAspGluPheAspLeuAsp 680  
Db 1981 CAGTCATTAAATAGACAAGGCATCACTATTATTATTAATATGACGAATTTGATGATTTAGAT 2040  
Qy 681 GluSerArgLysTyrrLlePheAsnLysThrAlaGluTyrrGlnGluGluLleAspLleLeu 700  
Db 2041 GAAAGTAGAAGATATATTTTCATTAACACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
Qy 701 LysAspLleLysLleLleGlnAsnLysAspAlaLysLleAlaValSerLlePheTyrrPro 720  
Db 2101 AAAGATATTAAATCATCCAGAAATAAGATGCCAAATCGCAATTCAGTATTTTATATCCC 2160  
Qy 721 AsnThrLeuAenGlyLeuValLysLysLeuAenAsnLleLleGluTyrrAsnLysAenLle 740  
Db 2161 AATACATTAAACGGCTTAGTGAATAAACTAAACCAATATTATTGAATATATAAAAAATATA 2220  
Qy 741 PheValLleValLeuHisValAspLysAsnHisLeuThrProAspLle 756  
Db 2221 TCGGTTATTGTTTACATGTTGATAAGAAATCATCTTACACCGATATC 2268

RESULT 13

ID ADP75698 standard; DNA; 2136 BP.  
XX ADP75698;  
XX  
XX 12-AUG-2004 (first entry)  
XX  
XX Pasteurella multocida truncated hyaluronid acid synthase gene #20.  
XX polymer production; hyaluronid acid polymer; chondroitin polymer;  
XX hyaluronid acid synthase; gene; ds; enzyme.  
XX  
XX Pasteurella multocida.

XX WO2003029261-A2.  
XX  
XX 10-APR-2003.  
XX  
XX 12-JUL-2002; 2002WO-US022386.  
XX  
XX 13-JUL-2001; 2001US-0305263P.  
XX 22-JAN-2002; 2002US-0350642P.  
XX 08-MAY-2002; 2002US-00142143.  
XX  
XX (DEAN/) DEANGELIS P L.  
XX  
XX Deangelis PL;  
XX  
XX WPI; 2003-532558/50.  
XX  
XX Producing polymer, e.g. hyaluronid acid or chondroitin polymer, by  
XX providing a functional acceptor, a synthase capable of elongating the  
XX acceptor and sugars such that the synthase elongates the acceptor to provide  
XX polymer.  
XX  
XX Disclosure; SEQ ID NO 51; 538pp; English.  
XX  
XX The invention comprises a method for producing a polymer, especially a  
XX hyaluronid acid (HA) or chondroitin (CD) polymer composed of less than  
XX 150 sugars. The method involves providing a functional acceptor,  
XX providing a synthase capable of elongating the functional acceptor, and  
XX providing sugars such that the synthase elongates the functional acceptor  
XX to provide the polymer. The method of the invention is useful for  
XX producing a hyaluronid acid or chondroitin polymer composed of 1-150  
XX sugars. The present DNA sequence encodes a truncated Pasteurella  
XX multocida hyaluronid acid synthase of the invention.  
XX  
XX Sequence 2136 BP; 754 A; 365 C; 388 G; 629 T; 0 U; 0 Other;  
SQ

Alignment Scores: 3.96e-311 Length: 2136  
Pred. No.: 3705.00 Matches: 702  
Score: 3705.00  
Percent Similarity: 99.72% Conservative: 7  
Best Local Similarity: 98.73% Mismatches: 2  
Query Match: 72.53% Indels: 0  
DB: 11 Gaps: 0  
US-10-642-248-2 (1-972) x ADP75698 (1-2136)  
Qy 1 MetAenThrLeuSerGlnAlaLleLysAlaTyrrAsnSerAenAspTyrrGlnLeuAlaLeu 20  
Db 1 ATGAACACATATACACAGCAATATAAGCATATATAACAGCAATGACTATCAATAGCACTC 60  
Qy 21 LysLeuPheGluLysSerAlaGluLleTyrrGlyArgLysLleValGluPheGlnLleThr 40  
Db 61 AAATTAATTTGAAAGTCGGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAAATACC 120  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen 60  
Db 121 AAATGCCAAGAAAACCTCTCAGCACATCTCTGTTAAATTCAGCACATCTTCTGTAAT 180  
Qy 61 LysGluGluLysValAenValCysAspSerProLeuAspLleAlaThrGlnLeuLeuLeu 80  
Db 181 AAAGAAGAAAAGTCAATGTTTGGCATGTCGGTAGATATTCGCAACACACTGTTACTT 240  
Qy 81 SerAenValLysLysLeuValLeuSerAspSerGluLysAenThrLeuLysAenLysTrp 100  
Db 241 TCCAACTGAAAATAATTTAGTACTTTTCTGACTCGCGAAAACACGTTAAAAATAAATGG 300  
Qy 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120  
Db 301 AAATTTGCTCACTGAGAAGAAATCTGAAATCGCGAGGTAAAGAGCGGCGCCCTTGTATCCA 360  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAenAspPheThr 140  
Db 361 AAAGATTTTCCCAAGATCTGGTTTTAGCGCTTTTACCTGATCATGTTAAATGATTTTACA 420  
Qy 141 TrpTyrrLysLysArgLysLysArgLysLysProGluHisGlnHisValGlyLysLeu 160  
Db 421 TGGTACAAAAGCGAAGAAAAGACTTGGCATATAAACTGAAACATCAACATGTTGGTCTT 480  
Qy 161 SerLleLleValThrThrPheAenArgProAlaLleLeuSerLleThrLeuAlaCysLeu 180  
Db 481 TCTATTATCGTTACACATTCATTCGACCACTTTTATCGATTACATTTAGCCCTGTTTA 540  
Qy 181 ValAenGlnLysThrHisTyrrProPheGluValLleValThrAspAspGlySerGlnGlu 200  
Db 541 GTAAACCAAAAACACACATTTACCCGTTTGAAGTTTATCGTCACAGATGATGGTAGTCAGGA 600  
Qy 201 AspLeuSerProLleLleArgGlnTyrrGluAenLysLeuAspLleArgTyrrValArgGln 220  
Db 601 GATCTATCACCGATCATTCGCCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 660  
Qy 221 LysAspAenGlyPheGlnAlaSerAlaAlaArgAenMetGlyLeuArgLeuAlaLysTyrr 240  
Db 661 AAAGATACGGTTTTTCAAGCCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 720  
Qy 241 AspPheLleGlyLeuLeuAspCysAspMetAlaProAenProLeuTrpValHisSerTyrr 260  
Db 721 GACTTTATTTGGCTTACTCGACTGTGATATGGCCCAATTCATTTATGGTTTCATCTTAT 780  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrLleLleGlyProArgLysTyrrLleAsp 280  
Db 781 GTTGCAAGACTATTAGAGAGATGATGATTTAACATCATTTGTTCCCAAGAAAATATACATCAT 840  
Qy 281 ThrGlnHisLleAspProLysAspPheLeuAenAenAlaSerLeuLeuGluSerLeuPro 300  
Db 841 ACACAACATATTGACCCCAAGACTTCTTAAATAACCGAGTTTCTGTTGAATTCATTACCA 900  
Qy 301 GluValLysThrAenAenSerValAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 901 GAAGTGAAAACCAATAATAGTGTTCGCCGCAAAAGGGAAGCAAGTTTCTCTGGATTGG 960

```
QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 961 CGCTTAGAACAAATTCGAAAGAAACAGAAATCTCCGCTTATCCGATTCGCCTTTCCGGTTTT 1020
QY 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPhePheAsp 360
Db 1021 TTTGGCGGGTAATGTTGCTTCGCTTAAATAATGGCTAAATAATCCGGTTCTTTTGAT 1080
QY 361 GluGluPheAenHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1081 GAGCAATTTAATCACTCGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCCGGTTAC 1140
QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1141 GGTAGTTTCTTTAAACTATTGATGGCATTATGGCTTACCATTCAAGAGCCACCAGGTAAA 1200
QY 401 GluAenGluThrAspArgGluAlaGlyLysAenIleThrLeuAspIleMetArgGluLys 420
Db 1201 GAAATCGAACCGATCGTAAGCGGGGAAAATATTACGCTCGATATTATGAGGAAAG 1260
QY 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAenArgValPro 440
Db 1261 GTCCCTTATATCTATAGAAAACCTTTTACCATAGAGATTTCGCATATTCATAGAAATACCT 1320
QY 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAenTyrIleGlnArgCysValAsp 460
Db 1321 TTAGTTTCTATTATATCCCGCTTTAATACGTGTCNAATATATATTCAAAGATGTGTAGAT 1380
QY 461 SerAlaLeuAenGlnThrValValAspLeuGluValCysIleCysAenAspGlySerThr 480
Db 1381 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTGTGTACGATGGTTCAACA 1440
QY 481 AspAenThrLeuGluValIleAsnLysLeuTyrGlyAenAenProArgValArgIleMet 500
Db 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGCTAATAATCTTAGGTCACGCATCATG 1500
QY 501 SerLysProAenGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAATGGCGAATAGCCCTCAGCATCAATAGCCGCTTCTTTTGTCTAAAGGT 1560
QY 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1561 TATTACATGGCGAGTTAGATTGATGATGATTATCTTGAGCTGTATGATGATGATGATGAT 1620
QY 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTATATACCACTAATAGAAACGTC 1680
QY 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580
Db 1681 AATCCGATGGTAGCTTAATCGCTTAATGGTTTACAAATGGCCAGAAATTTTACAGAGAAAA 1740
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1741 CTCAACCGGTATGATGCTCACCATTTTACAAATGTTAGCATTTAGAGCTTGGCATTTA 1800
QY 601 ThrAspGlyPheAenGluLysIleGluAenAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1801 ACGGATGGATTTAACGAAAAATATTGAAACCGCCGCGGATGATGATGATGATGATGATGAT 1860
QY 621 SerGluValGlyLysPheLysHisLeuAenLysIleCysTyrAenArgValLeuHisGly 640
Db 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAAAATCTGCTATAACCCGCTATTACATGGT 1920
QY 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValValAsn 660
Db 1921 GATTAACATCTCATTAAGAACTGGCATTTCAAAGAAAAACCAATTTTGTGTAGTCAAT 1980
QY 661 GlnSerLeuAenArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680
Db 1981 CAGTCATTAATAGACAAGGCATCAATATTATTAATATGACAAATTTGATGATTTAGAT 2040
```

```
QY 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2041 GAAAGTAGAAGATATATCTTCAATAAACCCTGAATATCAAGAAATGGATATTTTA 2100
QY 701 LysAspIleLysIleIleGlnAenLysAspAla 711
Db 2101 AAAGATCTTAAACTCATTCAGAATAAAGATGCC 2133

RESULT 14
AEA04964
ID AEA04964 standard; DNA; 2112 BP.
XX
AC AEA04964;
XX
DT 11-AUG-2005 (first entry)
XX
DE Hyaluronic acid synthase, PmHAS, coding sequence, SEQ ID 2.
XX
KW Hyaluronic acid synthase; polysaccharide; gene; ds.
XX
OS Pasteurella multocida.
XX
FH Key Location/Qualifiers
FT CDS 1..2112
FT /tag= a
FT /product= "PmHAS"
XX
PN US2005124046-A1.
XX
PD 09-JUN-2005.
XX
PF 16-JUL-2002; 2002US-00197153.
XX
PR 10-NOV-1999; 99US-00437277.
XX
PA (DEAN/) DEANGELIS P L.
XX
PI Deangelis PL;
XX
DR WPI; 2005-417007/42.
DR P-PSDB; AEA04963.
DR GENBANK; AF036004.
XX
PT Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin),
PT useful in polysaccharide polymer grafting, comprises providing hyaluronic
PT acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the
PT functional acceptor.
XX
PS Claim 4; SEQ ID NO 2; 41pp; English.
XX
CC The present invention relates to a method for elongating a functional
CC acceptor. The method comprises providing a hyaluronic acid (HA) synthase
CC (PmHAS; AEA04963) capable of elongating the functional acceptor and
CC providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid
CC synthase elongates the functional acceptor. PmHAS adds sugars to the
CC nonreducing end of a growing polymer chain. The PmHAS sequence is
CC significantly different from the other known HA synthases: there appears
CC to be only two short potential sequence motifs (AEA04967 and AEA04968) in
CC common between PmHAS and the other HA synthases. The method is useful in
CC polysaccharide polymer grafting, which may be utilized in the development
CC of biotechnological medical improvements. These may be used for producing
CC hybrid polysaccharides or for forming polysaccharide coatings. The
CC present sequence is the coding sequence for PmHAS.
XX
SQ Sequence 2112 BP; 746 A; 358 C; 387 G; 621 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1 93e-310 Length: 2112
Score: 3637.00 Matches: 703
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.38% Indels: 0
DB: 14 Gaps: 0
```

US-10-642-248-2 (1-972) x ABA04964 (1-2112)

Qy 1 MetAsnThrLeuSerGlnAlaIleGlyAlaTyrrhAsnSerhAsnAspTyrGlnLeuAlaLeu 20  
Db 1 ATGAATACATTTATCACAGCAATAAAAGCATATACAGCAATGATGATCAATATAGCACTC 60  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 61 AAATATTTGAAAAGTCGGCGGAATCTATGGACGGAAATTTGTTGAATTTCAAAATACC 120  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 121 AAATGCAAGAAAAAATCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTCTGTAAAT 180  
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 181 AAAGAAGAAAAAGTCAATGTTTGGATAGTCCTGATATATGCAACAACTGTTACTT 240  
Qy 81 SerhAsnValLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 241 TCCAACTGAAAAAATTTAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATAATGG 300  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValAlaAlaValAlaLeuValPro 120  
Db 301 AAATTTGCTCACTGAGAGAAATCTGAAATCGGAGGTAAGAGCGGTGCGCCCTTGTACCA 360  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 361 AAAGATTTTCCCAAGATCTGGTTTTAGCGCTTTTACCTGATCATGTTTAATGATTTACA 420  
Qy 141 TrpTyrLysLysArgLysLysArgLysGluLysProGluHisGlnHisValGlyLeu 160  
Db 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCAATAAACTGAACTGAACATCAACATGTTGGTCT 480  
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 481 TCTATTATCGTTACAACTTCAATCGACCAAGCAATTTTATCGATTACATTTAGCCCTGTTTA 540  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 541 GTAAACCAAAAAACACATTTACCGCTTTGAAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 601 GATCTATCACCGCATCATTCGCCAAATATGAAATAAATTTGGATTTTCGCTAGCTCAGACAA 660  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 661 AAAGATAACGGTTTTCAAGCCAGTCCCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 720  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
Db 721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGGTTCAATCTTTAT 780  
Qy 261 ValAlaGluLeuLeuGluAspAspPheThrIleIleGlyProArgLysTyrIleAsp 280  
Db 781 GTTGACAGAGCTATTAGAAGATGATGATTTAAACAATCAITGGTCCAGAAAAATACATCGAT 840  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 841 ACACAAACATATTGACCCAAAAGACTTCTTAATATACCGGAGTTTGGTGAATCATTTACCA 900  
Qy 301 GluValLysThrAsnAsnSerValAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 901 GAAGTGMAAACCAATAATAGTTGTGCGCAAAAGGGAAGGAAACAGTTTCTCTGGATTGG 960  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 961 CGCTTAGAACCAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTT 1020  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
Db 1021 TTTGCGGCGGGTAATGTTGCTTCGCTAAAAAATGGCTAAATAAATCCGGTTTCTTTTGAT 1080  
Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1081 GAGGAATTTAATCACTGGGCGTGAGAAGATGTGGAATTTGGATATCGCTTATTCCGTTAC 1140  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrrhHisGlnGluProProGlyLys 400  
Db 1141 GGTAGTTTCTTTAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCAGGTAAA 1200  
Qy 401 GluAsnGlnThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1201 GAAAAAGAAACCGATCGTGAAGCGGGAANAATAATTACGCTCGATATATGAGAGAAAAAG 1260  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1261 GTCCCTTATATATAGAAAACTTTTACCAATAGAGATTTCGCATATCAATAGAGTACCT 1320  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTTCAACGTTGCGTAGAT 1380  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTACGATGGTTCAACA 1440  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1441 GATANTACCTTAGAAGTGATCAATAAGCTTTATGTTAATAATCTAGGTTACGCATCATG 1500  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerhAsnAlaValSerPheAlaLysGly 520  
Db 1501 TCTAAACCAAAATGCGGAATAGCCTCAGCATCAAAATGCGCCGTTTCTTTTGTAAAGGT 1560  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCCTGATGCGTTGAACTGTGT 1620  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560  
Db 1621 TTTAAAGAAATTTTAAAGATATAAACCGTAGCTAGTTGTGTTTATACCACCTAATAGAAACGTC 1680  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1681 AATCGGATGTTAGCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTTCACGAGAAAA 1740  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaIleTrpHisLeu 600  
Db 1741 CTCACACGGCTATGATTGCTCACCCACTTTTAAAGATGTTTACGATTTAGAGCTTTGGCATTTA 1800  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1801 ACTGATGATTTCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGTGTATTACATGCT 1920  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsn 660  
Db 1921 GATAACACATCAATTTAGAAAACTTTGGCATTTCAAAAGAAAAAACCATTTTGTGTAGTCAAT 1980  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 1981 CAGTCATTTAATAGCAAGGCATTAATTTATTAATATGACGAATTTGATGATTTAGAT 2040  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluLysIleAspIleLeu 700  
Db 2041 GAAAGTAGAAGATATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTCATATCTTTA 2100  
Qy 701 LysAspIle 703  
Db 2101 AAAGATATTT 2109

## RESULT 15

AAA27448  
ID AAA27448 standard; cDNA; 2112 BP.

XX AC  
XX AAA27448;

DT 17-AUG-2000 (first entry)

XX P.multocida hyaluronic acid synthase-D coding sequence.

XX Hyaluronic acid synthase-D; HAS-D; enzyme; ophthalmic surgery; cataract;  
KW arthritis; ulcer; tissue abrasion; viscoelastic replacement;  
KW hyaluronic acid production; bioadhesive; ss.

XX Pasteurella multocida.

XX Key Location/Qualifiers

PH CDS 1..2112

FT /\*tag= a

FT /product= "PmHAS-D"

FT /transl\_except= (pos:1348..1353,aa:Asn)

XX WO200027437-A2.

XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-US026501.

XX 11-NOV-1998; 98US-0107929P.

XX 01-APR-1999; 99US-00283402.

XX (OKLA ) UNIV OKLAHOMA STATE.

XX Deangelis PL;

XX WPI: 2000-376319/32.

XX P-PSDB; AAY96212.

XX Novel method for the enzymatic transfer of sugar molecules to an  
PT acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or  
PT drug delivery systems, including hybrid molecules.

XX Claim 20; Page 84; 86pp; English.

XX The present sequence is the coding sequence of the soluble recombinant  
CC form of Pasteurella multocida hyaluronic acid synthase-D, PmHAS-D. This  
CC sequence encodes residues 1 to 703 of the 972 residues of the native  
CC PmHAS enzyme. PmHAS-D catalyses glycosaminoglycan polymerisation to  
CC produce hyaluronic acid. HA: a linear polysaccharide. HA has viscoelastic  
CC properties which makes it useful for a number of applications. HA can be  
CC used during ophthalmic surgery as a viscoelastic replacement for the  
CC vitreous humour e.g. during implantation of intraocular lenses in  
CC cataract patients. HA injections directly into joints is also used to  
CC alleviate pain associated with arthritis. HA can also be used to coat  
CC medical devices e.g. catheters and sensors to reduce tissue abrasion. HA  
CC can also be used as bioadhesives for haemostatic sealing and healing of  
CC wounds and surgical incisions; and as biomaterials that provide sustained  
CC delivery of encapsulated drugs, to wounds, ulcers, injuries or surgical  
CC sites. The present sequence can therefore be used to produce HA

XX Sequence 2112 BP; 745 A; 359 C; 387 G; 621 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 4.29e-310 Length: 2112  
Score: 3693.00 Matches: 702  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.86% Mismatches: 0  
Query Match: 72.30% Indels: 0  
DB: 3 Gaps: 0

US-10-642-248-2 (1-972) x AAA27448 (1-2112)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
DB |||||  
DB 1 ATGATATACATTATACACAGCAATAAAGCATATACAGCATGACTATCAATTAGCAGCTC 60  
QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
DB |||||  
DB 61 AAATTATTTGAAAAGTCGGCGGAAATCTATGACGCGGAAAATTTGTTGAAATTTCAAATTACC 120  
QY 41 LysCysGlyGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
DB |||||  
DB 121 AAATGCCAAGAAAACCTCTCAGCACATCTCTGTTAAATTCAGCACATCTTTCTGTAAT 180  
QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
DB |||||  
DB 181 AAAGAAGAAAAGTCAATGTTTCGGATAGTTCGTTAGATATTGCAACACACACTGTTACTT 240  
QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
DB |||||  
DB 241 TCCACAGTAAATAAATTTAGTACTTTCTGACTTCGAAAAAAAACACGTTAAAAATAAATGG 300  
QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
DB |||||  
DB 301 AAATTGCTCCTGAGAGAAATCTGAAAATGCGGAGGTAAAGACGCTCGCCCTTGATCCA 360  
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
DB |||||  
DB 361 AAAGATTTTCCCAAGATCTGGTTTTCGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
QY 141 TrpTyrLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
DB |||||  
DB 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATATAAAACCTGAACATCAACATGTTGGTCTT 480  
QY 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
DB |||||  
DB 481 TCTATTATCGTTACAACTTCAATCACCAGCAATTTTATCGAATATACATTAGCTGTGTTA 540  
QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
DB |||||  
DB 541 GTAAACAAAAAACAACATTAACCGTTTGAAATTCGTACAGATGATGGTAGTCAGGAA 600  
QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
DB |||||  
DB 601 GATCTATCACCAGATCATTCGCCAATATGAAATAAATAATTCGATATTCGTACGTACAGCAA 660  
QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
DB |||||  
DB 661 AAAGATAACCGTTTTCAGCCAGTCCGCTCGGAATATGGGATTCAGCTTAGCAAAATAT 720  
QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
DB |||||  
DB 721 GACTTTATGGCTTACTCCGACTGTGATATGGCGCAATCCATATATGGGTTCAATCTTAT 780  
QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
DB |||||  
DB 781 GTTTCAGAGCTATTAGAAGATGATGATTAAACAATCATTTGGTCCAAGAAAAATACATCGAT 840  
QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
DB |||||  
DB 841 ACACAACATATTGACCCAAAAGACTTCTTAAATAACCGGAGTTTGTGTAATCATTTACCA 900  
QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
DB |||||  
DB 901 GAAAGTGAACCAATTAATAGTGTTCGCGCAAAAGGGGAAGAACAGTTCCTCTGGATTGG 960  
QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
DB |||||  
DB 961 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCTTCCTCGTTTT 1020  
QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
DB |||||  
DB 1021 TTTTCGCGCGGGTAATGTTGCTTTTCGTAATAAATGGCTAAATAAATCCCGGTTCTTTGAT 1080  
QY 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380

Job time : 1299 secs

```
Db 1081 GAGGAATTTAATCACTGGGGTGGAGACAGTGTGGAATTTGGATATCGCTTATTCGGTTAC 1140
Qy GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1141 GGTAGTCTTTCTTTAAACATTAATGTCATATGCGCTTATGCGCTCAAGAGCCACCAAGGTAAA 1200
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1201 GAAATGAAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG 1260
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1321 TTAGTCTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1381 AGTCACACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTTATTTGTAACGATGGTTCAACA 1440
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1441 GATAATACCTTAGAAGTGCATCAATAAGCTTTATGCTTAATACTTAGGGTAGGCATCATG 1500
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCGCCGGTTCTTTTGTAAAGGT 1560
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1561 TATTACATTGGCAGTTAGATTTCAGATGATTAATCTTGAGCCTGATGCAGTTGAACTGTTG 1620
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1621 TTTAAAGAATTTTAAAGATAAAGCGTAGCTTGTTGTTATACCACATAATAGAAACGTC 1680
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580
Db 1681 AATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTTGCCAGAAATTTTTCACGAGAAAA 1740
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1741 CTCACAACGCGCTATGATTGCTCACCACCTTTAGAAATGTTCCAGATTAGACCTTGGCATTTA 1800
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1801 ACTGATGGATTCAATGAAAAAATTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAAACCGTGTATTACATGGT 1920
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
Db 1921 GATAACACATCAATTAAGAAACCTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1980
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 1981 CAGTCATTAATATAGACAGGCATTAATTAATTAATATGACGAATTTGATGATTAGAT 2040
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu 700
Db 2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGAGATTGATATCTTA 2100
Qy 701 LysAspIle 703
Db 2101 AAAGATATT 2109
```

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: January 8, 2006, 16:49:54 ; Search time 10619 Seconds  
(without alignments)  
5203.111 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQKAIKAYNSNDYQLAL.....SARGENIPVKNKFIINSITL 972

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlp  
-O=/cgn2\_1/USPTO.spool\_p/US10642248/runat\_06012006\_125010\_26868/app\_query.fasta\_1.1159  
-DB=GenEmbl -QFMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10642248 @CGN\_1\_1 8235 @runat\_06012006\_125010\_26868 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	5108	100.0	2920	1	AF036004 Pasteurel
2	5108	100.0	2937	6	AR616925 Sequence
3	5105	99.9	16727	1	AF067175 Pasteurel

4	5104	99.9	2919	1	AF237926
5	5104	99.9	2937	6	BD087261
6	5104	99.9	2937	6	BD205371
7	4502.5	88.1	2979	1	AF195517
8	4490.5	87.9	2979	6	BD228712
9	4490.5	87.9	2979	6	AR225814
10	4310.5	84.4	11885	1	AE006116
11	4306.5	84.3	3156	1	AY604234
12	4301.5	84.2	8838	1	AF302467
13	3693	72.3	2112	6	BD228711
14	3693	72.3	2112	6	AR225813
15	2209	43.2	2058	6	AX698176
16	2209	43.2	14483	6	AB079602
17	2209	43.2	14483	6	AX698178
18	1306	25.6	998	1	AY225345
19	1303	25.5	907	1	AY225347
20	1148.5	22.5	864	1	AY225346
21	432.5	8.5	11455	1	AY044868
22	418	8.2	12370	1	AY422196
23	417	8.2	12388	1	AF401529
24	410	8.0	11442	1	AF400048
25	404	7.9	13484	1	AF400047
26	404	7.9	13484	1	AY044156
27	404	7.9	282183	1	CJ11168X4
28	398.5	7.8	110000	1	AE017180_21
29	388.5	7.6	12390	1	AF401528
30	384.5	7.5	6047	1	AY644679
31	384.5	7.5	11474	1	AF130984
32	384.5	7.5	11474	1	AF215659
33	384.5	7.5	11474	6	BD249790
34	384.5	7.5	11474	6	AR271699
35	384.5	7.5	11474	6	AR481781
36	384.5	7.5	11474	6	AR527380
37	384.5	7.5	11474	6	AR609659
38	384.5	7.5	11474	6	AX934424
39	384.5	7.5	24437	1	AF167344
40	382.5	7.5	12576	1	AY297047
41	379	7.4	24425	1	AY422197
42	376	7.4	270050	1	AL591977
43	376	7.4	349980	6	AX641667
44	371	7.3	14157	1	AE007717
45	357	7.0	17250	1	CR931720

#### ALIGNMENTS

RESULT 1	AF036004	Pasteurella multocida hyaluronan synthase (PmHAS) gene, complete cds.	2920 bp	DNA	linear	BCT 04-MAR-2004
LOCUS	AF036004	Pasteurella multocida				
DEFINITION	AF036004.2	GI:44986831				
ACCESSION	AF036004	Pasteurella multocida				
VERSION	AF036004.2	GI:44986831				
KEYWORDS		Pasteurella multocida				
SOURCE		Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.				
ORGANISM		1 (bases 1 to 2920)				
REFERENCE		2 (bases 1 to 2920)				
AUTHORS		DeAngelis,P.L., Jing,W. and Achyuthan,A.M.				
TITLE		Identification and molecular cloning of a unique hyaluronan synthase from Pasteurella multocida				
JOURNAL		J. Biol. Chem. 273 (14), 8454-8458 (1998)				
PUBMED		9525958				
REFERENCE		2 (bases 1 to 2920)				
AUTHORS		DeAngelis,P.L., Jing,W. and Achyuthan,A.M.				
TITLE		Direct Submission				
JOURNAL		Submitted (26-NOV-1997) Biochem. & Molec. Biol., Univ. of Oklahoma Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City, OK 73104, USA				
REFERENCE		3 (bases 1 to 2920)				
AUTHORS		DeAngelis,P.L., Jing,W. and Achyuthan,A.M.				
TITLE		Direct Submission				

JOURNAL	Submitted (04-MAR-2004) Biochem. & Molec. Biol., Univ. of Oklahoma Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City, OK 73104, USA
REMARK	Sequence update by submitter
COMMENT	On Mar 4, 2004 this sequence version replaced gi:3043922.
FEATURES	Location/Qualifiers
source	1..2920 /organism="Pasteurella multocida" /mol_type="genomic DNA" /strain="P-1059; ATCC 15742" /db_xref="ATCC:15742" /db_xref="taxon:747" /note="Carter Type A strain"
gene	1..2919 /gene="PmHAS" /note="gene identified by transposon insertional mutagenesis and verified by functional expression in heterologous cells"
CDS	1..2919 /gene="PmHAS" /function="polymersizes hyaluronan (HA, hyaluronate, hyaluronic acid) polysaccharide using UDP-GlcA and UDP-GlcNAc precursors" /note="glycosyltransferase; HA synthase (synthetase); membrane-bound enzyme" /codon_start=1 /transl_table=11 /product="hyaluronan synthase" /protein_id="AAC38318.2" /db_xref="GI:44986832" /translation="MNTLSQAIKAYNSNDYQLALQLFEKSABEYGRKIVFQITKCKE KLSAHPVNSAHLNVNKEKVNCDSPDLDIATQLLLSNVKKLVLSDESKNTLKNKKL LTKESNSAERAVRALVPKDFPDLVLAPLPDVNDFTYKKRKRKLGIKPEHQHVL SIIVTTPRAIISITLACLVNQKTHYPFVITVDGSDQLSPIIRQYENKLDIRY RQKNGFQASAAARMGLAKYDFIGLLDCDMPNPLWVHSYVAELLEDLDTIIGPR KYIDTOHIDPKDFLNNALLESLEPEVTNNSVAAKGEGTVSLDWRLBOPFKTENLRUS DSPPFAAGNVAFAKWLKNGSPFDEFNHWGDEVEFGVRLPFGSGFVKTDGLMA YHEPPGKNETDREAGKNTLDIMREKVPYIYRKLPIEDSHINRVLVLSIYPAYN CANYIQRCDVSALNQTVDLEVCINCDSQDNTDLEVNKLYGNPNVRVIRMSKNGGIA SANAAYVSFARGYIGQLSDYLDPEDAVELCLKFLKDKTKLACVYTNRNVPDGLS IANGNNPEFSREKLTMAMTAHPRMFTIRAWHLTDGFNEKIENAVDYDMFLKLSVG KFHLNKICYNRVLHGNTSIIKLGIOKKNHFVVNOSLNKRGITTYNYDEFDLDSR RKYFNKTAEQVEIDILKDIKIQNKDAKIAVSIFYPNTLGLVKKLNNIIEYNKI FVILVHDKHLDPDIKEILAFYHKHQVNLILNNDISYTSNRNLKTEAHLNINKL SQLNLCXYIIFONHSLFVNDSYATMKKYDVGMPFSAUTHDWIEKINAHPPFKLI KTYPNNDLKSMMNVKGASQGMFTYALAHELLTIKEVITSCOSIDSVPEYNTEDIWF QFALLILLEKKTGHVFNKSTLTLYMPWERKLQWTNEQIESAKRGENIPVNKFIINSITL "
ORIGIN	
Alignment Scores:	
Pred. No.:	1.01e-309 Length: 2920
Score:	5108.00 Matches: 972
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	1 Gaps: 0
US-10-642-248-2 (1-972) x AF036004 (1-2920)	
Qy	1 MetAsnThrLeuSerGlnAlaIleLysAlaTyraSerAsnAapTytrGlnLeuAlaLeu 20 
Db	1 ATGAATACATATATCACAAGCAATAAAGCATATACAGCAATGATGATCAATTAGCACTC 60 
Qy	21 LysLeuPheGluLysSerAlaGluIleTytrGlyArgLysIleValGluPheGlnIleThr 40 
Db	61 AAATATTGAAAGACTCGCGGAAATCTATGAGCGGAAATTTGTGATTTCAATTTACC 120 
Qy	41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60 
Db	121 AAATGCAAGAAAAAATCTCAGCACATCTCTGTGTAATTCAGCACATCTTCTCTGTAAT 180 
Qy	61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80 
Db	181 AAGAGAGAAAAAGTCAATGTTTCGGATAGTCCGTTAGATATTCACACACACTGTTACTT 240 
Qy	81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100 
Db	241 TCCAAAGTAAAAAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTAAAAAAATAAATGG 300 
Qy	101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120 
Db	301 AAATTGCTCACTGAGAGAAATCTGAAAAATGCGAGGTAAGAGCGGTGCGCCCTTGTACCA 360 
Qy	121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140 
Db	361 AAGATTTTCCCAAGATCTGGTTTACGCCCTTTACCTGATCATGTTAATGATTTTACA 420 
Qy	141 TrpTytrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160 
Db	421 TGGTACAAAAAGCGAAAAAGAAAGACTTGGCATAAAAAAGCTTGAACATCAACATGTTGGTCTT 480 
Qy	161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180 
Db	481 TCTATTATCGTTTACACATTTCAATCGACCAGCAATTTTATCGATTACATTAGCCTGTGTTA 540 
Qy	181 ValAsnGlnLysThrHisTytrProPheGluValIleValThrAspAspGlySerGlnGlu 200 
Db	541 GTAAACCAAAAAACACATTTACCGCTTGAAGTTATCGTGACAGATGATGTTAGTCAGGAA 600 
Qy	201 AspLeuSerProIleLeuArgGlnTytrGluAsnLysLeuAspIleArgTytrValArgGln 220 
Db	601 GATCTATCACCGATCATTCGCCAATATGAAAAATAAATTTGGATATTCGTACTACGTACAGCAA 660 
Qy	221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTytr 240 
Db	661 AAAGATAACCGGTTTCAAGCCAGTCGCGCTCGGAAATGCGAATGCGCTTAGCCTTAGCAAAATAT 720 
Qy	241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTytr 260 
Db	721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCATATATGCGGTTCATCTTAT 780 
Qy	261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTytrIleAsp 280 
Db	781 GTTTCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT 840 
Qy	281 ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300 
Db	841 ACACAACATATTCACCAAAAGACTTCTTAAAAAAGCGAGTTTGTCTTGAATCATTTACCA 900 
Qy	301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320 
Db	901 GAAGTGAAAACCAATAATAGTTTGGCGCAAAAGGGGAGGACAGTTTCTCTGGATTGG 960 
Qy	321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340 
Db	961 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCCGCTTTCCGTTTT 1020 
Qy	341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTytrLeuAsnLysSerGlyPheAsp 360 
Db	1021 TTTTCGCGCGGTAATGTGCTTTTCGCTAAAAAATGCGTAATAATTCGCTTTCTTTGAT 1080 
Qy	361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTytrArgLeuPheArgTytr 380 
Db	1081 GAGGAATTTAATCCTCGGGGTGAGAGAGATGCGAATTTGGATATCGCTTATTCGCTTAC 1140 
Qy	381 GlySerPhePheLysThrIleAspGlyIleMetAlaTytrHisGlnGluProProGlyLys 400 
Db	1141 GGTAGTTTCTTTAAACTATTGATGGCATTATGCGCTTACCATCAAGACCAACAGGTAAA 1200 
Qy	401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420 
Db	1201 GAAAAATGAAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATATTATGAGAGAAAAG 1260 
Qy	421 ValProTytrIleTytrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440 

1261 GTCCCTTATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320 Db  
441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460 Qy  
1321 TTAGTTCCTCAATTTATATCCCGAGCTTATAACCTGTGCAACATATATTCACCGTTGCGTAGAT 1380 Db  
461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480 Qy  
1381 AGTCACCTGANTCAGACTGTTGTTGATCTCGAGGTTGTATTTGACGATGGTTCAACA 1440 Db  
481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500 Qy  
1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGCTAATAATATCTAGGAGTACGATCATG 1500 Db  
501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly 520 Qy  
1501 TCTAAACCAATGCGGAATAGCCTCAGCATCAATGCGCGGTTCTTTTGGCTTAAGGT 1560 Db  
521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540 Qy  
1561 TATTACATGGCGAGTTAGATTCAGATGATTTATCTTGAGCCTGATGCGAGTTGAACCTGTGT 1620 Db  
541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560 Qy  
1621 TTTAAAGAAATTTTAAAGATATAAACCGCTAGCTGTGTGTTTATACCACTAATAGAAACGTC 1680 Db  
561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580 Qy  
1681 AATCGGATGAGTGTAAATCGCTAATGTTTACAAATGCGCAGAAATTTTCACGAGAAAAA 1740 Db  
581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600 Qy  
1741 CTCACACGGCTATGATGCTCACCACTTTAGAAATGTTACGATTTAGAGCTTGGCATTTA 1800 Db  
601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620 Qy  
1801 ACTGATGATTCATGAAATGAAATGAAATGCGGTAGACTATGACATGTTCTCAAACTC 1860 Db  
621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640 Qy  
1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGTGTTATCATGGT 1920 Db  
641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660 Qy  
1921 GATAACACATCAATTAAGAACTTGGCAATCAAGAAACCAATTTGTTGTAGTCAAT 1980 Db  
661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680 Qy  
1981 CAGTCATTAATAGACAAAGGCATACTTATTATTAATATGACCAATTTGATGATTTAGAT 2040 Db  
681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700 Qy  
2041 GAAAGTAGAAGATATATTTTCAATAAAACCGCTGAAATATCAAGAAGAGATGATATCTTA 2100 Db  
701 LysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720 Qy  
2101 AAAGATATTTAAATCATCAGAAATTAAGATGCAAAATCGCAATCGAGTATTTTATATCCC 2160 Db  
721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740 Qy  
2161 AATACATTAACCGCTTAGTGAACAACTAAACATATATTTTGAATATAATAAAATATA 2220 Db  
741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760 Qy  
2221 TTCGTATTGTTCTACATGTTGATAAGATCATCTTTACACCAAGATATCAAAAGAAATA 2280 Db  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780 Qy  
2281 CTAGCCTCTTATCATAAACATCAAGTGAATATTTTACTAATAATGATATCTCATATTAC 2340 Db  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800 Qy  
2341 ACGAGTAAATAGATTAATAAAACTGAGGCGCATTTTAAAGTAAATATTAATAAATTAAGTCAG 2400 Db

801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820 Qy  
2401 TTTAAATCTAAATTTGTGAATACATCATTTTGTATAATCATGACAGCCTATTTCGTTAAAAAT 2460 Db  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840 Qy  
2461 GACAGCTATCTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTTAACACAT 2520 Db  
841 AspTyrIleGluLysIleAsnAlaHisProProPheLysLysLeuIleLysThrTyrPhe 860 Qy  
2521 GATTGGATCGAAAAATCAATGCGCATCCACCATTTTAAAGCTCATTTAAACCTTATTTT 2580 Db  
861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880 Qy  
2581 AATGACAATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGAGC 2640 Db  
881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900 Qy  
2641 TATCGCTAGCGCATGAGCTTCTGACGATTTAAGAAAGTCATCACATCTTGCAGTCA 2700 Db  
901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920 Qy  
2701 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAATTTGCACCTTTAATC 2760 Db  
921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940 Qy  
2761 TTAGAAAAAGAAACCGGCCATGTATTTAATAAAACATCGACCTGACTTATATGCTTTGG 2820 Db  
941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960 Qy  
2821 GAACGAAAAATTTACAAATGGACAAATGAAACAAATGAAAGTGCAAAAGAGGAGAAATATA 2880 Db  
961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972 Qy  
2881 CCTGTAAACAGTTTCATTTATTTAATAGTATAACTCTA 2916 Db

## RESULT 2

AR616925 LOCUS AR616925 2937 bp DNA linear PAT 14-FEB-2005  
DEFINITION Sequence 8 from patent US 6833264.

AR616925 ACCESSION AR616925.1 GI:59720260

VERSION AR616925.1

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE

1 (bases 1 to 2937)

AUTHORS Weigel,P.H., Kumari,K. and DeAngelis,P.

TITLE Hyaluronan synthase gene and uses thereof

JOURNAL Patent: US 6833264-A 8 21-DEC-2004;

The Board of Regents of the University of Oklahoma, Norman, OK

FEATURES

source

1..2937

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-309 Length: 2937

Score: 5108.00 Matches: 972

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-642-248-2 (1-972) x AR616925 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20

Db 19 ARGATACATATATCAACAGCAATAAAGCATATAACAGCATGACTATCAATAGCACATC 78

Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40

Db	79	AAATATTATTTGAAAGAGTCGGCGGAATCTATGCGACGGAAAAATGTTGTAATTTCAAATTACC	138
Qy	41	LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen	60
Db	139	AAATGCAAGAAAAACCTCAGCACATCCCTTCTGTTAATTCAGCACATCTTCTGTAAAT	198
Qy	61	LysGluGluLysValAenValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu	80
Db	199	AAAGAAGAAAAAGTCAATGTTTGGATAGTCGGTTAGATATGCAACACAACTGTACTT	258
Qy	81	SerAenValLysLysLeuValLeuSerAspSerGluLysAenThrLeuLysAenLysTrp	100
Db	259	TCCAACTGAAAAAATTAGTACTTCTGACTCGGAAAAAACACGTTAAAAAATAAATGG	318
Qy	101	LysLeuLeuThrGluLysLysSerGluAenAlaGluValAargAlaValAlaLeuValPro	120
Db	319	AAATGTCTCACTGAGAGAAATCTGAAAAATCGGAGGTAAAGCGGTGCGCCCTGTACCA	378
Qy	121	LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAenAspPheThr	140
Db	379	AAAGATTTTCCCAAGATCTGGTTTATAGGCCCTTACTGATCATGTTAATGATTTACA	438
Qy	141	TrpTyrLysLysArgLysLysArgLeuGluLysLysProGluHisGlnHisValGlyLeu	160
Db	439	TGGTACAAAAAGCGAAAGAAAGACTTGGCATATAAACCTGAACATCAACATGTGTGCTT	498
Qy	161	SerIleIleValThrThrPheAenArgProAlaIleLeuSerIleThrLeuAlaCysLeu	180
Db	499	TCTATTATCGTTACAACTCAATTCGACACAGCAATTTTATCGATTACATTAGCCTGTTA	558
Qy	181	ValAenGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu	200
Db	559	GTAACCCAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGAA	618
Qy	201	AspLeuSerProIleIleArgGlnTyrGluAenLysLeuAspIleArgTyrValArgGln	220
Db	619	GATCTATCACCGATCAATTCGCCAATATGAAATTAATTTGGATATTCGTACGTCAGACAA	678
Qy	221	LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr	240
Db	679	AAAGATAACGGTTTTTCAAGCCAGTCCCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT	738
Qy	241	AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr	260
Db	739	GACTTTATTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGGTTCACTTAT	798
Qy	261	ValAlaGluLeuLeuGluAspAspLeuThrIleGlyProArgLysTyrIleAsp	280
Db	799	GTTGCAGAGCTATTAGAAGATGATGATTTAAACAATCATCTTGGTCCAGAAAAATACATCGAT	858
Qy	281	ThrGlnHisIleAspProLysAspPheLeuAenAenAlaSerLeuLeuGluSerLeuPro	300
Db	859	ACAAACAATATTTGACCCAAAAGACTTCTTAATAACCGAGTTTGGCTTGAATCAATTACCA	918
Qy	301	GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp	320
Db	919	GAAGTGAAACCAATATATGTTTGGCGCAAAAGGGAGAACAGTTTCTCTGGANTGG	978
Qy	321	ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe	340
Db	979	CGCTTAGAACAAATTCGAAAAAACAGAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTTT	1038
Qy	341	PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPhePheAsp	360
Db	1039	TTTCGGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATCCGGTTCTTTGAT	1098
Qy	361	GluGluPheAenHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr	380
Db	1099	GAGGAATTTAATCACTGGGGTGGAGAGAGTGGAAATTTGGATATCGCTTATTCGTTAC	1158
Qy	381	GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys	400

1159	GGTAGTTCCTTTAAACATATGTAGTGGCATATATGGCCCTACCATCAAGAGGCCACAGGTAAA	1211
401	GLuAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys	420
1219	GAAATGAAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAG	1278
421	ValProTyrIleTyrArgIysLeuLeuProIleGluAspSerHisIleAsnArgValPro	440
1279	GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAAGATTTCGATATATCAATAGAGTACCT	1338
441	LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp	460
1339	TTAGTTTCAATTTATATCCCGAGCTTATAACTGTGCAAACTATATTCACCGTTCGGTAGAT	1398
461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480
1399	AGTGCACCTGAATCAGACTGTTGTTGATCTCGAGGTTGTATTGTAACGATGGTTCAACA	1458
481	AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet	500
1459	GATAATACCTTAGAAGTGATCAATAAGCTTTATGCGTAATAATCCTTACGGGTACGCATCATG	1518
501	SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly	520
1519	TCTAAACCAAAATGGCGAATAGAGCTCAGCATCAAAATGCAGCCGTTCTTTTGCTAAAGGT	1578
521	TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys	540
1579	TATTACATTGGGCAGTTAGATTCCAGATGATTATCTTGAGCCTGATGCAGTTGAACGTGT	1638
541	LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal	560
1639	TTAAAGAAATTTTAAAGATAAAACCGTAGCTTGTTGTTTATACCACTAATAGAAACGCT	1698
561	AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys	580
1699	AAATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCAGAAATTTTCCACGAGAAAA	1758
581	LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrHisLeu	600
1759	CTCAACAGGCTATGATTGCTCACCATTTAGAATGTTTCAGATTAGAGCTTGGCATTTA	1818
601	ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu	620
1819	ACTGATGGATTCAATGAAAAAATTGAAAAATGCCGTAGACTATGCATGTTTCTCCAAACTC	1878
621	SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly	640
1879	AGTGAAGTTCCGAAAAATTTAAACAATCTTAATAAAAATCTGCTATAACCGGTGTTATCATGGT	1938
641	AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn	660
1939	GATAACACATCAATTAGAAACCTTGGCATTCAAAAGNAAAAACCATTTTGTGTAGTCAAT	1998
661	GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp	680
1999	CAGTCAITTAATAAGACAGGCATAACTTATTAATAATTATGACGAATTTGATGATTTAGAT	2058
681	GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu	700
2059	GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAAATATCAAGAAGAGATTGATATCTTA	2118
701	LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro	720
2119	AAAGATTATTAATCATCCAGATTAAGATGCCAAAATCCGAGTCAGTATTTTTTATCCC	2178
721	AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle	740
2179	AATACAITTAACCGCTTAGTGAAAAAACAATAATAATTTGAATATAATAAAAAATATA	2238
741	PheValIleValLeuHisValAspLysAsnHisIleuThrProAspIleLysLysGluIle	760
2239	TTCCGTTATGTTCTCACATGTTGTAGAAATCATCTTACCCAGATATCAAAAAGAAATA	2298

COMMENT		On May 5, 2000 this sequence version replaced gi:3435183.
Qy	LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAnAspIleSerTyrTyr	Location/Qualifiers
	761	1. .16727
Db	CTAGCCTCTATCATCAAAACATCAAGTGAATATTTTACTAATATGATATCTATATAC	/organism="Pasteurella multocida"
	2299	/mol_type="genomic DNA"
Qy	ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln	/db_xref="taxon:747"
	781	complement (1157. .2383)
Db	ACGAGTAATAGATTAAATAAAACCTGAGCGCATTTAAGTAATATTAAATAAATTAAGTCAG	/gene="phxB"
	2359	complement (1157. .2383)
Qy	LeuAsnLeuAnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValIysAsn	/gene="phxB"
	801	/note="LipB, Kps homolog"
Db	TTAAATCTAAATCTGTAATACATCATCTTTTGATATCATGACGCTATTCGTTAAATAAT	/codon_start=1
	2419	/transl_table=11
Qy	AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis	/product="PhyB"
	821	/protein_id="AAC67247.1"
Db	GACAGCTATGCTTATATGAAATAATATGATGTCGCGCATGAAATTTCTGACGATTAAACAT	/db_xref="GI:3435184"
	2479	/translation="MDVLKHNDELLESSTNYLLQGPIGPFFTELSAWLTKFKQVF
Qy	AspTrrIleGluLysIleAsnAlaHisProPhetLysLysLeuIleLysThrTyrPhe	KINFSGDEAFYNSIPOTFAYGQLDQDFQYLRFFCHOSIDAIICFGDTRAVHRIA
	841	XIVADKQKISFWFEEGLRPEVTLKSGVNDYSQLPRIANFSLQAACCSAISAP
Db	GATTGGATCGAGAAATCAATGCGCATCCACCATTTTAAAGAGCTCATTTAAACCTATATTT	KLAKGFTPLATIAIKYTKAYFNQDKYPDYOHRILDLKTYIKLWLTSGIKRAYYQ
	2539	DRSGKKVAAGKGLDFPLQVDDSVRIHCDYESDAFLKELSLPIHHAPSALN
Qy	AsnAspAsnLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr	LIIRKHPMDRGVDYGHVIKQYQYPAFKRIIFYVHDVPTPIILLRKGKMITLNSTS
	861	GISALLARMPVLTIGRASYNFEGLTQCNLHSFWHNKGLPEAKVFEAYRKVHLSKTOI
Db	AATGACAATGACTTAAAGAAAGTATGAATCTGAAAGGGGCATCACAAGGTATGTTATGACG	NGSFYKVIILRYPNQ"
	2599	complement (2393. .4483)
Qy	TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer	/gene="phxA"
	881	complement (2393. .4483)
Db	TATGCGCTAGCGCATGAGCTTCTGACGATTATTAAAGAGTCATCACAATCTTGCCAGTCA	/gene="phxA"
	2659	/note="KpsA, LipA homolog"
Qy	IleAspSerValProGluTyrAsnThrGluAspIleTrrPheGlnPheAlaLeuLeuIle	/codon_start=1
	901	/transl_table=11
Db	ATTGATAGTGGCAGATATAAACAATGAGGATATTTGTTCCCAATTTGCATTTTAATC	/product="PhyA"
	2719	/protein_id="AAC67248.1"
Qy	LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp	/db_xref="GI:3435185"
	921	/translation="WSTLYDYIRLNMYOEFLIFSKGMUKIPVLSGFFTQRLKMFSPFV
Db	TTAGAAAAGAAACCGCGCATGTATTATTAATAAACAATGACGCTGACTTATATGCTTGG	TWKERTICILEWGYKASAKKARHFAQQHDLPEATIEDGFLRSIGLVDPYPPFSLVYD
	2779	DIGIYDINQPSRLNLSQDLVKQDVQVEYAIELICTHNLKYNHAIIDTFLONT
Qy	GluArgLysLeuGlnTrrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle	KRPTLVVDQTYGDMAVTFNAEQSDFLHMLERAIIEPTAEIWLKTHPDMWCKKQG
	941	YLTSYQQPFRVKLSSEDFNSISLLKLVQKVCVTSHTGFEALLLKTVTYVFGAASFQ
Db	GAACGAAATATCAATGACAAATGAACAAATTTGAAGATGCAAAAGAGGAGGAAATATA	WGLTDRHAYIRQLKQSKRWRKRVQVFPFQPCRLHFLVNLVHVKRCIHEKAQAKI
	2839	OAKVTQIAGDIYCVGMRWKRKVQVFPFQPCRLHFLVNLVHVKRCIHEKAQAKI
Qy	ProValAsnLysPheIleAsnSerIleThrLeu	VWGHSHLEVVEYAKQQQLPRLRMEDGFLRSVGLSGNLTPISLVLDVGVYFDASQV
	961	SRLEDILQHSQFTLQDLQRAETLAKTLIEQHIQKYNVGHVTHLCLTHIRQNKLTVGVQ
Db	CCTGTTAACAGTTCAATTATTAATAGTATACTCTA	ENDASIQGSPHIRTNAELCTVRKNNPAYIITYKPHDVPVAVGNKRTDRLDQYQYA
	2899	DFVVEKVNILDINQVDEVTMTSLAGFEALLREKKVHCYGLPFYSNGLTVDLHLSLN
RESULT 3		RRSRKLILLEIAGVLIYYPQYIDPKTKTMIDVQRAVDILIEQRRKIKNKLHTNYFM
LOCUS	AF067175	NIFMKLNKXVSVLR"
	AF067175	4832. .6700
DEFINITION	Pasteurella multocida capsule biosynthesis gene cluster, complete sequence.	/gene="hyaB"
	AF067175	4832. .6700
ACCESSION	AF067175.2	/gene="hyaB"
	GI:7710189	/note="KfiB homolog"
KEYWORDS	Pasteurella multocida	/codon_start=1
	Pasteurella multocida	/transl_table=11
SOURCE	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;	/product="HyaE"
	Pasteurellaceae; Pasteurella.	/protein_id="AAC67249.1"
REFERENCE	1 (bases 1 to 16727)	/db_xref="GI:3435186"
	Chung, J. Y., Zhang, Y. and Adler, B.	/translation="WKVIIIGHKQSNQYDVEKVPQCYGMNPPLPSKREKMSPIBIGH
AUTHORS	The capsule biosynthetic locus of Pasteurella multocida A:1	VLNKVLPSFHTPKNVLSLNKSKIKKNSAKNKHAKTNTTIQTSSIWDLNSLD
	FEMS Microbiol. Lett. 166 (2), 289-296 (1998)	LMLANIEQNFQWSDPNAIQIDYWNLDPNHIFVYVDKPENLQYHSLEALKLDK
JOURNAL	9770287	HTVQKPEEQWQTYNEKILTYFNKYKDRSVLLNTQOLQTKTSLSEIYKHISAPDALV
	2 (bases 1 to 16727)	KKLNEPSLNKEMEIIENVQDLSHQDECPLSNFIVSQIITNSFTVTVQVEELSHQDLDP
PUBMED	Chung, J. Y., Zhang, Y. and Adler, B.	YISEQLVNDADFALLAKMDIQVDANQYQHEKELSLTKEQLESTYQVLETKYQLETEQ
	Submitted (19-MAY-1998) Microbiology, Monash University, Wellington	KLSETOKEIEQIKDENRKVKSEKAKLTSVOSTSKILSEKEKEI6CIKSENKTKKEK
REFERENCE	3 (bases 1 to 16727)	IKIDAYHLTKTSLSDSKALKTHQDEIEALKIIFENISVQEDQKQFOENKRRKOE
	Chung, J. Y., Zhang, Y. and Adler, B.	LEQELUKASDKKALLETNSQTKVSELENENKVLQAQLQIQLELEKLYIDNQVLK
AUTHORS	Direct Submission	AKPRLYGAADRIKNQLYRGLYGRHSRSLFGLIFLFFTLFFTYLFGAKEMKTEWN
	Submitted (05-MAY-2000) Microbiology, Monash University, Wellington	TLPTTHEYEDAEANRIKSHLSYKLGVLQFLOBINNPFKWLTPYKLIKEGKRFQO"
JOURNAL	Road, Clayton, VIC 3168, Australia	6717. .9635
	3 (bases 1 to 16727)	/gene="hyaD"
REFERENCE	Chung, J. Y., Zhang, Y. and Adler, B.	6717. .9635
	Submitted (05-MAY-2000) Microbiology, Monash University, Wellington	/note="hyaD"
AUTHORS	Road, Clayton, VIC 3168, Australia	
	Sequence update by submitter	

```
/codon_start=1
/transl_table=11
/product="glycosyl transferase"
/protein_id="AAC67250.2"
/db_xref="GI:7710190"
/translation="MNTLSQAIKAYNSNDYELALKLPKSAEIVGRKIVFQITKCKE
KLSAHPNSVAHLSVNRKEKYNVCDSPDIATOLLNSNVKVLISDSEKNTLKNKKL
LTEKTSNENRAVALVPKPPDQDLVLAIPLDHVNDFTWYKRRKLRIKPEHQHVL
LIIKVTNPAIISITLACLVNQKTHYFFVEI VTDGSGEDLSPIIRQYENKLDIRIV
RQDNGQSAANRMLRLAKYDFI GLLLCDMAFNPLVHWSYVAELLEDDLTIIIGPR
KYIDTHIDPKDNLNALSLESLEPEVKTNNSAAGGEGTSLDWRLEQFEETENLRIS
DSRPFPAAGNAFAKKWLNKSGFFDEEFNHGGEDEVFGYRLFRYGSFFKTDGIMA
YHQEPCKNETREAGKNTLIDIMREKVPYIYRKLPIEDSHINRVLVSIYIPAN
CANYIQRCDUSALNQTVLDLEVCINDGSDTNDILEVINKLYGNRPVRIMSKNGGIA
SASNAVFAFGYIIGDSDYLDPAVELCKLDFLOKTLACVYITNTRNVNPDGSL
IANGYNWPFSEKRLTAMIAHFRMFTIRAMHLTDGFNEKIEINAVDIFMLKLSVYG
KFHLNKICYNRVLHGNTSIKKLGIQKQNHVVVNOGSLNRQGITVYNYDEFDLDES
RYIFENKTAQVBEIDILDKIILQNKDAKIAVSI FYPNTLGLVKKLNNI IEVNKNI
FVILVHDKNHLTPDI KKEILA FVHKQVNLNNDISVYTSNRLIKTEAHLNINKL
SQNLNCEYIIFDNHDSLFVNDSYATMKKYDVGMNPSALTWDIEKINAHPPFKKLI
KTYFNDNDLKSMMVKGASQGMFTYALAHELLTIIKEVITSCQSIDSPYENTDIWF
QFALLILEKTHGVFNKTSITLTYPWERKLQWNTNEQIESARGENIPVNFIIINSITL
"
```

gene

CDS

```
9699. .10871
/gene="hyaC"
9699. .10871
/gene="hyaC"
/notes="hyaC"
/codon_start=1
```

```
/transl_table=11
/product="UDP-glucose dehydrogenase"
/protein_id="AAC67251.2"
/db_xref="GI:7710191"
```

```
/translation="MKKTIAGAGYVGLSNVLAQHHNVILLIDQNKVDLINNKKKS
PITDKEDELQNSLTMWATTDEKVALKNADFVI IATPTDYNTETGYNTSTVEAVI
EQTLSINQATIIKSTIPVGFTEENREKENTNLIFSPFEVREGKALVNLVPSRII
VGSYSQAKVPADMLTQCARKQDVVLFTHNTEBAVKLPANTYLANRVAFPNELDTY
ASLHLNKTIDINGISITDPRIGTHYNNPSFGYGYCLPQKTKQLLANYADVPQNLIEA
IVKSNRETRKFI THVLNKKPKTVGIYRLIMKSGSDNFRASAILDIMPHLKNGEVEI
IYEPFLNQAFEDVPYINQLSEFINRSDVILANRSEPDNLNQCSHKIYTRDIFGDA"
10864. .12297
/notes="glycosyl transferase"
/codon_start=1
```

CDS

```
/transl_table=11
/product="Hyab/HyaA fusion protein"
/protein_id="AAC67252.2"
/db_xref="GI:7710192"
```

```
/translation="MLNLKIIKKYVHIQSLHKKVEALLVAKYINLLSINOQAYVIC
QLKLYDLPLDPKWSHVSFQGLIARGHADNDWMYRLITCTDFSKNQLILSOLL
AYSPQIATILCPKTYRYRALYLSLVANLKFVRLKERLNKLPSCLVKNTHYCLLQNF
VENKSKJENINQFLYFKLGEITTIKTEDPPNTNNIVSHSMVNDNTYVNLAPLITI
LVITFNSQKIKNTLSLNFQSYENIBI IVIDHSQDNTWSILQAYTKYKNIKIISL
KENVGTYVAKNIIGLYKASGFITCQSDDWAHPOKALQVAPLLOHKELIYVTFKWR
LDPTGNPYARTIYPLMRNPSSALFRKKEVCEKLTALDWVRIGADSEFNARLKLIFGH
KGYTVNKPPLTFGAHRENSLMTAQSTGYVNGVSLPREAYWKANNIWHISQLQRHAFL
LSSSPKREFQYDQHPIMDVISYAIIN"
```

gene

CDS

```
/gene="hexD"
/notes="CpxD, BexD homolog"
/codon_start=1
/transl_table=11
/product="HexD"
/protein_id="AAC67254.1"
/db_xref="GI:3435191"
```

```
/translation="MKPIKTLISITFITLILAGCHSMPTSGPAQNHIILGLKPKQNESL
PSVDVIMENDKVAHTLPKQKQSFTQFKQNSNYADIINVGDTLDLVDLWEAPAILIF
GSLVTSQTGGGANLTLPEQIVARNGKITIIPFGILPVKGTPEQIQORDIAHALSILA
NKQPIVRLNKNNSKNVTILRQNSVRMPLTSQGERVLDATAAAGGATENLODTSVOL
TRKEVKMLSLIKLEKLAHPEENILLNRSNDVVTLLNKLPSFTGLGALGTNKQVKANGL
TLARGICEMGSLNDRADPKGVFVRYIPFNKLSLABQTKWARGYDNDMEIPTVYSV
NLLNPNALFWLQRPPIQDKDLVYVSNAPMAEFQKFLKLVFSITSPVTGTLHNINVIK
```

```
gene
CDS
```

```
L"
13507. .14643
/gene="hexC"
13507. .14643
/gene="hexC"
/notes="BexC, CpxC homolog;
MIETKIQNQFKKSRKPKISTLPKYMVILPTCCSLFYFSLWASDIYISQSSFVVVRT
PKNOALSCVGGALLQSSGFARAQDDTYTVQEFMRSRSTLELLEKSIPIRQFYEDKGL
FRFNPLIPSEQAEYQFYSKLSVNFVSIGIATNLINRAFPKQAQINQLBLLKQG
EYLINLNEARKDTVMFAELAVSEAKKVTTSALSERYIRKNGVDFDLOSQSEVQUS
LSTLQNELIITQTQDQVRSISPNPNQVQVTLARANSIRKEMQOQVQVILGGNSIV
TYNTEYQRLVNLNTLAQQQLGTAITSLQNSRSEADQQLYLEIISIYPNEPDLAEPYR
LYNLAITFLSILYGITLLLLASIREHKN"
```

```
/codon_start=1
/transl_table=11
/product="HexC"
/protein_id="AAC67255.1"
/db_xref="GI:3435192"
/translation="MIETKIQNQFKKSRKPKISTLPKYMVILPTCCSLFYFSLWA
SDIYISQSSFVVVRTPKNOALSCVGGALLQSSGFARAQDDTYTVQEFMRSRSTLELLEK
SIPIRQFYEDKGLFRFNPLIPSEQAEYQFYSKLSVNFVSIGIATNLINRAFPD
KQAQINQLBLLKQGEYLINRLNEARKDTVMFAELAVSEAKKVTTSALSERYIRK
GVDFDLOSQSEVQVLSLTLQNELIITQTQDQVRSISPNPNQVQVTLARANSIRKEMQ
QVQVQVILGGNSIVTQAEYQRLVNLNTLAQQQLGTAITSLQNSRSEADQQLYLEI
SYNPEPDLALEPVLNLAITFLSILYGITLLLLASIREHKN"
```

```
14643. .15440
/gene="hexB"
14643. .15440
```

```
gene
CDS
```

Alignment Scores:

Pred. No.:	1.07e-108	Length:	16727
Score:	5105.00	Matches:	971
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.90%	Mismatches:	0
Query Match:	99.94%	Indels:	0
DB:	1	Gaps:	0

US-10-642-248-2 (1-972) x AF067175 (1-16727)

Qy	1	MetAsnThrLeuSerGlnAlaLalleLysAlaTyrAsnSerAenAepTyrGlnLeuAlaLeu	20
Db	6717	ATGAATACATTATCACAGCAATAAAGCATATAACAGCAATGACTATGAAATTAGCACTC	6776
Qy	21	LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr	40
Db	6777	AAATATTATTGAGAAGTCGCGGAAATCTATGGACGGAATAATTGTGAAATTTCAAAATACC	6836
Qy	41	LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn	60
Db	6837	AAATGCAAGAAAAAATCTCAGCACATCTCTCTGTTAATTCAGCACATCTTCTGTAAT	6896
Qy	61	LysGluGluLysValAenValCysAepSerProLeuAepIleAlaThrGlnLeuLeuLeu	80
Db	6897	AAAGAAGAAAAAGTCAATGTTTCGATAGTCCGTTAGATATTGCAACACACACTGTTACTT	6956
Qy	81	SerAsnValLysLysLeuValLeuSerAepSerGluLysAsnThrIleLysAsnLysTyr	100
Db	6957	TCCAACGTAATAAAAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTAAAAATAATGG	7016
Qy	101	LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro	120
Db	7017	AAATTGCTCACTGAGAAGAANAATCTGAAAATCGGAGGTAGAGCGGTGCGCCTTGTTACCA	7076
Qy	121	LysAepPheProLysAepLeuValLeuAlaProLeuProAepHisValAsnAepPheThr	140
Db	7077	AAAGATTTTCCCAAGATCTGTTTTTAGCGCCTTTACTCTCATCATGTGTAATGATTTTACA	7136
Qy	141	TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu	160
Db	7137	TGTTACAAAAAGGCAAGAAAGACTTGGCATATAAAACCTGAAACATCAACATGTTGGTCTT	7196
Qy	161	SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu	180



Db 7197 TCTATTATCGTTACAAACATTCAATCGACCAGCAATTTTATCGATTACATTAGCCTGTTTA 7256  
Qy 181 ValAenGlnIyThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 7257 GTAACCAAAACACACATTACCCGTTTGAAGTTATCGTGACAGATGATGTTAGTCAGGAA 7316  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAepIleAArgTyrValArgGln 220  
Db 7317 GATCTATCACCGATCAITTCGCCAATATGAAATAATTAATTTGGATATTCGCTACGTCAGACAA 7376  
Qy 221 LysAepAenGlyPheGlnAlaSerAlaAlaArgAenMetGlyLeuArgLeuAlaIyTyr 240  
Db 7377 AAAGATAACGGTTTTCAGCCAGTCGCCCTCGGAATATGGGATTACGCTTAGCAAAATAT 7436  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAenProLeuTyrValHisSerTyr 260  
Db 7437 GACTTTATTTGGCTTACTCGATGTGATATGGCGCAATCCATTATGGGTTTCATCTTAT 7496  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAep 280  
Db 7497 GTTCGAGAGCTATTAGAAGATGATGATTAACAATCATTTGTCCTCAAGAAATAACATCGAT 7556  
Qy 281 ThrGlnHisIleAepProLysPheLeuAenAenAlaSerLeuLeuGluSerLeuPro 300  
Db 7557 ACACAAATATTGACCCAAAGACTTCTTAAATAACCGAGTTTGTGTAATCATTTACCA 7616  
Qy 301 GluValIyThrAenAenSerValAlaAlaIyGlyGluGlyThrValSerLeuAspTyr 320  
Db 7617 GAAGTGAACCAATAATAGTTGTTCGCCCAAAAGGGAAGAACAGTTTCTCTGATTTGG 7676  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe 340  
Db 7677 CGCTTAGAACCAATTCGAAACAAACAGAAATCTCCGCTTATCCGATTCGCCCTTTCGTTT 7736  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaIyLysTyrLeuAenLysSerGlyPhePheAep 360  
Db 7737 TTTGGCGCGGTAAATGTTGCTTCGCTAAATAATGGCTAAATAATCGGTTTCTTTCGAT 7796  
Qy 361 GluGluPheAenHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 7797 GAGGAATTCATACCTCGGTTGGAGAGATGTGGAAATTTGGATATTCGCTTATTCGGTTTAC 7856  
Qy 381 GlySerPhePheLysThrIleAepGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 7857 GGTAGTTCTTTTAAACCTATTGATGGCATATTGGCTACCATCAGAGCCACCAGGTAA 7916  
Qy 401 GluAenGluThrAspArgGluAlaGlyLysAenIleThrLeuAepIleMetArgGluLys 420  
Db 7917 GAAATGAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG 7976  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAepSerHisIleAenArgValPro 440  
Db 7977 GTCCCTTATATATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGATACCT 8036  
Qy 441 LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAep 460  
Db 8037 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 8096  
Qy 461 SerAlaLeuAenGlnThrValValAepLeuGluValCysIleCysAenAepGlySerThr 480  
Db 8097 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAACGATGGTTCAACA 8156  
Qy 481 AspAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet 500  
Db 8157 GATAATACCTTAGAAGTATCAATAAGCTTTATGTTGTAATAATCCTAGGGTAGCATCATG 8216  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAenAlaAlaValSerPheAlaIyGly 520  
Db 8217 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCGAGCGGTTCTTCTTCTAAGGT 8276  
Qy 521 TyrTyrIleGlyGlnLeuAepSerAspTyrLeuGluProAepAlaValGluLeuCys 540  
Db 8277 TATTACATTTGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGTCAGTTGCACTGTGT 8336

Qy 541 LeuLysGluPheLeuLysAepLysThrLeuAlaCysValTyrThrThrAenArgAenVal 560  
Db 8337 TTTAAAGAAATTTTAAAGATAAAACCGTAGCTTGTGTTTATACCACTAAATAGAAACGTC 8396  
Qy 561 AsnProAspGlySerLeuIleAlaAenGlyTyrAenTyrProGluPheSerArgGluLys 580  
Db 8397 AATCCCGATGGTAGCTTAATCGCTTAATGGTTACAAATTTGGCAGAAATTTTCCAGAGAAA 8456  
Qy 581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTyrPheLeu 600  
Db 8457 CTCAACACGGCTATGATTGCTCACCACTTTTGAATGTTCCAGATTAGAGCTTGGCAITTA 8516  
Qy 601 ThrAspGlyPheAenGluLysIleGluAenAlaValAepTyrAspMetPheLeuLysLeu 620  
Db 8517 ACTGATCGAATTCATGAAATTTGAAATTCGCGTAGCATATGCATGATGCTCTCAAACTC 8576  
Qy 621 SerGluValGlyLysPheLysHisLeuAenLysIleCysTyrAenArgValLeuHisGly 640  
Db 8577 AGTGAAGTTGGAAAATTTAAACATCTTAAATAATCTGCTATTAACCGTGTATTTACATGGT 8636  
Qy 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValAen 660  
Db 8637 GATTAACACATCAATTAGAACAATTTGGCATTCAAAGAAACCACTTTTGTGTAGTCAAT 8696  
Qy 661 GlnSerLeuAenArgGlnGlyIleThrTyrTyrAenTyrAspGluPheAspLeuAep 680  
Db 8697 CAGTCATTAATAAGCAAGGCATTAATTTATTAATATGACGAATTTGATGATTAGAT 8756  
Qy 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluGluIleAepIleLeu 700  
Db 8757 GAAATGTAAGATATATTTTCAATTAACCGCTGAAATATCAAGAGAGATGATATCTTA 8816  
Qy 701 LysAepIleLysIleIleGlnAenLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 8817 AAAGATTTAAATCTCCAGAAATTAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 8876  
Qy 721 AsnThrLeuAenGlyLeuValLysLysLeuAenAenIleIleGluTyrAenLysAenIle 740  
Db 8877 AATACATTAACCGCTTAGTGAAATACTAAACAATATTTATGAATATAATAATAATA 8936  
Qy 741 PheValIleValLeuHisValAspLysAenHisIleThrProAepIleLysLysGluIle 760  
Db 8937 TTCGTTATTGTTTACATGTTGATGAAGAAATCATCTTACCCAGATATCANAAAAAGAAATA 8996  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAenIleLeuLeuAenAenAspIleSerTyrTyr 780  
Db 8997 CTAGCTTCTATCATTAACATCAAGTGAATATTTTACTAATATATGATATCTCATATTAC 9056  
Qy 781 ThrSerAenArgLeuIleLysThrGluAlaHisLeuSerAenIleAenLysLeuSerGln 800  
Db 9057 ACGAGTAAATGATTAATAAAACCTGAGCGCATTTTAAGTAATATTAATAATAATAAGTCAG 9116  
Qy 801 LeuAenLeuAenCysGluTyrIleIlePheAepAenHisAspSerLeuPheValLysAen 820  
Db 9117 TTAATCTAAATTTGTAATACATCATCTTTTGTATATCATGACGCTATTCGTTAAAAAT 9176  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAenPheSerAlaLeuThrHis 840  
Db 9177 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 9236  
Qy 841 AspTyrIleGluLysIleAenAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
Db 9237 GATTGGATCGAGAAAATCAATCGCATCCACCACTTAAAAAGCTCATTTAAAACTTATTTT 9296  
Qy 861 AenAepAenAepLeuLysSerMetAenValLysGlyAlaSerGlnGlyMetPheMetThr 880  
Db 9297 AATGCAATGACTTAAAAAGTATGAATGTGAAGGGGCATCACAAGGTATGTTTATGACG 9356  
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 9357 TATGCGCTAGCGCATGAGCTTCTCGCATTTTAAAGAAAGTCATCACATCTCTGCCAGTCA 9416



```
Qy 901 IleAspSerValProGluTyrAenThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 9417 ATTGATAGTGGCAGAAATAAACACATGAGGATATTTGGTTCCAAATTTGCACATTTTAATC 9476
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940
Db 9477 TTAGAAAAGAAACCGGCCATGATTTTAAATAAACAATCGACCCCTGACTTATATGCTTGG 9536
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 9537 GAACGAAAATTTACAATGCACAAATGAACAAATTTGAAAGTGCAAAAGAGGAGAAATATA 9596
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 9597 CCTGTTAACAGTTTCATTTAATAGTATACTCTA 9632
RESULT 4
LOCUS AF237926 2919 bp DNA linear BCT 08-MAY-2000
DEFINITION Pasteurella multocida hyaluronan synthase (has) gene, complete cds.
ACCESSION AF237926
VERSION AF237926.1 GI:7716512
KEYWORDS
SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
1 (bases 1 to 2919)
Fuller,T.E., Kennedy,M.J. and Lowery,D.E.
Identification of Pasteurella multocida virulence genes in a
septicemic mouse model using signature-tagged mutagenesis
Unpublished
2 (bases 1 to 2919)
Fuller,T.E., Kennedy,M.J. and Lowery,D.E.
Direct Submission
Submitted (24-FEB-2000) Discovery Research, Pharmacia & Upjohn
Animal Health, 7923-25-43*, 7000 Portage Road, Kalamazoo, MI
49001-0199, USA
FEATURES
source
1. .2919
/organism="Pasteurella multocida"
/mol_type="genomic DNA"
/db_xref="taxon:747"
1. .2919
/gene="has"
1. .2919
/gene="has"
/note="pmhas"
/codon_start=1
/transl_table=11
/product="hyaluronan synthase"
/protein_id="AAF68412.1"
/db_xref="GI:7716513"
/translation="MNTLSQAIKAYNSNDYQLALKLFKSAEYIGRKIVFQITKCOE
KLSHPVNSAHUSVNEEKVNCVSDPLDIATQLLSNVKKLVLSDSKNTLKNMKL
LTKESNAEVAVALVPKDFPKDLVLAPLPHVDNFTYKRGKRLGKIPKHQVGL
SIIVTNRPAILISITLACLNVQKTHYPFEVITVDGDSQSDLSPIIRQYENKLDIRY
ROKNGFQAASARNMGLAKYDFIGLDCDMAPNPLWHSYVAELDEDDDLATIIGPR
KYIDTOHIDPKDPLNNALLESLEPVKTNNSVAAGKGTGTVSLDWRLQEPKTNRLS
DSPPRFAAGNAFAKWLKNSGFFDEFNHWGGEDEVFGYRLPRVGSFFKTIIDGINA
IYHPPKGETNETDREAGNITLIDIMREKVPYIYKGLPIEDSHINRVLPSYIYPATN
CANYIQCVSALNQTVVDLEVCINCDSGTDNTLEVINKLYGNNPRVRIMSKNGGIA
SASNAAYSFARGYIGLSDSDYLDPAVELCLKFLDKDTLACVYTNRNVPDGLS
IANGYNWPEFSREKLTAMTAHHPMTIRAWHLTDGFNEKIENAVYDMFLKLSVGL
KFHKLNIQYRVLHGNTSIIKLGIOKXHFVVVGNLNARQGTYYNYNDEFDLDES
KRYIPNKTAQOEIDIDKIIQNKDAKIVSIFYPNTLGLVKLNNIIEYNKI
FVIVHVKHNLTPDIKEILAFYHKHQVILLNNDISYTSNKLITKTEAHLNSNKL
SQLNLCYEYIFDNHSLFQKNDYSAYMKYDVGMNFSALTDHWEIKINAHPPFKLI
KTYFNDNLKSMNVKSGAQGMFTYALAHELLITIKEVITSCQSIDSVPEYNTEDIWF
QFALLILEKKTGHVFNKTSITLYMPWERKLQWNTNEQIESAKRGENIPVNFKIINSITL
"
```

ORIGIN

```
Alignment Scores: 1.79e-309 Length: 2919
Pred. No.: 5104.00 Matches: 971
Score: 100.00% Conservative: 1
Percent Similarity: 100.00%
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.92% Indels: 0
DB: 1 Gaps: 0
US-10-642-248-2 (1-972) x AF237926 (1-2919)
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 1 ATGANTACATTATCACAGCAGCATATAAAGCATATAACAGCAATGACTATCAATTAGCACATC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTATTTGMAAAGTCGCGGAAATCTATGAGACGGAAAAATTCCTGAATTTCAAAATTACC 120
Qy 41 LysCysGlyGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AAATGCCAAGAAAAACTCTCAGCACATCTCTTGTTAATTCAGCACATCTTTCTGTAAAT 180
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeu 80
Db 181 AAAGAGAAGAAAAGTCAATGTTGCGATAGTCCGTTAGATATTGCAACACAACTGTACTT 240
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db 241 TCCAACGTAAAAAATTTAGTACTTTCTGACTCGCAAAAAACACGTTAAAAAATAAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTTGCTCCTGAGAGAAGAAATCTGAAATGCGGAGGTAAAGACGGTCGCCCTTGTACCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAAGATTTTCCCAAGAGATCTGGTTTGTAGCGCTTTACCTGATCATGTAAATGATTTTACA 420
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisIleValGlyLeu 160
Db 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAAACCTGAACATCAACATGTGTGGTCTT 480
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTTACAACATTTCAATCGACAGCAAAATTTATTCGATTAACATTAGCTGT 540
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAAACACACATTTACCCTTTGAAGTTATCGTGACAGATGATGGTAGCAGAA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 601 GATCTATCACCGATCATTCGCCAAATATGAAAAATAAATTTGGATATTGCTACGTCAGACAA 660
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetClyLeuArgLeuAlaLysTyr 240
Db 661 AAAGATAACCGGTTTCAAGCCAGTCGCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT 720
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db 721 GACTTTATGGCTTACTCGACTCTGTGATATGGCGCCAAATCCATATATGGGTTCATCTTAT 780
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db 781 GTTGCAGAGCTATTAGAAGATGATGATTAAACAATATTGCTCGTCCAGAAAAATACATCGAT 840
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 841 ACAACAATATTGACCCCAAAAGACTCTTTAAATAAACGCGAGTTGCTTGAATCATTTACCA 900
Qy 301 GluValLysThrAsnAsnSerValAlaLysGlyGluGlyThrValSerLeuAspTyr 320
Db 901 GAAGTGAACCAATTAATAGTTGTTGCGCAAAAGGGGAGGACAGTTTCTCTGGATTGG 960
```



JOURNAL	Patent: JP 2001521741-A 13 13-NOV-2001; THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
COMMENT	OS Pasturella multocida PN JP 2001521741-A/13 PD 13-OCT-2001 PF 30-OCT-1998 JP 2000519083 PR 31-OCT-1997 US 60/064435,26-OCT-1998 US 09/178851 PI PAUL H WEIGEL,KSHAWA KUMARI,PAUL DEANGELIS PC C12N15/09,A61K31/728,A61P43/00,C12N1/21,C12N9/10,C12P19/04, PC C12Q1/68// PC (C12N15/09,C12R1:46),C12N15/00,(C12N15/00,C12R1:46) CC Hyaluronan synthase gene and utilization thereof FH Key Location/Qualifiers FT source 1..2899 FT /organism='Pasturella multocida'. FEATURES source 1..2937 Location/Qualifiers /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644' ORIGIN Alignment Scores: Pred. No.: 1..81e-309 Length: 2937 Score: 5104.00 Matches: 971 Percent Similarity: 100.00% Conservative: 1 Best Local Similarity: 99.90% Mismatches: 0 Query Match: 99.92% Indels: 0 DB: 6 Gaps: 0 US-10-642-248-2 (1-972) x BD087261 (1-2937) Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20 Db 19 ATGAATACATTATCACAGCAATTAAGCAATATTAACAGCAATGACTATCAATTAGCACTC 78 Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40 Db 79 AAATTATTGAAAGTCGGCGGAANTCTATGAGCGGAAATTTGTGAATTTCAAAATTACC 138 Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60 Db 139 AAATGCCAGAAAACTCTCAGCACATCCCTCTGTTAATTCAGCACATCTTCTGTAAT 198 Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeu 80 Db 199 AAAGAAGAAAGCAATGTTTGGATAGTCGCTAGATATTGCAACACAACTGTTACTT 258 Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100 Db 259 TCCAAACGTAAAAAAATTAGTACTTCTTGACTCGGAAAAAAACACGTTAAAAAATAAATGG 318 Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120 Db 319 AAATTGCTCACTGAGAGAAATCTGAAATCGGAGGTTAAGCGGTCGCCCTGTACCA 378 Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140 Db 379 AAAGATTTCCCAAGATCTGGTTTACGCGCTTTACCTGATCATGTTAATGATTTTACA 438 Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160 Db 439 TGGTACAAAAAGCGGAAAGAAAGACTTGGCAATAAAACCTGAACATCAACATGTTGGTCTT 498 Qy 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180 Db 499 TCTATTATCGTTTACACATTCATCGACCAACCAATTTTATCGATTACATTAGCCGTGTTA 558 Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200 Db 559 GTAAACCAAAAAACACATTACCCTGTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGAA 618 Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220 Db 619 GATCTATCACCGATCATTTGCCCATATGAANAATAATTTGGATATTCGTACGTACAGCAA 678 Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240 Db 679 AAAGATAACCGTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 738 Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260 Db 739 GACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCATATATGGGTTCATCTTAT 798 Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280 Db 799 GTTGCAGAGCTATTAGAAGATGATGATTTAAACATCATTTGGTCCAGAGAAATACATCGAT 858 Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300 Db 859 ACACAACATATTGACCCAAAGACTTCTTAAATAACCGAGTTTGTCTTGAATCATTACCA 918 Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320 Db 919 GAAAGTGAAACCAATAATAGTGTTCGCCAAAAAGGGAAGGACAGTTCCTCTGGATGG 978 Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340 Db 979 CGCTTAGAACATTCGAAAAACAGAAATCTCCGTTATCCGATTCGCTTCGCTTTT 1038 Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp 360 Db 1039 TTTGCGGCGGTAAATGTTGCTTTCCGCTAAAAAATGGCTAAATAAATCCGCTTTCTTTGAT 1098 Qy 361 GluGluPheAsnHisTyrGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380 Db 1099 GAGCAATTTAAATCACTGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGCTTAC 1158 Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400 Db 1159 GGTAGTTTCTTTAAACTATTGATGGCATTTAGCCCTACCATCAAGAGCCACCGGTAA 1218 Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420 Db 1219 GAAATGAAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAG 1278 Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440 Db 1279 GTCCCTTATATCTATAGAAACCTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT 1338 Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460 Db 1339 TTAGTTTCAATTTATATCCAGCTTATTAATCTGTGCAAACTATATTCNAACGTTGGTAGAT 1398 Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480 Db 1399 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA 1458 Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500 Db 1459 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCTTAGGGTACGCATCATG 1518 Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520 Db 1519 TCTAAACCAANTGGCGAATAGCTCAGCATCAAAATGACAGCCGCTTCTTTTGTAAAGGT 1578 Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540 Db 1579 TATTACATTCGGCAGTTAGATTGATGATTTATCTTGAGCTGATGAGTGAACCTGTGT 1638 Qy 541 LeuLysGluPheLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560 Db 1639 TTAAGAAGATTTTAAAGATAAAACGCTAGCTGTGTGTTATACCATTAATAGAAACGCTC 1698 Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580

```
Db 1699 AATCGGATGCTAGCTTAATCGCTAATGGTTACAAATGGCCAGCAAAATTTTACAGAGAAAA 1758
Qy 581 LeuThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1759 CTCACACGGCTATGATGCTCACACCTTTAGAATGTTACGATTAGAGCTTGCGATTTA 1818
Qy 601 ThrAspGlyPheAenGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1819 ACTGATGGATTCAATGAAAGAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1878
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1879 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTACATGGT 1938
Qy 641 AspAsnThrSerIleLysLeuLysGlyIleGlnLysLysAsnHisPheValValValAsn 660
Db 1939 GATAACACATCAATTAAGAAACTTGCGCAITCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1998
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 1999 CAGTCATTAATAGACAGGCACTAATCTTATTAATATGACGAATTTGATGATTTAGAT 2058
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluLysIleAspIleLeu 700
Db 2059 GAAAGTGAAGATATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA 2118
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2119 AAAGATATTAAATCCTCAGAAATAAGATGCAAAATCGCAGTCAGTATTTTATATCCC 2178
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 2179 AATACATTAACCGCTTAGTGAAAACTAACAATATTATTAATATAATAAAATATA 2238
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2239 TTCGTTATTGTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAspIleSerTyrTyr 780
Db 2299 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATAAATGATATCTCATATTAC 2358
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2359 ACCAGTAAATAGTTAATAAATACTAGCGGCATTTAAGTAAATTAATAAATTAAGTCAG 2418
Qy 801 LeuAsnLeuAsnCysGluTyrIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2419 TTAATATCTAAATTTGTGAATACATCATTTTGTATAATCATGACAGCCTATTCTGTTAAAAAT 2478
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538
Qy 841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2539 GATTGATCGAGAAATCAATCGCATCCACCATTTTAAAGAACTCATTAATAACTTATTTT 2598
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2599 AATGACAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGACG 2658
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2659 TATCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAAAGTCAATCACAATCTTCCAGTCA 2718
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2719 ATTGATAGTGTGCCAGATATAACACTGAGGATATTGTTGTTCAATTTGACATTTTAAATC 2778
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2779 TTAGAAAAAGAAAAACCGCCATGATTTTAATAAAACATCGACCTTGACTTATATGCTTGG 2838
```

```
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2839 GAACGAAAAATTACAATGGACAAATGAACAAATTGAAAGTGCAAAAAGAGAGAAAAATATA 2898
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrIleu 972
Db 2899 CCTGTTAAACAAGTTTCATTATTAAATAGTATAACTCTA 2934
RESULT 6
BD205371 Nucleic acid encoding hyaluronan synthase and method of using the
LOCUS same.
DEFINITION
ACCESSION BD205371
VERSION BD205371.1 GI:33015141
KEYWORDS JP 2002510648-A/1.
SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
REFERENCE Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
1 (bases 1 to 2937) Pasteurellaceae; Pasteurella.
AUTHORS Deangelis, P.
TITLE Nucleic acid encoding hyaluronan synthase and method of using the
JOURNAL Patent: JP 2002510648-A 1 09-APR-2002;
COMMENT BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
OS Pasteurella multocida
PN JP 2002510648-A/1
PD 09-APR-2002
PF 01-APR-1999 JP 2000542035
PR 02-APR-1998 US 60/080414, 26-OCT-1998 US 09/178851 P1
PAUL DEANGELIS
PC A61K39/102, A61K39/00, A61K47/36, A61P31/04, C12N1/15, C12N1/19, PC
C12N1/21,
PC
C12N5/10, C12N9/00, C12N15/09, C12P19/04, C12Q1/02, C12Q1/68, G01N33/ PC
48,
PC G01N33/53, G01N33/566, C12N5/00, C12N15/00
CC Nucleic acid encoding hyaluronan synthase and method of using
the same.
FH Key Location/Qualifiers
FT source 1. .2937
/organism='Pasteurella multocida'.
/organism='Pasteurella multocida'
/mol_type='genomic DNA'
/db_xref='taxon:747'
FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 1.81e-309 Length: 2937
Score: 5104.00 Matches: 971
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.92% Indels: 0
DB: 6 Gaps: 0
US-10-642-248-2 (1-972) x BD205371 (1-2937)
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 19 ATGAATACATATTATCAAGCAATAAAGCAATATAACAGCAATGACTCAATTAATAGCCTC 78
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 79 AAATATTATTGAAGTCGCGGAAATCTATGACGCAAAATTTGTTGAATTTCAATTTACC 138
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 139 AAATGCCAAGAAAAAACTCTCAGCATCTCTCTGTTAATTCAGCACATCTTCTCTGAAT 198
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
```

Db 199 AAAGAGAAAAGTCATGTTGGCATAGTCGGTTAGATATTGCAACACAACTGTACTT 258  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
Db 259 TCCAAACGTAAAAAAATAGTACTTCTGACTCGGAAAAAAACACGTTAAAAAAATAAATGG 318  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 319 AAATTGCTCACTGAGAGAAATCTGAAAATCGCGAGGTAAGACGGTCGCCCTTGTACCA 378  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 379 AAAGATTTTCCCAAGAATCTGGTTTTAGCGCCTTACTGATCATGTATGATTTTACA 438  
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
Db 439 TGGTACAAAAGCGAAGAAAGACTTTGGCATAAAACCTGAACATCAACATGTTGGTCTT 498  
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 499 TCTATTATCGTTACAACATTCATCGACCCAGCAATTTTATCGATTACATTAGCCTGTTTA 558  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 559 GTAAACCAAAAACACAAATACCCGTTTGAAGTTATCGTGACAGATGATGTTAGTCAGGAA 618  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 619 GATCTATCACCGATCATTCGCCAATATGAAATAAATTTGGATATTTCGTACGTCAGACAA 678  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 679 AAAGATAACCGTTTCAAGCCAGTCGCGCTCGGAATATGGGATTTACGTTAGCAAAAATAT 738  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
Db 739 GACTTTATGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGGTTCACTCTTAT 798  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 799 GTTCAGAGCTATTAGAAGATGATGATTTAACATCATTTGGTCCACAGAAAAATACATCGAT 858  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 859 ACACAACATATTGACCCAAAAGACTTCTTAATAACCGAGTTTGTCTGAATCAATTACCA 918  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320  
Db 919 GAAGTGAAACCAATATATGTTTGGCGCAAAAGGGAGNACAGTTTCTCTGGATTGG 978  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGAACAAATTCGAAAAAACAGAAAACTCCGCTTATCCGATTCGCTTTCCGTTTT 1038  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
Db 1039 TTTGCGCGGGTAATGTTGCTTTCGCTAAAAAATGGCTAATAATAATCCGGTTCTTTGAT 1098  
Qy 361 GluGluPheAsnHisTyrGlyGlyAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1099 GAGGAAATTTATCTCGGGTGGAGAGATGTGAATTTGGATATCGCTTATTCGGTTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1159 GGTAGTTCTTTAAAACTATTGATGGCATTATGGCTTACCATTCAAGACCCACAGGTAAA 1218  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAATGAACCGATCGTGAAGCGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG 1278  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440

Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCATAAGAGATTGCGCATATCAATAGAGTACCT 1338  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAAAGTTCCGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1399 AGTGCACTGATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA 1458  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1459 GATAATACCTTTAGAACTGATCAATAAGCTTTATGGTAAATACTCTAGGGTACGCATCATG 1518  
Qy 501 SerLysProAsnGlyLysIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1519 TCTAAACCAAAATGGCGAATAGCCTCAGCATCAAAATGCAGCGGTTTCTTTTGTAAAGGT 1578  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTTGGGCGATGATTTCAGATGATATCTTGAGCCTGATGCGAGTTGAACTGTGT 1638  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1639 TTTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1698  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1699 AATCCGGATGGTATTAATCGCTAATGGTTACAATTTGGCCAGATTTTTCACGAGAAAAA 1758  
Qy 581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1759 CTCAACACGGCTAGATGCTCACCACTTTAGAAATGTTACGATTTAGAGCTTGGCATTTA 1818  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATTAACCGTGTTACATGGT 1938  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1939 GATPACACATCAATTAAGAAACCTTGCACTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1998  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
Db 1999 CAGTCATTTAAATAGACAAGCATAACTTATTATAATTATGACGAAATTTGATGATTTAGAT 2058  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATATCAAGAGAGATTTGATATCTTA 2118  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2119 AAAGATATTAAATATCATCCAGATAAAGATGCCAAAATCCAGTCACTAGTATTTTTTATCCC 2178  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2179 AATACATTTAAACCGCTTAGTGAAAAAACATAAACATATTATTGAATATATAAAAAATATA 2238  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysGluIle 760  
Db 2239 TTCGTTATTGTTCTACATGTTGATAAGAAATCATCTTACACCAAGATATCAAAAAAGAAATA 2298  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
Db 2299 CTAGCCTTCTATCATTAACATCAAGTGAATATTTTACTAATAATGATATCTCATATTAC 2358  
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
Db 2359 ACCGAGTAATAGATTAAATAAACTGAGGCGCAATTTAAGTAAATATTATAAAATTAAGTCAG 2418

```
QY 801 LeuAenLeuAenCysGluTyriLeilePheAenHisAaspSerLeuPheVallyAen 820
Db 2419 TTAATCTAAATTTGGAATACATCATTTTTCATATCATGACAGCTATTCGTTAAAAAT 2478

QY 821 AspSerTyraLalTyMetLysLysTyAspValGlyMetAenPheSerAlaLeuThHis 840
Db 2479 GACAGCTATGCTTATATGAAAAATATATGTCGCGCATGAATTTCTCAGCATTAACACAT 2538

QY 841 AspTrpIleGluLysIleAenAlaHisProPheLysLysLeuLysLysThTyPhe 860
Db 2539 GATTGGATCGAGAAAAATCAATCGCATCCACCATTTTAAAAAGGCTCATTTAAAACTTATTTT 2598

QY 861 AenAenAenAenLeuLysSerMetAenVallyLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2599 AATGCAATGACTTTAAAAAGTATGATGTAAGAGGGCATCAAGGATGTTTATGAGC 2658

QY 881 TyraLeuAlaHisGluLeuLeuThriLeileLysGluValIleThrSerCysGlnSer 900
Db 2659 TATGCGCTAGCGCATGAGCTTCGACGATTTTAAAGAAGTCATCACATCTTGCCAGTCA 2718

QY 901 IleAepSerValProGluTyraenThrGluAepIleTrpPheGlnPheAlaLeuLeu 920
Db 2719 ATTGATAGTGCAGAGATATAAACACTGAGGATATTTGGTTCCAAATTTGCCACTTTTAATC 2778

QY 921 LeuGluLysLysGlyHisValPheAenLysThrSerThrLeuThTyMetProTrp 940
Db 2779 TTAGAAAAAGAAACCGCGCATGTATTTAATAAACAATCGACCTGACTTATATGCTTGG 2838

QY 941 GluAryLysLeuGlnTrpThrAenGluGlnIleGluSerAlaLysAryGlyGluAenIle 960
Db 2839 GAACAAAAATTACATGCAAAATGAACAATTTGAAGTGCAAANAGAGGAGAAAAATATA 2898

QY 961 ProValAenLysPheIleAenSerIleThrLeu 972
Db 2899 CCTGTTAAACAGTTCATTATTAAATAGTATAACTTA 2934

RESULT 7
AF195517
LOCUS AF195517 2979 bp DNA linear BCT 04-MAR-2004
DEFINITION Pasteurella multocida chondroitin synthase CS gene, complete cds.
ACCESSION AF195517
VERSION AF195517.2 GI:44985817
KEYWORDS
SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
1 (bases 1 to 2979)
DeAngelis,P.L. and Padgett-McCue,A.J.
Identification and molecular cloning of a chondroitin synthase from
Pasteurella multocida type F
J. Biol. Chem. 275 (31), 24124-24129 (2000)
10818104
2 (bases 1 to 2979)
DeAngelis,P.L. and Padgett-McCue,A.J.
Direct Submission
Submitted (04-MAR-2004) Biochem. & Molec. Biol., Univ. of Oklahoma
Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City,
OK 73104, USA
3 (bases 1 to 2979)
DeAngelis,P.L. and Padgett-McCue,A.J.
Direct Submission
Submitted (04-MAR-2004) Biochem. & Molec. Biol., Univ. of Oklahoma
Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City,
OK 73104, USA
REMARK
COMMENT On Mar 4, 2004 this sequence version replaced gi:9716369.
FEATURES
Location/Qualifiers
1..2979
/organism="Pasteurella multocida"
/mol_type="genomic DNA"
/strain="P4679"
source
```

```
/db_xref="taxon:747"
/country="USA: Arkansas"
/note="capsule type F
isolated from face lesion of turkey from Arkansas; strain
obtained from USDA"
61..2958
/functions="synthesizes the chondroitin polymer backbone (a
polysaccharide composed of repeating disaccharide units
consisting of beta(1,4)glucuronic acid linked to
beta(1,3)N-acetylgalactosamine) involved in capsule
biosynthesis"
/note="polysaccharide-forming glycosyltransferase; similar
to Pasteurella multocida type A hyaluronan synthase"
/codon_start=1
/transl_table=11
/product="chondroitin synthase CS"
/protein_id="AAF97500.2"
/db_xref="GI:44985818"
/translation="MNTLSQAIKAYNSNDYELALKLFEKSAETVGRKIVRQIIKCKE
KLTNSVSDKKNSSCDSDIATOLLNNVKKLTLSSEKNSKNKMKISITQKSE
NAETRKVELVPKDPKDLVLAEPDHVNDFTWYKRRKSLGIKVKNIGIISITPF
NRSRLIDI TLACLNVQNTNYPFEVAVDDGSKENLTIQVKEQKLDIKYVRQKDYG
QLCAVRNLGLRTAKYDFVSLDCDMPQOLWVHSYLTLEEDNDIVLIGPKYQVDYH
ITAQFLNDPLYLSLPETATNNPNSITSKGNISLDNRLEHFKTDNLRLCDSPRYF
SCGVAFSKWLNKVGWDFEFNHGWDVEFGYRLFAGCFRVIDGGMAYHQBPFG
KENETDREAGKSIITLKI VKSKVPYIYRKLPLIEDSHRIPLVSIYIPAYNCANTYQ
CVDALNOTVVDLEVCICNDGSTDNTLEINKLYGNRPVRINSKPNGISASNAAY
SFAGYIIGQLSDSDYLEPDAVELCKEFLKDKTLCACVYTTNRNVNPOGSLIANGYNW
PEFSREKLITAMIAHFMPTIRAFHLTDGENENIENADVDMFLKLESEVKFHLNK
ICNRLHGDNTSICKLGIQKKNHFVVVQSLNRQGINNYNYNDFDLDSESKYLFNK
TAEYOBEMDILKDLKIQNDKAKI AVSIFYPNTLNGLVKLNNTIENYKNI FVILHV
DKNHLTPDIIKEILAFYHQVNILLNNDISYTNRLIKTEANLSNKLNSQLNLC
EYIIFDNHSLFVKNDVSAYVMKFDVGNFSAFTHDIKINAHPPFKLIGKTYFNDL
DLRSMNVKSGASQGMFKYALPHELLTIKIVITSCSIDSVPEYNTEDWIFQFALLIL
SKTKGHVFNKSTLTITYPWERLQWTHNEIQISAKKENIPVNFIIINSITL"
ORIGIN
Alignment Scores:
Pred. No.: 6,74e-272 Length: 2979
Score: 4502.50 Matches: 845
Percent Similarity: 93.21% Conservative: 61
Best Local Similarity: 86.93% Mismatches: 59
Query Match: 88.15% Indels: 7
DB: 1 Gaps: 2
US-10-642-248-2 (1-972) x AF195517 (1-2979)
QY 1 MetAenThrLeuSerGlnAlaIleLysAlaTyraenSerAenAaspTyGlnLeuAlaLeu 20
Db 61 ATGAATACATTATCACAGCAATTAAGCATATATAACAGCAATGACTATGAATTAGCACTC 120
QY 21 LysLeuPheGluLysSerAlaGluIleTyrglyArglyLysIleValGluPheGlnIleThr 40
Db 121 AAATATTATTGAGAAAGTCTGCTGAAACCTACGCGGCGGAAAATCGTTGAATTCCAAATTATC 180
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen 60
Db 181 AAATGTAAGAAAAAATCTC-----TCGACCAATTCI-----TATGTAAGT 219
QY 61 LysGluGluLysValAenValCysAaspSerProLeuAaspIleAlaThrGlnLeuLeuLeu 80
Db 220 GAAGATAAAAAAACAAGTGTTCGATAGCTCATTAGATATATCGAACACACAGCTCTTACTT 279
QY 81 SerAenValLysLeuLeuValLeuSerAaspSerGluLysAenThrLeuLysAenLysTTP 100
Db 280 TCCAACGTAAAAAAAATTAACCTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATG 339
QY 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120
Db 340 AAATCTATCACTCGGAAAAAATCGGAGAACCGCAGAAATCAGAAAGGTGGAACCTAGTACCC 399
QY 121 LysAaspPheProLysAaspLeuValLeuAlaProLeuProAaspHisValAenAaspPheThr 140
```



Db	400	AAAGATTTTCTCTAAAGATCTTGTGTTCTTCTGCTCCATGCGCAGATCATGTAAATGATTTTACA	459
Qy	141	TTPYRLYLSYLSAQLYLSYLSArgLeuGluGlyLeuSerLeuHisGlnHisValGlyLeu	160
Db	460	TGGTACAAAATCGAAAAAAGCTTAGGTATAAAGCTGTAAATAAGATATCGGTCCT	519
Qy	161	SerileileValThrPheAsnArgProAlaileLeuSerileThrLeuAlaCysLeu	180
Db	520	TCTATTATTCTCATTTAATCGTAGCGGTATTTTAGATATAACGTTAGCCTGTTTG	579
Qy	181	ValAsnGlnYthrHisYrProPheGluValleValThrAspAspGlySerGlnGlu	200
Db	580	GTCAATCAGAAAAACAACTACCCATTTGAAATCGTGTTCAGATATGCTAGTAGTAA	639
Qy	201	AspLeuSerProileileArgGlnYrGluAsnLysLeuAspIleArgYrValArgGln	220
Db	640	AACCTTACTTACCATTGTGCAAAATACGACAAAACCTTGACATAAAGTATGTAAACAA	699
Qy	221	LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysYr	240
Db	700	AAAGATTATGATATCAATTGTGTGAGTCAGTAAACCTTAGGTTTACGTACAGCAAACTAT	759
Qy	241	AspPheileGlyLeuLeuAspCysAspMetAlaProAsnProLeuYrValHisSerYr	260
Db	760	GATTTTCTCGATTCCTAGACTGCGATATGCGCACCAACAATATATGGGTTCAATCTTAT	819
Qy	261	ValAlaGluLeuLeuGluAspAspAspLeuThrileileGlyProArgLysYrIleAsp	280
Db	820	CTTACAGAACTATTAGAAGCAATGATATGTTTAAATTTGACCTAGAAATATGTGGAT	879
Qy	281	ThrGlnHisileAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro	300
Db	880	ACTCATAATATTACCGCAGAACAAATTCCTTAAACGATCCATATTTAATAGAACTACCTACCT	939
Qy	301	GluValLysYthrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspYr	320
Db	940	GAACCCGCTACAAATAACAATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATGG	999
Qy	321	ArgLeuGluGlnPheGluYrThrGluAsnLeuArgLeuSerAspSerPropheArgPhe	340
Db	1000	AGATTAGAACAATTTCAAAAACCGATAATCTAGCTGTATGTGAATCTCCGTTTCGTTAT	1059
Qy	341	PheAlaAlaGlyAsnValAlaPheAlaLysLysYrTrpLeuAsnLysSerGlyPheAsp	360
Db	1060	TTTAGTTCCGGTAATGTTGCATTTCTTAAAGAAATGGCTAAATAAAGTAGGTTCGTTCCAT	1119
Qy	361	GluGluPheAsnHisYrTrpGlyGlyGluAspValGluPheGlyYrArgLeuPheArgYr	380
Db	1120	GAAGAAATTTAATCATTTGGGGGGGCAAGATGTAGAAATTTGGTTACAGATTATTTGCCAAA	1179
Qy	381	GlySerPhePheYthrIleAspGlyLleMetAlaYrHisGlnGluProProGlyLys	400
Db	1180	GGCTGTTTTTTCAGAGTAATTTGACGGCGGAATGGCATCCATCAAGAACCACTCGGTAAA	1239
Qy	401	GluAsnGluThrAspArgGluAlaGlyLysAsnileThrLeuAspIleMetArgGlyLys	420
Db	1240	GAATAATGAACAGACCGGAAGCTGTAAAAGTATTACGCTTAAAAATGTTGAAGAAAAG	1299
Qy	421	ValProYrIleYrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro	440
Db	1300	GTACCTTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCAATATTTACAGAATACCT	1359
Qy	441	LeuValSerileYrIleProAlaYrAsnCysAlaAsnYrIleGlnArgCysValAsp	460
Db	1360	TTAGTTCTTATTATATCCCGCTTATAACTGTGCAAAATATATTTCAAGATGTGTAGAT	1419
Qy	461	SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr	480
Db	1420	AGTGCTCTTAATCAACTGTTGTGCATCTCGAGGTTTGTATTGTACAGATGGTTCACCA	1479
Qy	481	AspAsnThrLeuGluValIleAsnLysLeuYrGlyAsnAsnProArgValArgIleMet	500
Db	1480	GATAAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATATCTTAGGTACGATCATG	1539

Qy	501	SerLysPro	AsnGlyGlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGly	520
Db	1540	TCTAAACCAAAATGCGGAATAGCCTCAGCATCAAAATGCGAGCCGTTCTTTTGTCTAAAGGT	1599	
Qy	521	TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys	540	
Db	1600	TATTACATTTGGCAGTTAGATTTCAGATGATTAATCTTTGAGCCTGATGCAGTTGAACATGTGT	1659	
Qy	541	LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal	560	
Db	1660	TTAAAGAAATTTTTAAAGATTAACAGCTAGCTTGTTTATACCACTAATAGAAAGCTC	1719	
Qy	561	AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys	580	
Db	1720	AATCCGGATGGTAGCTTAATCGCTAATGGTTACAAATTTGGCCAGAAATTTTTCACGAGAAAAA	1779	
Qy	581	LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu	600	
Db	1780	CTCAACACGGCTGATGATGTCTCACCAATTTTAGAAATGTTTACGATTAAGAGCTTGCCATTTA	1839	
Qy	601	ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu	620	
Db	1840	ACGGATGGATTTAACGAAATATTTGAAACCGCTGGATTATGACATGTTCTCTTAAACTC	1899	
Qy	621	SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly	640	
Db	1900	AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGCGATTACATGGT	1959	
Qy	641	AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn	660	
Db	1960	GATTAACACATCCATTAAAGAACTCGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT	2019	
Qy	661	GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp	680	
Db	2020	CAGTCATTTAAATAGACAAAGGCATCAATATTATAATTATGACAAATTTGATGATTAGAT	2079	
Qy	681	GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluLysIleAspIleLeu	700	
Db	2080	GAAGTTAGAAGATATATCTTCATATAAACCGCTGAATATCAAGNAGAAATGGATATTTTA	2139	
Qy	701	LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro	720	
Db	2140	AAAGATCTTAAACTCATTTCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCC	2199	
Qy	721	AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle	740	
Db	2200	AATACATTTAAACCGCTTAGTGAAAAAACTAAACAATAATTATTGAATATAATAAAAAATATA	2259	
Qy	741	PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle	760	
Db	2260	TTTCGTTATTATTCTACATGTTTGATAAGAAATCACTTTACACGACATCAAAAAGAAATA	2319	
Qy	761	LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr	780	
Db	2320	TTGCTTCTTATCATATAAGCAACCAAGTGAATATTTTACTAAATAATGACATCTCATATTAC	2379	
Qy	781	ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln	800	
Db	2380	ACGAGTAAATAGACTAAATAAAAAAGCTAGAGGCCATTTAAGTAAATATAATAAAATTAAGTCAG	2439	
Qy	801	LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn	820	
Db	2440	TTAAATCTAAATTTGTAATACATCAATTTTTTGATTAATCATGACGCTATTTCGTTAAAAAT	2499	
Qy	821	AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis	840	
Db	2500	GACAGCTATGCTTATATGAAAAATAATGATGTCGGCATGAATTTCTCAGCATTAACACAT	2559	
Qy	841	AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe	860	
Db	2560	GATTGGATCGAAGAAATCAATGGCGATCCACCAATTTAAAAGCTGATTTAAACACCTATTTT	2619	



QY 861 AsnAspAsnLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
 DB 2620 AATGACAAATGCTTAAGAAAGTATGAATGTGAAGGGGCATCAACAGGTATGTTATGAAG 2679  
 QY 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
 DB 2680 TATGGCTACCGCATAGCTTCTGACGATTATTAAAGAAAGTCATCACATCTGCGCAATCA 2739  
 QY 901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuIle 920  
 DB 2740 ATTGATAGTGTGCCAGATATAAACAACACTGAGATATTGGTTCCCAATTTGGCACTTTTAAATC 2799  
 QY 921 LeuGluLysValThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940  
 DB 2800 TTAGAAAAGAAAACCGGCATGATTATTAAACATCGACCTGACTTATATGCTTGG 2859  
 QY 941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
 DB 2860 GAACGAAAATACATATGACAAATGAACAAATTCAAAGTGCAGAAAAGGCGCAAAATATC 2919  
 QY 961 ProValAsnLysPheIleAsnSerIleThrLeu 972  
 DB 2920 CCCGTTAACAAAGTTCATTATTAAATAGTATAACGCTA 2955

## RESULT 8

BD228712 2979 bp DNA linear PAT 17-JUL-2003  
 LOCUS Polymer grafting by polysaccharide synthases.

DEFINITION BD228712  
 ACCESSION BD228712.1 GI:33038482  
 VERSION JP 2002529064-A/2.0  
 KEYWORDS Pasteurella multocida  
 SOURCE Pasteurella multocida  
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 Pasteurellaceae; Pasteurella.

## REFERENCE

1 (bases 1 to 2979)  
 Deangelis,P.L.

Polymer grafting by polysaccharide synthases

TITLE Patent: JP 2002529064-A 2 10-SEP-2002;

JOURNAL THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA

## COMMENT

OS Pasteurella multocida  
 PN JP 2002529064-A/2  
 PD 10-SEP-2002  
 PF 10-NOV-1999 JP 2000580666  
 PR 11-NOV-1998 US 60/107929, 01-APR-1999 US 09/283402 PI  
 PAUL L DEANGELIS  
 PC C12N15/09, A61K47/36, C12N1/21, C12P19/26//C12N9/26, C12N15/00 CC  
 Polymer grafting by polysaccharide synthases  
 FH Key Location/Qualifiers  
 FT source 1..2979  
 FT Location/Qualifiers  
 /organism='Pasteurella multocida'.  
 /organism='Pasteurella multocida'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:747'

## FEATURES

Source

## ORIGIN

Alignment Scores:  
 Pred. No.: 3,78e-271 Length: 2979  
 Score: 4490.50 Matches: 843  
 Percent Similarity: 93.11% Conservative: 62  
 Best Local Similarity: 86.73% Mismatches: 60  
 Query Match: 87.91% Indels: 7  
 DB: 6 Gaps: 2

US-10-642-248-2 (1-972) x BD228712 (1-2979)

QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
 DB 61 ATGAATACATTATCACAGCAATAAAGCATATAACAGCAATGACTATGAATAGCACTC 120  
 QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40

DB 121 AAATTATTGAGAAGTCTGCTGAAACCTACGGCGCAAAAAATCGTTGAATTCCAAATATATC 180  
 QY 41 LysCysLysGluLysValSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
 DB 181 AAATGTAAAGAAAAACCTC-----TCGACCAATTC-----TATGTAAGT 219  
 QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
 DB 220 GAAGATAAAAAAACACAGTGTTCGATAGCTCATTAGATATCGCAACACACACTCTTACTT 279  
 QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
 DB 280 TCCAACCTAAAAAAATTAACCTCTATCCGAATCAGAAAAAACAGTTTAAAAAATAAATGG 339  
 QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
 DB 340 AAATCTATCACTGGGAANAANAATCGAGAACGCAAGAAATCAGAAAGGTGGAACCTAGTACCC 399  
 QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
 DB 400 AAAGATTTCCTAAGATCTTGTCTTCCTCAATTCGACATCATGTTAATGATTTTACA 459  
 QY 141 TrpTyrLysLysArgLysLysArgLysGlyLysProGluHisGlnHisValGlyLeu 160  
 DB 460 TGGTACAAAAATCGAAAAAAAGCTTAGGTATAAGCCTGTANAATAAGAAATATCGGCTCTT 519  
 QY 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
 DB 520 TCTATTATTATCTCTACATTTAATCGTAGCCGTATTTTAGATATAACGTTAGCCCTGTTTG 579  
 QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
 DB 580 GTCAATCAGAAAAACAACCTACCCATTTGAAGTTCGTTGTCAGATGATGGTAGTAAGAA 639  
 QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
 DB 640 AACTTACTTACCATTTGTCAAAAAATACGAAACAAAACCTTGACATAAAGTATGTAAAGCAA 699  
 QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
 DB 700 AAAGATTATGATATCAATTTGTGCACTCAGAAACCTTAGGTTTACGTACAGCAAAAGTAT 759  
 QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260  
 DB 760 GATTTTGTCTCGATTCCTAGACTCGCATATGGCACCACCAACAATTTATGGTTCATTCTTAT 819  
 QY 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
 DB 820 CTTACAGAACTATTAGAAAGACAATGATATTGTTTAAATTTGGACCTAGAAAATATGTGGAT 879  
 QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
 DB 880 ACTCATATAATTACCGCAGAACAAATTCCTTACGATCCATATTTAATAGAATCATTACCT 939  
 QY 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
 DB 940 GAAACCGCTACAAATAAACAATCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999  
 QY 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
 DB 1000 AGATTAGAACATTTCAAAAAAACCGATAATCTACGCTCTATGTGATTTCCCGTTTCGTTAT 1059  
 QY 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPheAsp 360  
 DB 1060 TTTTGTGGGGTAATGTTGCAATTTTCTAAAGAAATGGCTAAATAAAGTAGGTGGTTCCGAT 1119  
 QY 361 GluGluPheAsnHisTyrGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
 DB 1120 GAAGAATTTTAATCATTTGGGGGGGGCCAGAGATGTAGAATTTGGTTACAGATTTATTTGCCAAA 1179  
 QY 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400

```
Db 1180 GGCTGTTTTTTCAGAGTAATTTGACGGCGAATGGCCATCCATCAAGAACACACCTGGTAAA 1239
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
Db 1240 GAAATGAAACAGAACGCGAGCTGGTAAAGTATTACGCTTAAATTTGTGAAGAAAAG 1299
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGATTCACATATTCATAGATACCT 1359
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1360 TTAGTTTCTATTTATATCCCGCTTATAAAGTGTGCAATATATTTCAAAGATGTAGAT 1419
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1420 AGTGCCTTAAATCAAACTGTTGTGCATCTCGAGGTTTGATTTTGTAAACGATGGTTCAACA 1479
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1480 GATAAATACCTTAGAAGTGTATCAATAGCTTTATGGTAAATATCTTAGGGTACGCATCATG 1539
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaIleValSerPheAlaLysGly 520
Db 1540 TCTAAACCAATGGCGAATAGCCTCAGCATCAATGCAGCGTTCTTTTGTCTAAAGGT 1599
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrIleuGluProAspAlaValGluLeuCys 540
Db 1600 TATTACATTTGGCAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCGAGTTGAAGTGTGT 1659
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1660 TTTAAAGAAATTTTAAAGATATAAACCGCTAGCTGTGTGTATATACCACTAATAGAAACGTC 1719
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580
Db 1720 AATCCGATGGTAGCTTAATCGCTTAATGGTTACAAATGGCCAGAAATTTTCACGAGAAAAA 1779
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTyrPheIleLeu 600
Db 1780 CTCACACGGCTATGCTTGCCTACCAATTTTGAATGTTTACGATTAGAGCTTGGCATTTA 1839
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1840 ACGGATGGATTTAACGAAATATTGAAACCGCCGGTGAATATGACATGTTCTCTTAAACTC 1899
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1900 AGTGAAGTTGAAAATTTAAACATCTTAATAAATCTGCTATAACCGCGTATTACATGGT 1959
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
Db 1960 GATAACACATCCATTAAAGAACTCGGCATTCGAAAGAAAAACCAATTTTGTGTAGTCAAT 2019
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 2020 CAGTCATTAAATAGACAGGCGATCAATATTATTAATATTATGACAAATTTGTAGTATTAGAT 2079
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2080 GAAAGTAGAAGTATATCTTCAATAAACCCTGATATCAAGAGAAATCGATATGTTA 2139
Qy 701 LysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2140 AAAGATCTTAAACTCAATCAAAATAAAGATGCCAAAATCGCAGTCAGTATTCTTCTATCCC 2199
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnIleIleGluTyrAsnLysAsnIle 740
Db 2200 AATACATTAAACGGCTAGTGAAGAAAACTAAACAAATATTATTGAATATAATAAAAAATATA 2259
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2260 TTCGTTATTCTTACATGTTGTATGAAGATCATCTTACACCAGACATCAAAAAAGAAATA 2319
```

```
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAspIleSerTyrTyr 780
Db 2320 TTGGCTTTCTATCATAGCACCAAGTGAATATTTTCTAAATATGACATCTCATATTAC 2379
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2380 ACCAGTAATAGACTAATAAAACTGAGGCACATTTAAGTAATATTATAAATAAAGTCAG 2439
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2440 TTAATCTAAATTTGTGAATACATCAATTTTGTGAATACATCACAGCCTATTTCGTTAAAAAT 2499
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTGGCATGAATTTCTCAGCATTAACACAT 2559
Qy 841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2560 GATTGGATCGAAGAAATCAATGGCATCCACCATTTTAAAAAGCTGATTAAACCTATTTT 2619
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2620 AATGACAAATGACTTAAGAAGTATGAATGTGAAAGGGGCATCAACAAGGTATGTTTATGAAG 2679
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2680 TATGCGCTACCGCATGAGCTTCTGACGATTTATTAAGAAGTCATCACATCTGCGCAATCA 2739
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTyrPheGlnPheAlaLeuLeuIle 920
Db 2740 ATTGATAGTGTGCAGAAATATAACACTGAGGATATTGGTTCCAAATTTGCACITTTAATC 2799
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940
Db 2800 TTAGAAAAAGAAAACCGCCCATGTATTATTAATAAACATCGACCTGACTTATATGCTTGG 2859
Qy 941 GluArgLysLeuGlnTyrThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2860 GAACGAAAAATTACAAATGGACAAATGAACAAATTCAAAGTGCAAAAAANGCGAAAAATATC 2919
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCGGTTAACAAAGTTCATTATTATATAGTATTAACGCTA 2955

RESULT 9
AR225814
LOCUS AR225814 Sequence 4 from patent US 6444447.
ACCESSION AR225814
VERSION AR225814.1 GI:27263929
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Source
1. .2979
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 3,78e-271 Length: 2979
Score: 4490.50 Matches: 843
Percent Similarity: 93.11% Conservative: 62
Best Local Similarity: 86.73% Mismatches: 60
Query Match: 87.91% Indels: 7
DB: 6 Gaps: 2
```



Qy	721	AsnThrLeuAenGlyLeuValLysLeuAenAenIlelleGluTyrAenLysAenIle	740
Db	2200	AAATACATTAACCGCTAGTGAAGAAATTAACATATTAATGAATATAATAAATAATA	2259
Qy	741	PheValIleValLeuHisValAspLysAenHisLeuThrProAepIleLysLeuGluIle	760
Db	2260	TTGGTTATTAATTCACATGTTGATGAAGATCATCTTACACGAGCATCAAAAAGAATA	2319
Qy	761	LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAenAenAepIleSerTyrTyr	780
Db	2320	TTGGCTTTCTATCATAGACCAAGTGAATATTTTACTAAATATGACATCTCATATTAC	2379
Qy	781	ThrSerAenArgLeuIleLysThrGluAlaHisLeuSerAenIleAenLysLeuSerGln	800
Db	2380	ACGAGTAATAGACTAATAAAGAACTGAGCGACATTTAAGTGAATATTAATAAATTAAGTCAG	2439
Qy	801	LeuAenLeuAenCysGluTyrIleIlePheAspAenHisAepSerLeuPheValLysAen	820
Db	2440	TTAAATCTAAATGTGAATACATCATTTTGTATTAATCATGACAGCCTATTCTGTTAAAAAT	2499
Qy	821	AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAenPheSerAlaLeuThrHis	840
Db	2500	GACAGCTATGCTTATATGAAGAAATATGATCTCGCATGAATTTCTCAGCATTAACACAT	2559
Qy	841	AspTrpIleGluLysIleAenAlaHisProPheLysLysLysLeuIleLysThrTyrPhe	860
Db	2560	GATTGGATCGAGAAATCAATCGCATCCACCATTTAAAAAGCTGATTAAAAACCTATTTT	2619
Qy	861	AsnAepAenAepLeuLysSerMetAenValLysGlyAlaSerGlnGlyMetPheMetThr	880
Db	2620	AATGACAAATGACTTGAAGATGATGAATGTGAAGGGGCATCACAAGGTATGTTTATGAAG	2679
Qy	881	TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer	900
Db	2680	TATCGCTACCGCATGAGCTTCGACGATTAATAAGAGTCATCATCTCGCAATCA	2739
Qy	901	IleAepSerValProGluTyrAenThrGluAepIleTrpPheGlnPheAlaLeuLeuIle	920
Db	2740	ATTGATAGTGTCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAATC	2799
Qy	921	LeuGluLysLysThrGlyHisValPheAenLysThrSerThrLeuThrTyrMetProTyr	940
Db	2800	TTAGAAAGAAACCGGCCATGATATTAATAAAACATCGACCCGATATATGCCCTGG	2859
Qy	941	GluArgLysLeuGlnTyrThrAenGluGlnIleGluSerAlaLysArgGlyGluAenIle	960
Db	2860	GAACGAAAAATACAAATGGACAAATGAACAAATTCAAAGTGCACAAAAAGCGAAAAATATC	2919
Qy	961	ProValAenLysPheIleIleAenSerIleThrLeu	972
Db	2920	CCCGTTAAACAGTTTCATTATTAATAGTATACGCTA	2955
RESULT 10			
AE006116			
LOCUS			
DEFINITION Pasteurella multocida subsp. multocida str. Pm70 section 83 of 204			
of the complete genome.			
ACCESSION AE006116 AE004439			
VERSION AE006116.1 GI:12721075			
KEYWORDS			
SOURCE			
ORGANISM			
Pasteurella multocida subsp. multocida str. Pm70			
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
Pasteurellaceae; Pasteurella.			
1 (bases 1 to 11885)			
REFERENCE			
AUTHORS			
May, B.J., Zhang, Q., Li, L., Paustian, M.L., Whittam, T.S. and Kapur, V.			
TITLE			
Complete genomic sequence of Pasteurella multocida, Pm70			
JOURNAL			
Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)			
PUBMED			
11248100			
REFERENCE			
2 (bases 1 to 11885)			
AUTHORS			
Zhang, Q. and Kapur, V.			

TITLE		Direct Submission	
JOURNAL		Submitted (24-OCT-2000) Department of Veterinary Pathobiology, University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN 55108, USA	
FEATURES		Location/Qualifiers	
source		1. .11885	
		/organism="Pasteurella multocida subsp. multocida str. Pm70"	
		/mol_type="genomic DNA"	
		/strain="PM70"	
		/sub_species="multocida"	
		/db_xref="taxon:272843"	
gene		205..2073	
		/gene="hyaE"	
		/note="synonym: PM0774"	
CDS		205..2073	
		/gene="hyaE"	
		/codon_start=1	
		/transl_table=11	
		/product="HyaE"	
		/protein_id="AAK02858.1"	
		/db_xref="GI:12721076"	
		/translation="MKKVIIGHKOSNYQDVEKVFQCYGMNPLPKSKREKMSPIEIGH VLNKVLPSEHTPKVSVLLSNKSKTKKNSAKNGHKUAKTNTIOTTSIMDNLSLD LMLANTEQFWGSDPNALQILDYWANLDPNIHFVYDKPENLFQYHSEALAKLDK HTVQEPQEWQYNEKILYFYFNKYKDRSVLNTQLOQNTKTSLSIYKHISAPDALV KLNPSLNKMEIIEVNQDLSHQBECPISNFIVSQIKNPSPTVQYVEELQSHADLP YSEQLVNDADFPALLAKWDMIQKVDVNOYQHEKELELSITIKEROLEVTERVOLTEQ KLSQKEIEIQIKDENRKVKSKAKTASVQSTLSBSKEKEISCTKSNTKIKEEK KIDEAYHLTKTILSDKEKALATHODEIBALKIIFNENISVQEDMOBKFOEANKRQOE LEQELAKISDKKALLETENSOKTOVSELENENKVLAAQLIQELEKLYIDNOVLK AKPRLGAADRINKQUTYRGLYKIQRHGRLSGLIIFLPILFTFYFGFKREMKKYENN TUPPIHEYEDAHEANRIKSHLSYKGLGVLFQEIINNPFKMTLPLFKLKEGKRPAQG 2090..4987	
gene		2090..4987	
		/gene="PM0775"	
CDS		2090..4987	
		/gene="PM0775"	
		/codon_start=1	
		/transl_table=11	
		/product="unknown"	
		/protein_id="AAK02859.1"	
		/db_xref="GI:12721077"	
		/translation="NMTLSQAKAYNSNDYELAKLFEKSAETVGRKIVFQIICKKE KUSTNSYSEDKKNVCDSSLDIATQALLSNVKKILSSEKSNLKNKWSITGKSE NABIRKVELVPDFPKDLVLAFLPDHVNDFWTYNNRKKSLGIRPNKNKIGLSIIPF NSRIIDITLACLNVOKTNYPFVAVDADGSKENLLTIYQKYQKLDIKVQRQDYGN QLCAVNGLRTAKYDFVSLDCDMAAPQMLVHSYLTLELNDIIVLIGPRKYVDTHN ITAEQFLNDPPLYIESLPETATNNPSITSGNISLDWRLEHFKKLTNLRCLDSPFRYF SCGNVAFSKMLNKVGFDEEFNHWGGEVFCGYRLFAKGCFFRVIDGWAYHQEPG KENETREAGKSTILKIVKEVPYIYRKLPIEDSHIRIPLVSIYPAANCANYIQR CVDNALQTVVDLEVCICNDGSDNTLEVNKUGNNPRVIRMSKNGGSIASNAAY SFAGYYIQQLSDDDYLEPDAVELCKELKDKTLACVYTTNRNVNPDGSLIANGYV ICYVNLHGDNITSIKNLDTKQKHFFVVVNSQSLNRQSVNYSYVDFONLSEKRYFNK PEPFREKLTTAMIAHFRMFTIRAMHLTDGFNEKIENAVDYDMFLKLSEVGKPKHLNK TADYQSEIDILKDIKIVQRDAKVAISIPNRLDGLVKKLANIIEYKNVLIIVLHI DNKHLSDIKKEILEFHNKQNIILLANDVSYTNNRLIKTAKHLSNMNKLQNLNL EYIIFDNHDSLEIFKNDYINHKYIDGMNPFSSLTNDWINKINAHSPKNIUKTFNDN DLKTIINKGASQGMFIKYTLAHDIAITIMKEVITLCQSDSVPEYNTEDIWFQALLIL EKKTGHVFNKTSITLYMPWERKLQWTNEQIESARGENIPVNKFIINSITL" 5051..6223	
gene		5051..6223	
		/gene="PM0776"	
CDS		5051..6223	
		/gene="PM0776"	
		/codon_start=1	
		/transl_table=11	
		/product="unknown"	
		/protein_id="AAK02860.1"	
		/db_xref="GI:12721078"	
		/translation="MKKTIAGAGYVGLSNAVLAAQHNVILLIDONKVDLNNKKS PITDKSEIDFQNKSLTMMATTDKEVALKNADEVIITATPDYNTETGYFNSTVEAVI EQTLSINPQATIIIKSTIPVGTENNREKFNPLNIFSPFEFLREGKALYDNLVPSRII VGSTSYOAKVFADMLTQCARKKDVTLFTHNTEAEAVKLFANTYLAARVAFVFNELDTY ASLHLNTKDIINGISTDPRIGTHYNNPSFGYGYCLPKDTKQLLANYADVQNLI EA	

gene  
CDS  
10789..11448  
/gene="hexa"  
/codon\_start=1  
/transl\_table=11  
/product="Hexa"  
/protein\_id="AAK02865.1"  
/db\_xref="GI:12721083"  
/translation="MIYVENCKKYLNRCTWHTVLDVVSLSLRGKQKVGILGKNGAGK  
STLIRLSGVEPTSGKITRMSISWPLGFGAPQGSITGMDNURFIARIYNADIDYV  
KRTEPESELGKLYLEPVTYSKMKARLAFALSLSIEFCYLDDEIYAVGDARFADK  
KXKPELPEKRDRLSLVSHSPNAIREYCDNAVVLHNGIMHHPNSIDIAIYQPHNALQT  
K"  
complement(11484..11813)  
/gene="PM0782"  
complement(11484..11813)  
/gene="PM0782"  
/codon\_start=1  
/transl\_table=11  
/product="unknown"  
/protein\_id="AAK02866.1"  
/db\_xref="GI:12721084"  
/translation="METLDKIKKQISENPILIIYMKGSPKFPSCGFSARAVALMHCKV  
PFGYVDILQHPDIRAELPAYANWPTFFQLWVDGELVGCDIILEMFQOGLQTLIADV  
AAKYPQE"  
gene  
CDS  
ORIGIN  
Alignment Scores:  
Pred. No.: 3.06e-259 Length: 11885  
Score: 4310.50 Matches: 803  
Percent Similarity: 91.56% Conservative: 85  
Best Local Similarity: 82.61% Mismatches: 77  
Query Match: 84.39% Indels: 7  
DB: 1 Gaps: 2  
US-10-642-248-2 (1-972) x AB006116 (1-11885)  
QY 1 MetAenThrLeuSerGlnAlaIleLysAlaTyrAenSerAenApyTyrGlnLeuAlaLeu 20  
Db 2090 ATGAATACATTATCACAGCAATAAAGCATATATACAGCAATGACTATGAAATTAGCCTC 2149  
QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 2150 AAATATTATTGAGAAGTCTGCTGAAACCTACGGCGGCAAAATCGTTTGAATTTCCAAATTATC 2209  
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen 60  
Db 2210 AAATGTAAGAAATAACTC-----TCGACCAATTCT-----TATGTAAGT 2248  
QY 61 LysGluGluLysValAenValCysAenSerProLeuAenAlaThrGlnLeuLeuLeu 80  
Db 2249 GAAGATAAAAAAACAAGTGTTCGATAGCTCATAGATATATCGCAACACAGCTCTTACTT 2308  
QY 81 SerAenValLysLysLeuValLeuSerAenSerGluLysAenThrLeuLysAenLysTyr 100  
Db 2309 TCCACAGCTAAAAAATAACTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 2368  
QY 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120  
Db 2369 AAATCTATCACTCGGAAAAAATAATCGAGAACGAGAAATCAGAAAGTGGAACTAGTACCC 2428  
QY 121 LysAenPheProLysAenLeuValLeuAlaProLeuProAenPHisValAenAenPheThr 140  
Db 2429 AAAATTTTCTTAAAGATCTTGTCTTCCTCCATTCAGATCATGTAAATGATTATTACA 2488  
QY 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
Db 2489 TGGTACAAAAATCGAAAAAACAAGCTTAGGTATAAAGCCCTGTAAATAAGAAATATCGCTCT 2548  
QY 161 SerIleIleValThrThrPheAenArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 2549 TCTATTATTATTCCTACATTTTAATCGTACCGCTATTATAGATATTAACGTTAGCTGTTG 2608  
QY 181 ValAenGlnLysThrHisTyrProPheGluValIleValThrAenAenPheGlySerGlnGlu 200

IVKSNTRKRFITHVLNKKPKTVGIYRILIMKSGDNFRASAILDIMPILKENGVEIV  
IYEPTLQAQPEDYPVINQLSEFINRSDVILANRSEPLNQCSHKIYTRDIFGDA"  
6216..7649  
/gene="PM0777"  
/codon\_start=1  
/transl\_table=11  
/product="unknown"  
/protein\_id="AAK02861.1"  
/db\_xref="GI:12721079"  
/translation="MLNLFKLIKIKYHIQSLHKEVALLYAKIINQLSINQQAIVIC  
QLKLYDLFIDPKWSHSVFFQLGIARGHDSDEMVRRLITCDFSKNQLILSOLL  
AYEQIATVLCPTVRYRALYLSLLANKDFEKLKELNKLPSCLVKNTPHYCILLQNF  
VEKSKKLENIQFLPYKLGELTIKTEDPPTNNIVSHSIVNDNTYKNIAPIITI  
LVTFNSQKSKINTLSLFPQSYENIEIIVDDHSQDNTWSILOAYTKOVKNIKIISL  
KENGVTVAKNIGYKAGSEFITCQSDDDWAHPQKALQVAPLQHKELIVTFKWR  
LDPIGNFYATYPLMRNPSLSALFRKKEVCEKALMDWRIGADSEFNARLKLIFGH  
KGYTVNKPFLTFGAHRNLSMTAQSTGYVGVSLPREAYWKAWNWIHSIQORGHAPL  
LSSSPKREFFOYDQHPIMDVISAIIN"  
7668..8849  
/gene="hexd"  
/note="synonym: PM0778"  
7668..8849  
/gene="hexd"  
/codon\_start=1  
/transl\_table=11  
/product="Hexd"  
/protein\_id="AAK02862.1"  
/db\_xref="GI:12721080"  
/translation="WKPKITLSISFTTILLAGCHSMPTSGPAQNHIIGLKKPQNESL  
PSVDIENKDVANTLFRKQKOSFTQPKQSNYADIINVGDITLDVLIWEAAPAILF  
GSVLSQTSGGANLTLPQIIVARGKITIPLGLILVKGTPEQIORDIAHALSSLA  
NKQVIVLRNKNNSKNTILKQGNVRLNLSNDVTLNKLPLSLTGLAAGLTNNKQVFSANGL  
TRGEVKMLSLKATHPEENILNLSNDVTLNKLPLSLTGLAAGLTNNKQVFSANGL  
TLAEGIGEMGQLLRADPKGVFPYRPIYFPNKLSLAECQTKWARGYDNDMEIPTVYSV  
NLLNPNALFWLQRPFIQDKDLVYVSNAPMAEFQKFLKLVFSITSPVTGLHNINVIKN  
1"  
8859..9995  
/gene="hexc"  
/note="synonym: PM0779"  
8859..9995  
/gene="hexc"  
/codon\_start=1  
/transl\_table=11  
/product="HexC"  
/protein\_id="AAK02863.1"  
/db\_xref="GI:12721081"  
/translation="MIETKMKQKPKWKRFRKISTLPKYMVILPTCCSLFYFLSLWA  
SDIYISQSFVVRTPKQALSGVALLQSSGFARAQDDTVTQEFMRSLTELEK  
SIPKQFEDKGLFSRPNLNIQSEAEAFQYFYSKLSVNFDSVSGIATINIRAFDP  
KEAQINGELKQGBYLINRNERAKOTVMAELAVSEAEKKVTSLSAISEYRIKN  
GVFDLQSSQEVQLSISTIQNELITITQLOQVRSISPNPQVOTLLARANSIRKEMQ  
QQVQVLGGNSIVTQAEYQRLVNLTLAQQLGTAITSIQNARSEADROQLYLEII  
SYNPEPDALBRYLNLATLFIISILYGITLLLASIREHKN"  
9995..10792  
/gene="hexb"  
/note="synonym: PM0780"  
9995..10792  
/gene="hexb"  
/codon\_start=1  
/transl\_table=11  
/product="HexB"  
/protein\_id="AAK02864.1"  
/db\_xref="GI:12721082"  
/translation="MLYDDQTTLKHAFIIONRIVIGALLMREIITRYGRKNLGLFLWLFV  
EPLTWGLMILWMSFRADQFSNAINMAFMITGYPLMMWRNRAICGANSANSTLL  
YHRNVRVLTILVRMILEISGATIAQVLMSPCIALDMLPMPQDDI FYMLLAWFLAIF  
AIGFGFICISIHLEVFQKWLGSFAMPLUSGTFFFVYNLPQAREVILLWMPMIGH  
SEMFRHGVGDSVITLENPYFLILCDLIFLLIGLLMVAHFSGKIGBPR"  
10789..11448  
/gene="hexa"  
/note="synonym: PM0781"

2609	Db	 GTCAATCAGAAAA	 CAAAACTACCC	 ATTGAAAGTCGTTGTTG	 TCAGATGATGGTAGTAAGGAA	2668	
201	Qy	AspLeuSerProIlelle	ArgGlnTy	GluasnLysLeu	AspIleArgTy	ValArgGln	220
2669	Db	AACTTACTTACCAT	TGTGCAAAATACG	AAACAACTTGACAT	AAATATGATGTAAAGCAA	2728	
221	Qy	LysAspAsnGlyPhe	GlnAlaSer	AlaAlaArgAsnMet	GlyLeuArgLeuAlaLysTy	240	
2729	Db	AAAGATTATGGAT	ATCAATTGTGTGCAGT	CAGAAACTTAGGTTACGT	CACGCAAGTAT	2788	
241	Qy	AspPheIleGlyLeu	LeuAspCysAspMet	AlaProAsnProLeu	TyrValHisSerTy	260	
2789	Db	GATTTTGTCTCGAT	CTTAGACTCGGATATG	GCACCAACAATAT	TATGGGTTCTATCTTAT	2848	
261	Qy	ValAlaGluLeuLeu	GluAspAspAspLeu	ThrIleIleGlyPro	ArgLysTyIleAsp	280	
2849	Db	CTTACAGAACCT	TATTAGAAACAATGAT	TATTTTAAATTTGGAC	TACAGAAATATGTCGAT	2908	
281	Qy	ThrGlnHisIleAsp	ProLysAspPheLeu	AsnAsnAlaSerLeu	LeuGluSerLeuPro	300	
2909	Db	ACTCATTAATAT	TACCGCAGAACAA	TTCTTAAACGATCCAT	TATTTAATAGATCACTACCT	2968	
301	Qy	GluValLysThrAsn	AsnSerValAla	AlaLysGlyGluGlyThr	ValSerLeuAspTyr	320	
2969	Db	GAACCCGCTACA	AAATAACAATCTTCGAT	TATACATCAAAAGGAA	TATATCGTTGGATTGG	3028	
321	Qy	ArgLeuGluGlnPhe	GluLysThrGlu	AsnLeuArgLeuSer	AspSerProPheArgPhe	340	
3029	Db	AGATTAGAACAT	TTTCAAAAAACCGAT	ATCTACGTCTATGTGAT	TATCACCGTTTCGTAT	3088	
341	Qy	PheAlaAlaGlyAsn	ValAlaPheAla	LysLysTyPheLeu	AsnLysSerGlyPhePheAsp	360	
3089	Db	TTTAGTTGGGT	TAATGTTGCATTTCT	TAAAGAATGGCTTAA	TAAATAGGTGGTTGCAT	3148	
361	Qy	GluGluPheAsnHis	TyrGlyGlyGlu	AspValGluPheGlyTyr	ArgLeuPheArgTy	380	
3149	Db	GAAGAAATTTAT	CAATTTGGGGGGCG	AGATGTAGAAATTTG	TTGTACAGATATTTGCCAAA	3208	
381	Qy	GlySerPhePheLys	ThrIleAspGlyL	IleMetAlaTyHis	GlnGluProProGlyLys	400	
3209	Db	GGCTGTTTTTT	TCAGAGTAATTTG	ACGGCGGAATGGC	ATCACCAATCAAGAACACACCTGGTAA	3268	
401	Qy	GluAsnGluThrAsp	ArgGluAlaGlyLys	AsnIleThrLeuAsp	IleMetArgGluLys	420	
3269	Db	GAAATGAAACAG	ACCGGAAGCTGTT	AAAGTATTACGCTT	AAAAATTTGGAAGAAAAG	3328	
421	Qy	ValProTyrIleTy	ArgLysLeuLeuPro	IleGluAspSerHis	IleAsnArgValPro	440	
3329	Db	GTACCTTACAT	CTATAGAAAGCTTTT	ACCAATAGAGATT	CACATATTCATAGAAATACCT	3388	
441	Qy	LeuValSerIleTy	IleProAlaTy	zAsnCysAlaAsnTy	IleGlnArgCysValAsp	460	
3389	Db	TTAGTTTCTAT	TTTATATCCCGCTT	ATACTGTGCAATTA	TATATCAAAAGATGTGTAGAT	3448	
461	Qy	SerAlaLeuAsnGln	ThrValValAspLeu	GluValCysIleCys	AsnAspGlySerThr	480	
3449	Db	AGTGCCTCTTA	ATCAAACTGGTTCG	ATCTCGAGGTTGTAT	TTTGTACGATGGTGTCAACA	3508	
481	Qy	AspAsnThrLeu	GluValIleAsnLys	LeuTyGlyAsnAsnPro	ArgValArgIleMet	500	
3509	Db	GATAATACCT	TAGAGTGATCAATA	AGCTTTATGGTAAT	TAATCTCCTAGGTACGCATCATG	3568	
501	Qy	SerLysProAsnGly	IleIleAlaSer	AlaSerAsnAlaVal	SerPheAlaLysGly	520	
3569	Db	TCTAAACCAAAT	TGGCGGAATAGCCT	CAGCATCAAAATG	CAGCGCGTTTCTTTTGTCTAAAGGT	3628	
521	Qy	TyrTyIleGlyGln	LeuAspSerAspTy	IleLeuGluProAsp	AlaValGluLeuCys	540	
3629	Db	TATTACATTGGC	AGTTAGATTTCAGAT	GAATATCTTGAGCC	TGATGACGATGCGATGTTGAATCTGT	3688	
541	Qy	LeuLysGluPheLeu	LysAspLysThrLeu	AlaCysValTyThr	ThrAsnArgAsnVal	560	

3689	Db	TTTTAAAGAAATTTTAAAAAGATAAAAACGCTAGCTTGTTGTTTATACCACTAATAGAAACGCT	3748
561	Qy	AsnProAspGlySerLeuIleAlaAsnGlyTyrrAsnTrpProGluPheSerArgGluLys	580
3749	Db	AATCCGGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTCCACGAGAAAAA	3808
581	Qy	LeuThrThrAlaMetIleAlaHisHispeArgMetPheThrIleArgAlaTrpHisLeu	600
3809	Db	CTCACAAACGGCTATGATTTGCTCACCACTTTAGAAATGTTTACAGATTAGAGCTTGCGCATTTA	3868
601	Qy	ThrAspGlyPheAsnGluLysIleGluAenAlaValAspTyrrAspMetPheLeuLysLeu	620
3869	Db	ACTGATGGATTCATGAAAAATTTGAAAAATGCCGTAGACTATGACATGTTTCCCTAAAAAATC	3928
621	Qy	SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrrAsnArgValLeuHisGly	640
3929	Db	AGTGAGGTTGGAAATTTTAAGCATCTTAATAAAATTTGTTATAACCGCGTATTACATGGT	3988
641	Qy	AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn	660
3989	Db	GATAATACATCAATTAATAAATCTAGACACTCAAAAGAAAAATCATTTGTTGTCGTTAAT	4048
661	Qy	GlnSerLeuAsnArgGlnGlyIleThrTyrrTyrrAsnTyrrAspGluPheAspAspLeuAsp	680
4049	Db	CAATCATTAATAATAGGCAGAGAGTAAGTAATTAATTAACCTATGATGAATTCGATAATCTTAGAT	4108
681	Qy	GluSerArgLysTyrrIlePheAsnLysThrAlaGluTyrrGlnGluGluIleAspIleLeu	700
4109	Db	GAAAGTAGAANAATACATTTTCATTAACACAGCAGATTAATCAGAGNAATTTGATATTCTA	4168
701	Qy	LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrrPro	720
4169	Db	AAAGATATCAAAATAGTACAGCGTAAAGATGCAAAAGTTGCAATAAGTATATTTTATCCCA	4228
721	Qy	AsnThrLeuAsnGlyLeuValLysLysLysLysAsnAsnIleIleGluTyrrAsnLysAsnIle	740
4229	Db	AATAGATTAGATGGGTGTTAGTTAAAAAATTAACAAATATTATCGAATATAACAATAATGTA	4288
741	Qy	PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle	760
4289	Db	CTCATTTATGTTTACCATTTGACAAANAATCATCTCACATTCAGACATCAANAAGGAATA	4348
761	Qy	LeuAlaPheTyrrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrrTyr	780
4349	Db	CTAGAAATTTTCATAACAGAATCAAAATCAATATCTTGTAAATAATGATGTTCTTTATATAT	4408
781	Qy	ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln	800
4409	Db	ACAACAACAGCGCTCAATAAAATCTAAAGCTCATTTAAGCAATATAGAACAGTTTAAGACAA	4468
801	Qy	LeuAsnLeuAsnCysGluTyrrIleIlePheAspAsnHisAspSerLeuPheValLysAsn	820
4469	Db	CTAAATCTTAATTTAGANAATATATATTTTTTGACACCAATGACAGCCTATTTATTAANAAT	4528
821	Qy	AspSerTyrrAlaTyrrMetLysLysTyrrAspValGlyMetAsnPheSerAlaLeuThrHis	840
4529	Db	GATAGTTATAACCATATAAAAAATATGATATCGGCATGAATCTCTCTCATTAACCAAT	4588
841	Qy	AspTrpIleGluLysIleAsnAlaHisProProPheLysLysIleLysThrTyrrPhe	860
4589	Db	GAITGGATAAATAAATAATATGACACATCAACCAATTTAAAAATCTCGATAAAAAAATATTTT	4648
861	Qy	AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr	880
4649	Db	AATGATTAATGATTTTAAANAACATAAATAATGAAAGCGCGTCACAGGAATTTTCATAAAA	4708
881	Qy	TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer	900
4709	Db	TACACTTTAGCACATGATATTGCTACGATTATGAAGAAGTCATTACATTATGCAATCT	4768
901	Qy	IleAspSerValProGluTyrrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle	920
4769	Db	ACAGATAGTGTCTCGAATAATAATCTGAAGAATATTTGGTTCCAAATTTGCACTTTAATC	4828



```
Qy 921 LeuGluLysValThrGlyHisValPheAsnLysThrSerThrLeuThrTyMetProTyr 940
Db 4829 TTAGAAAGAAACCGGCATGATATTTAATAAATCGACCTGACTTATATGCTTGG 4888
Qy 941 GluArgLysLeuGlnTrrThrAsnGluGlnLeuGluSerAlaLysArgGlyGluAunle 960
Db 4889 GAACGAAATTTACAAATGGACAAATGAACAAATGAAAGTGCAGAAAGAGGAGAAATATA 4948
Qy 961 ProValAsnLysPheLeuLeuAsnSerLeuThrLeu 972
Db 4949 CCTGTAAACAGTTTCATTTAATAGTATACTCTA 4984

RESULT 11
LOCUS AY604234 3156 bp DNA linear BCT 12-MAY-2004
DEFINITION Pasteurella multocida strain J-4103 glycosyltransferase Fcbd (fcbb)
gene, complete cds.
ACCESSION AY604234
VERSION AY604234.1 GI:47080018
KEYWORDS Pasteurella multocida
SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
1 (bases 1 to 3156)
Jaglic,Z. and Bartos,M.
The first detection of Pasteurella multocida serogroup F in
rabbits: analysis of serogroup F specific fcbd gene
Unpublished
2 (bases 1 to 3156)
Jaglic,Z. and Bartos,M.
Direct Submission
Submitted (22-APR-2004) Bacteriology, Veterinary Research
Institute, Hudcova 70, Brno 62132, Czech Republic
FEATURES
source
1. 3156
/organism="Pasteurella multocida"
/mol_type="genomic DNA"
/strain="J-4103"
/db_xref="taxon:747"
/note="serogroup: F"
143. 3040
/gene="fcbd"
143. 3040
/gene="fcbd"
/note="chondroitin synthase"
/codon_start=1
/transl_table=11
/product="glycosyltransferase Fcbd"
/protein_id="AA10183.1"
/db_xref="GI:47080019"
/translation="NNTLSQAIAKAYNSNDYELALFKSAETVGRKIVFQIKKKE
KLSVTSYSEDKNSVCDSSLDIATQLLSNVKLTLSSEKNSLNKWSITGKKE
NAEIKVELVPKDPKDLVPLPDVNDFTWKNRKSGLGKPVNKGILSIIPTF
NRSRLDITLACLVNKNTPYEVVADGSKENLITVQKYEQKLDI KYVRKDYGY
QUCVNRGLRTAKDYFVSLDCDMPQQLWVHSLTELLEDNDIVLIGPRKYVDTH
ITAEQFLNDPYLIESLPETATNNPSITSGNLSUDWRLEHFKFTDNDLRUCDSPRYF
SCGNVAFSKWLNKGVFDEEFHWGDEVEFGRLPFKGCTFRVIDGGMAYHQBPYP
KENEDTAGKSIITLKI VKEKVPYIYRKLIEDSHIRIPLVSIYI PAYNCANTYQR
ICYNVLHGDNSTIKNLTQKQNFVFNQSLNRQVSNNTYDFNDESRYI FNK
SPAKGYI GQLSDSDYLPDPAVELCLKEFLDKTLACVYTNRNVPDGLSIANGYNV
PEFSREKLTAMIAHFRTIRAWHLTDGDFNEKENIENAVDYMFLKLSVEGKFKLAK
1CYNVLHGDNSTIKNLTQKQNFVFNQSLNRQVSNNTYDFNDESRYI FNK
TADYQBEDILDKIKIVORKDAVAISIFYPNRLDGLVKLNNIIEYNKNVLIIVLHI
DKQHLTSDIKLEIFHNKQINILNNDVSYNTNRLIKTKAHLNNKRLQLNLI
EYIIFDNDLSLFIKNDSYNHI KKYDIGNFFSLDWINKINAHSPFNKLIKYPNDN
DLKTNMKGASQGMFKYTLAHDIAITIMEVITLCQSDTSVEYNTDWFQFVLLIL
EKKTHGVFNKTSITLTPWKRKLQWNEQIESAKGGENIPVKNFIINSITL"
```

Alignment Scores:  
Pred. No.:

1.25e-259 Length: 3156

```
Score: 4306.50 Matches: 802
Percent Similarity: 91.26% Conservative: 85
Best Local Similarity: 82.51% Mismatches: 78
Query Match: 84.31% Indels: 7
Db: Gaps: 2

US-10-642-248-2 (1-972) x AY604234 (1-3156)
Qy 1 MetAsnThrLeuSerGlnAlaLeuLysAlaLeuTyAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 143 ATGAATACATTATCACAAGCAATATAAAGCATATAACAGCAATGACTATGAATTAGCACTC 202
Qy 21 LysLeuPheGluLysSerAlaGluLeuTyrGlyArgLysLeuValGluPheGlnLeuThr 40
Db 203 AAATTATTGAGAGTCTGCTGAAACCTACGGCGGAGAAATCGTTGAATTCCTCAATATC 262
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 263 AAATGTAAAGAAATACATC-----TCGACCAATCT-----TATGTAAGT 301
Qy 61 LysGluLysValAsnValCysAspSerProLeuAspLeuAlaThrGlnLeuLeuLeu 80
Db 302 GAGCATAAATAAACAGTGTTCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 361
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db 362 TCCAAACGTAAATAAATTAACCTATCCGAAATCAGAAAAAACAAGTTTAAAAAATAATGG 421
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 422 AAATCTATCACTCGGAAAAAATCGAGAACCGCAGAAATCAGAAAGGTGGNACTAGTACCC 481
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 482 AAAGATTTCCTTAAGATCTTGTTCCTTCATTCATTCAGATCATGTTAATGATTTTACA 541
Qy 141 TrpTyrLysLysArgLysLysArgLysGlyLysProGluHisGlnHisValGlyLeu 160
Db 542 TGGTACAAAAATCGAAAAAAGCTTAGGTATNAAGCCTGTAAATAAGAAATATCGGCTT 601
Qy 161 SerLeuLeuValThrThrPheAsnArgProAlaLeuSerLeuThrLeuAlaCysLeu 180
Db 602 TCTATTATTCTTACATTTTAACTAGCCGTATTTAGATATATACCTTAGCCTGTGTTG 661
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValLeuValThrAspAspGlySerGlnGlu 200
Db 662 GTCAATCAGAAACAACTACCCATTTGAAGTCGTTGTCGAGATGATGGTAGTAAGGAA 721
Qy 201 AspLeuSerProLeuLeuArgGlnTyrGluAsnLysLeuAspLeuArgTyrValArgGln 220
Db 722 AACTTACTTACCATTTGTCAAAAATACGAAACAAACCTTGACATAAAGTATGTAAAGACAA 781
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 782 AAAGATTATGATATCAATTTGTGTCATCGATCGAATACTTAGTTTACGTACGCAAAAGTAT 841
Qy 241 AspPheLeuGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db 842 GATTTTGTCGATTCAGATTCGATATGCACCAACCAATTTATGGTTTCATCTTAT 901
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrLeuLeuGlyProArgLysTyrLeuAsp 280
Db 902 CTTACAGAACTATTAGAAGACAAATGATATGTTTTTAAATTTGGACCTAGAAAAATATG 961
Qy 281 ThrGlnHisLeuAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 962 ACTCATATATATCCGCGAGAACTTCTTACGATCCATTTTATAGATCCTACTTACCT 1021
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluThrValSerLeuAspTyr 320
Db 1022 GAAACCGCTACAAATACAAATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATTG 1081
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerPropheArgPhe 340
```

```
Db 1082 AGATTAGAACCTTTCAAAAACCGATATACCTGCTCTGTGATTCACCGTTTCGTAT 1141
Qy PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360
Db 1142 TTTAGTTGCGGTAAATGTTGCATTTTCTAAAGAAATGGCTAAATAAAGTAGGTTGGTTCGAT 1201
Qy GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1202 GAAGAAATTAATCAATGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTATTTCGCCAAA 1261
Qy GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1262 GGCCTGTTTTTCAGAGTAATTCACGGCGGAATGGCATACCAATCAAGAACCACTGGGTAAA 1321
Qy GluAsnGluThrAspArgGluAlaGlyAsnIleThrLeuAspIleMetArgGluLys 420
Db 1322 GAAATGAACAGACCGCGAAGCTGGTAAAAGTATTACGCTTAAATTTGTGAAGAAAAG 1381
Qy ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1382 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGATTACATATTTTCATAGAAATACCT 1441
Qy LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 1442 TTAGTTCTATTTATATCCCGCTTATAACTGTGCAAAATATATTTCAAGATGTGTAGAT 1501
Qy SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1502 AGTCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTTGTTAAGCATGGTTCAACA 1561
Qy AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1562 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATATCTTAGCGTAGCATCATG 1621
Qy SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 1622 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCGCCGGTTCTTTTGTCTAAAGGT 1681
Qy TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1682 TATTACATGGCGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCAGTTGAACGTGT 1741
Qy LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1742 TTAAGAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTTTATACCACCTAATAGAAACGTC 1801
Qy AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580
Db 1802 AATCCGATGGTAGCTTAATCGCTTAATGGTTTACAAATTTGCCAGAAATTTTACAGAGAAAA 1861
Qy LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 1862 CTCACACGGCTATGATTGCTCACCACCTTTAGATGTTTCAGATTAGAGCTTGSCATTTA 1921
Qy ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1922 ACTGATGGATTCAATGAAAAAATTCAAAAATGCCCGTAGCATATGCATGTTCTCTAAAACTC 1981
Qy SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 1982 AGTGAGGTGGAAAAATTTAAGCATCTCTAAATAAAAATTTGTTATAACCGCGTATTACATGGT 2041
Qy AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
Db 2042 GATAATACATCAATTAAAAATCTAGACACTCAAAAGAAAAATCATTTTCGTTGCTGTTAAT 2101
Qy GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680
Db 2102 CAATCATTAATAGCGCAGAGTAAGTAATTAATAACTATGATGTAATTCGATTAACATAGAT 2161
Qy GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
```

```
Db 2162 GRAAGTAGAAAAATACATTTTCAATAAAAACAGCAGATTATTCAAGAAGAAATTTGATTATCTA 2221
Qy LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2222 AAAGATATCAAAATAGTACAGCGTAAAGATGCAGAAAGTTGCAATAAGTATATTTTATCCA 2281
Qy AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 2282 AATAGATTAGATGGGTAGTTAAAAAATTAACAATATTTATCGAATATAACAANAATGTAT 2341
Qy PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2342 CTCATTATTGTTTTTACACATTGCAGAAAATCATCTCACATTCACACATCAAAAAGGAATA 2401
Qy LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
Db 2402 CTAGAATTTTCATAACAAGAAATCAATCATCTGTTAAATTAATGATGTTCTTCTTATAT 2461
Qy ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2462 ACAACAACAGCGCTCAAAAACTAAAGCTCATTTAAGCAATATGAACAAGTTAAGACAA 2521
Qy LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2522 CTAAATCTTAAATTTAGAAATATATTTTGTGACACCATGCACAGCCTATTTTATAAAAAT 2581
Qy AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2582 GATAGTTATAACCATATAAAAAATATGATATCGCATGAACCTTCTCTCATTAACAAAT 2641
Qy AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2642 GATTGATAAATAAAAAATTAATGCACACTCACCATTTTAAAAATCTGATAAAAAATATTTT 2701
Qy AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2702 AATGATAATGATTTAAAAACAATAATATGAAGGCGGTCAACAAGGAATGTTCAAAAA 2761
Qy TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900
Db 2762 TACACTTTAGCACATGATATTGCTAGCATTTATGAAAGAAGTCAATTACATTATGCCAATCT 2821
Qy IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2822 ACAGATAGTGTTCCTGAATATAATACTGAAGATATTTGGTTCCAAATTTGTACTTTTAAATC 2881
Qy LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940
Db 2882 TTAGAAAAAGAAAACCGCCATGTTATTTAATAAACATCGACCTGACTTATATGCCTTGG 2941
Qy GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2942 GAACGAAAAATTACAATCGCAAAATGAACAAATTTGAAAGTGAAGAGAGAGAGAGAAATATA 3001
Qy ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 3002 CCTGTTAAACAAGTTCAATTATTAATAGTATAACTCTA 3037

RESULT 12
AF302467 8838 bp DNA linear BCT 12-MAR-2001
LOCUS Pasteurella multocida P4218 region 2 capsule biosynthesis gene
DEFINITION cluster, partial sequence.
ACCESSION AF302467
VERSION AF302467.1 GI:13274373
KEYWORDS Pasteurella multocida
SOURCE Pasteurella multocida
ORGANISM Pasteurella multocida
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
REFERENCE 1 (bases 1 to 8838)
AUTHORS Townsend, K.M., Boyce, J.D., Chung, J.Y., Frost, A.J. and Adler, B.
TITLE Genetic organization of Pasteurella multocida cap loci and
```

development of a multiplex capsular PCR typing system  
J. Clin. Microbiol. 39 (3), 924-929 (2001)

11230405  
JOURNAL PUBLISHED  
REFERENCE 2 (bases 1 to 8838)  
Townsend,K.M., Boyce,J.D., Chung,J.Y., Frost,A.J. and Adler,B.  
Direct Submission  
TITLE Submitted (03-SEP-2000) Veterinary Pathology and Anatomy, The  
University of Queensland, School of Veterinary Science, Brisbane,  
QLD 4073, Australia  
FEATURES  
source

1..8838  
/organism="Pasteurella multocida"  
/mol\_type="genomic DNA"  
/strain="P4218"  
/serotype="F:3"  
/db\_xref="taxon:747"  
complement (<1..351)  
/gene="phya"  
complement (<1..351)  
/gene="phya"  
/note="similar to KpsS, LipA"  
/codon\_start=1  
/transl\_table=11  
/product="PhyA"  
/protein\_id="AAK17919.1"  
/db\_xref="GI:13274374"  
/translation="MSILYDRLNMYQEFLLFSKGLMKIPYLSGFFTORLKMSPFV  
TWKERTCILBWKYKASSKARHFAQQHDLFIATIEDGFLRSLGLGVNDGYPPFSLVYD  
DIGIYYDINQPSRLS"  
699..2567  
/gene="fcbg"  
699..2567  
/gene="fcbg"  
/note="similar to HyaB, KfiB"  
/codon\_start=1  
/transl\_table=11  
/product="Fcbg"  
/protein\_id="AAK17920.1"  
/db\_xref="GI:13274375"

gene  
CDS  
699..2567  
/gene="fcbg"  
699..2567  
/gene="fcbg"  
/note="similar to HyaB, KfiB"  
/codon\_start=1  
/transl\_table=11  
/product="Fcbg"  
/protein\_id="AAK17920.1"  
/db\_xref="GI:13274375"

gene  
CDS  
2584..5481  
/gene="fcbd"  
2584..5481  
/gene="fcbd"  
/note="similar to PmcS"  
/codon\_start=1  
/transl\_table=11  
/product="glycosyltransferase Fcbb"  
/protein\_id="AAK17921.1"  
/db\_xref="GI:13274376"

gene  
CDS  
2584..5481  
/gene="fcbd"  
2584..5481  
/gene="fcbd"  
/note="similar to PmcS"  
/codon\_start=1  
/transl\_table=11  
/product="glycosyltransferase Fcbb"  
/protein\_id="AAK17921.1"  
/db\_xref="GI:13274376"

gene  
CDS

5545..6717  
/gene="fcbc"  
5545..6717  
/gene="fcbc"  
/codon\_start=1  
/transl\_table=11  
/product="UDP-glucose dehydrogenase Fcbb"  
/protein\_id="AAK17922.1"  
/db\_xref="GI:13274377"

gene  
CDS  
6710..8143  
/gene="fcbg"  
6710..8143  
/gene="fcbg"  
/codon\_start=1  
/transl\_table=11  
/product="glycosyltransferase Fcbb"  
/protein\_id="AAK17923.1"  
/db\_xref="GI:13274378"

gene  
CDS  
8162..>8838  
/gene="hexD"  
8162..>8838  
/gene="hexD"  
/note="similar to hexD"  
/codon\_start=1  
/transl\_table=11  
/product="hexD"  
/protein\_id="AAK17924.1"  
/db\_xref="GI:13274379"

gene  
CDS  
8162..>8838  
/gene="hexD"  
8162..>8838  
/gene="hexD"  
/note="similar to hexD"  
/codon\_start=1  
/transl\_table=11  
/product="hexD"  
/protein\_id="AAK17924.1"  
/db\_xref="GI:13274379"

#### ORIGIN

Alignment Scores:  
Pred. No.: 8,03e-259 Length: 8838  
Score: 4301.50 Matches: 802  
Percent Similarity: 91.15% Conservative: 84  
Best Local Similarity: 82.51% Mismatches: 79  
Query Match: 84.21% Indels: 7  
DB: 1 Gaps: 2

US-10-642-248-2 (1-972) x AF302467 (1-8838)

Qy 1 MetAenthLeuSerGlnAlaIleValTyAenSerAenAseTyGlnLeuAlaLeu 20  
Db 2584 ATGAATACATTATCAACAGCAATAAAGCATATACAGCAATGACTAGTAATAGCACTC 2643  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyGlyArgLysIleValGluPheGlnIleThr 40  
Db 2644 AAAATTATTGAGAGCTGCTGCTGAAACCTACGGGGGAGAAATCGTTGAAATTCCTCAATTATC 2703

DKNHLTSDIKKEILEFHNKNQINILNNDVSYTNRLIKTKAHLNMMKLRQLNLNL  
EYIIFDNHSLFKNDKSYNHIKKYDIGNMFPSSLTNDWINKINAHSPKLIKKTFNDN  
DLKTIINMGASQGMFIKYTHLAIDIATIMKEVITLCQSDSPBYNTEDIFQFALLIL  
EKKTGHVFNKSTLTLYMPWERKLTQWNEQIESARGENIPVNKFIINSITL"

5545..6717  
/gene="fcbc"  
5545..6717  
/gene="fcbc"  
/codon\_start=1  
/transl\_table=11  
/product="UDP-glucose dehydrogenase Fcbb"  
/protein\_id="AAK17922.1"  
/db\_xref="GI:13274377"

gene  
CDS  
6710..8143  
/gene="fcbg"  
6710..8143  
/gene="fcbg"  
/codon\_start=1  
/transl\_table=11  
/product="glycosyltransferase Fcbb"  
/protein\_id="AAK17923.1"  
/db\_xref="GI:13274378"

gene  
CDS  
8162..>8838  
/gene="hexD"  
8162..>8838  
/gene="hexD"  
/note="similar to hexD"  
/codon\_start=1  
/transl\_table=11  
/product="hexD"  
/protein\_id="AAK17924.1"  
/db\_xref="GI:13274379"

ORIGIN  
Alignment Scores:  
Pred. No.: 8,03e-259 Length: 8838  
Score: 4301.50 Matches: 802  
Percent Similarity: 91.15% Conservative: 84  
Best Local Similarity: 82.51% Mismatches: 79  
Query Match: 84.21% Indels: 7  
DB: 1 Gaps: 2

US-10-642-248-2 (1-972) x AF302467 (1-8838)

Qy 1 MetAenthLeuSerGlnAlaIleValTyAenSerAenAseTyGlnLeuAlaLeu 20  
Db 2584 ATGAATACATTATCAACAGCAATAAAGCATATACAGCAATGACTAGTAATAGCACTC 2643  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyGlyArgLysIleValGluPheGlnIleThr 40  
Db 2644 AAAATTATTGAGAGCTGCTGCTGAAACCTACGGGGGAGAAATCGTTGAAATTCCTCAATTATC 2703

```
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 2704 AAATGTAAGAGAAAACATC-----TCGACCAATTCCT-----TATGTAAGT 2742
Qy 61 LysGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 2743 GAAGATAAAAAACACAGTGTTCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 2802
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100
Db 2803 TCCAAACGTAAAAAAATTAACCTCTATCCGAATCAGAAAAAACACAGTTTAAAAAATAAATGG 2862
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 2863 AAATCTATCACTGGGAAAAAATCGGAGAACCGAANAATCAGAAAGGTGGAACTAGTACCC 2922
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 2923 AAAGATTTTCTTAAGATCTTGTTCTTCCTCCATTCGACAGATCATGTTAATGATTTTACA 2982
Qy 141 TrpTrpLysLysArgLysLysArgLeuGluLysLysProGluHisGlnHisValGlyLeu 160
Db 2983 TGGTACAAAAATCGAAAAAAGCTTAGGTATAAGCCTGTAATAAAGAAATATCGGTCTT 3042
Qy 161 SerIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 3043 TCTATTATTACTCTCATTTAATCGTAGCGGTATTTTAGATATAAGCTCAGCCTGTGTTG 3102
Qy 181 ValAsnGlnLysThrHisTrpProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 3103 GTCAATCAGAAAAACAACTACCCATTTGAAGTCTGTTGCAGATGATGGTAGTAAGGAA 3162
Qy 201 AspLeuSerProIleIleArgGlnTrpGluAsnLysLeuAspIleArgTrpValArgGln 220
Db 3163 AACTTACTTACCATTTGCAAAAAATAGCAACAAAACTTGACATAAAAGTATGTAAAGCAA 3222
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 3223 AAAGATTATGGATATCAATTGTGTGCAGTCAGAACTTAGGTATTACGTACAGCAAAAGTAT 3282
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260
Db 3283 GATTTTGTCTCGATTCAGATCGCATATGCCACCAACAATTTATGGTTTCACTTCTAT 3342
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTrpIleAsp 280
Db 3343 CTTACAGAACTATTAGAAGACAAATCATATGTTTAAATTTGGACCTAGAAAAATATGTGGAT 3402
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db 3403 ACTCATATATTACCGCAGAAACAATTCCTTAACGATCCATATTTAATAGAAATCACTACCT 3462
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320
Db 3463 GAAACCGCTACAATAACAATCCTTCGATTACATCAAAAGGAATATATCCTGTGGATTGG 3522
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 3523 AGATTAGAACTTTCAAAAAAACCCGAAATCTACGTCTATGTGATTCACCGTTTCGTTAT 3582
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysTrpLeuAsnLysSerGlyPheAsp 360
Db 3583 TTTAGTTGCGGTAAAGTTTTCATAAGAAATGGCTAAATAAAGTAGGTGGTTGGTTCGAT 3642
Qy 361 GluGluPheAsnHisTrpGlyGlyLeuAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 3643 GAAGAAATTAATCATTTGGGGGGCGAAGATGATAGAAATTTGGTTACAGATTATTTGCCAAA 3702
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 3703 GGCTGTTTTTTCAGAGTAATTTGACGGCGGAATGGCATACCATCAAGAACCACTCGTAA 3762
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420
```

```
Db 3763 GAAAATGAACACAGACCGCGAGCTGCTAAAAGTATTACGCTTAAATTTGTGAAGAAAAG 3822
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 3823 GTACCTTACATCTATAGAAAAGCTTTTACCAATAGAAAGATTCACATATTCATAGAACTCT 3882
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db 3883 TTAGTTTCTATTATATCCCGCTTATAACTGTGCAAAATATATATCAAGATGTGTAGAT 3942
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 3943 AGTGTCTCTTAATCAAACTGTTCGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA 4002
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 4003 GATAATACCTTTAGAACTGATCAATAAGCTTTATGGTAATAATCTTAGGGTACGCATCATG 4062
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db 4063 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCAGCCGTTCTTTTGTCTAAAGGT 4122
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 4123 TATTACATTTGGGCAGTTAGATTTCAGATGATTATCTTGAGCCTCATGCAGTTGAACGTGT 4182
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560
Db 4183 TTAAGAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAAACGTC 4242
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580
Db 4243 AATCCCGATGGTAGCTTAATCGCTAATGGTTTACAATTTGGCCAGAAATTTTCCAGGAGAAA 4302
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600
Db 4303 CTCACAACGGCTATGATGCTCACCACTTTAGTAATGTTTCAGCATTAGAGCTTGGCAATTA 4362
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db 4363 ACTGATGATTTCAATGAAAAAATGAAAAATGCGGTAGACTATGACATGTTCTCTAAAAACTC 4422
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
Db 4423 AGTGAGGTGGAATAATTAGCATCTTAATAAATTTGTTATAACCCCGTATTACATGCT 4482
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660
Db 4483 GATAATACATCAATTAATAATCTTAGACACTCAAAAGAAAAATCATTTTCGTTGCTTAAT 4542
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 4543 CAATCATTAATAGGCAGAGAGTAAGTAATATATAACTATCATGTAATTCGATAACTTAGAT 4602
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 4603 GAAAGTAGAAAAATACATTTTCAATAAAACAGCAGATATTCAAGAAAGAAATTTGATTCTTA 4662
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 4663 AAAGATATCAAAATAGTACAGCGTAAGATGCAAAAGTTGCAATAGTATATTATTATCCA 4722
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740
Db 4723 AATAGATTAGATGGTTAGTTAAATAAATAAATAATTAATATCAATAATAACAATAATGTA 4782
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 4783 CTCATTATTGTTTACACATTTGACAAAAATCATCTCACTTCAGACATCAAAAGGAATA 4842
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
```



```
Qy 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTir 320
Db 901 GAGGTGAACCAATAATAGTTTCCGCCAAGGGAAGGAAACAGTTTCTCTGGATGG 960
Qy 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAspSerProPheArgPhe 340
Db 961 CGCTTAGAACAAATTCGAAAAACACAGAAAAATCTCCGCTTATCCGATTCGCCTTCCTCGGTTTT 1020
Qy 341 PheAlaAlaGlyAenValAlaPheAlaLysLysThrLeuAenLysSerGlyPhePheAsp 360
Db 1021 TTTTCGCGCGGTATGTGTCTTCGCTAAAAAATGGCTAAATAAATCCGGTTCTTTTGAT 1080
Qy 361 GluGluPheAenHisTirGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1081 GAGGAATTTAATCACTCGGGTGGAGAAGATGTGGAATTTGGATATCCCTTATTCGGTTAC 1140
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db 1141 GGTAGTTTCTTTAAACTATTGATGGCATTATGSGCTTACCATTCAAGAGCCACCAGGTAAA 1200
Qy 401 GluAenGluThrAspArgGluAlaGlyLysAenIleThrLeuAspIleMetArgGluLys 420
Db 1201 GAAAAATGAAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGACAGAAAAAG 1260
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAenArgValPro 440
Db 1261 GTCCCTTATATCTATAGAAACCTTTTACCATAAGATTCGCATATCAATAGAGTACCT 1320
Qy 441 LeuValSerIleTyrIleProAlaTyrAenCysAlaAenTyrIleGlnArgCysValAsp 460
Db 1321 TTAGTTTCAATTTATATCCCGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380
Qy 461 SerAlaLeuAenGlnThrValValAspLeuGluValCysIleCysAenAspGlySerThr 480
Db 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGTTTGTATTGTTAAACGATGGTTCAACA 1440
Qy 481 AspAenThrLeuGluValIleAenLysLeuTyrGlyAenAenProArgValArgIleMet 500
Db 1441 GATAAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATATCTTAGGGTACGCATCATG 1500
Qy 501 SerLysProAenGlyIleAlaSerAlaSerAenAlaAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAATGSCGAATAGCTCAGCATCAATGCAGCGTTCTTCTTGTCTAAAGGT 1560
Qy 521 TyrTyrIleGlyGlnLeuAenSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540
Db 1561 TATTACATTGGCAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCAAGTTGAACCTGTG 1620
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAenArgAenVal 560
Db 1621 TTTAAAGAAATTTTAAAGATAAACCCTAGCTTGTGTGTATTATACCACTAATAGAAACGTC 1680
Qy 561 AsnProAspGlySerLeuIleAlaAenGlyTyrAenTirProGluPheSerArgGluLys 580
Db 1681 AATCCGATGTTAGCTTAATCGCTAATGGTTACAATTTGGCCAGAAATTTTCCAGAGAAAA 1740
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTirPheLeu 600
Db 1741 CTCACACGGGTATGATTGCTCACCACCTTTAGAAATGTTCCAGATTAGAGCTTGGCATTTA 1800
Qy 601 ThrAspGlyPheAenGluLysIleGluAenAlaValAspTyrAspMetPheLeuLysLeu 620
Db 1801 ACTGATGGATTCAATGAAATAAATGAAATGCCGTAGCATATGACATGTTCTCTCAAACTC 1860
Qy 621 SerGluValGlyLysPheLysHisLeuAenLysIleCysTyrAenArgValLeuHisGly 640
Db 1861 AGTGAAGTTGGAAATTTAAACATCTTAATAAATAATCTGTATTAACCGTGTATTACATGGT 1920
Qy 641 AspAenThrSerIleLysLysLeuGlyIleGlnLysLysAenHisPheValValAen 660
Db 1921 GATAACACATCAATTAAGAACTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980
Qy 661 GlnSerLeuAenArgGlnGlyIleThrTyrAenTyrAspGluPheAspAspLeuAsp 680
```

```
Db 1981 CASTCATTAAATAGACAGGCATACTATTATAAATTATGACGAATTTGATGATTTAGAT 2040
Qy 681 GluSerArgLysTyrIlePheAenLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2041 GAAAGTAGAAGATATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100
Qy 701 LysAspIle 703
Db 2101 AAAGATATT 2109
RESULT 14
LOCUS AR225813 2112 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6444447.
ACCESSION AR225813
VERSION AR225813.1 GI:27263928
KEYWORDS SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2112)
DeAngelis,P.L.
TITLE Polymer grafting by polyaccharide syntheses
JOURNAL Patent: US 644447-A 2 03-SEP-2002;
The Board of Regents of the University of Oklahoma; Norman, OK
FEATURES
source
1. 2112
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.65e-221 Length: 2112
Score: 3693.00 Matches: 702
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.86% Mismatches: 0
Query Match: 72.30% Indels: 0
DB: 6 Gaps: 0
US-10-642-248-2 (1-972) x AR225813 (1-2112)
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 1 ATGAATACATTATCACAGCAATPAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTTATTTGAAAAGTCGGCGGAAAATCTATGGACGGAAAATTTGTGAATTTCAAAATTACC 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAen 60
Db 121 AAATGCCAGAAAAAATCTCAGCACATCCTTCTGTTAATTCAGCACATCTTCTGTAAAT 180
Qy 61 LysGluGluLysValAenValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAAGAGAAAAAAGTCAATGTTTCGGATAGTCCGTTAGATTATGCACACACTGTTACTT 240
Qy 81 SerAenValLysLysLeuValLeuSerAspSerGluLysAenThrLeuLysAenLysTirp 100
Db 241 TCCAACGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTAAAAAATAAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAenAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTCGCTCATCAGAGAATAATCTGAAAAATTCGGAGGTAAAGAGCGTCGCCCTTGTACCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAenAspPheThr 140
Db 361 AAAGATTTTCCCAAGATCTGGTTTATAGCCCTTTTACCTGATCATGTTAATGATTTTACA 420
Qy 141 TirpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 421 TGGTACAAAAGCGAAGAAAGACTTGGCATAAACCTGAAACATCAACATGTTGGTCTT 480
```



```
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTACAAACATTCATCGACCAACAAATTTATCGATTACATTAGCCCTGTTTA 540
Qy 181 ValAsnGlnIysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnIysLeuAspIleArgTyrValArgGln 220
Db 601 GATCTATCACCGATCAATTCGCAATATGAAATAAATGGATATTCGCTACGTCAGACAA 660
Qy 221 LysAspGlnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaIysTyr 240
Db 661 AAAGATAACGGTTTCAAGCCAGTCCGCTCGGAATATGGGATTCAGCGTTAGCAAAATAT 720
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db 721 GACTTATGGCTTACTCGACTGTGATATGGGCCAATCCATTATGGTTTCATCTTAT 780
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgTyrIleAsp 280
Db 781 GTTCAGAGCTATTAGAAGATGATGATTAACAATCATTTGGTCCAAAGAAAAATACATCGAT 840
Qy 281 ThrGlnHisIleAspProIysAspPheLeuAsnAsnAlaSerLeuGluSerLeuPro 300
Db 841 ACACAACATATGACCCCAAGAGCTCTTAATAACCGGAGTTTGCCTTGAATCATTTACA 900
Qy 301 GluValIysThrAsnAsnSerValAlaAlaIysGlyGluGlyThrValSerLeuAspTrp 320
Db 901 GAAGTGAACCAATATATAGTTGTCCCGCAAAAGGGGAAGNACAGTTTCTCTGGATTGG 960
Qy 321 ArgLeuGluGlnPheGluIysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCGCTTTT 1020
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaIysIysTyrLeuAsnIysSerGlyPhePheAsp 360
Db 1021 TTTGCGCGGGTAATGTGCTTTCGCTAAAAAATGGCTAAATAAATCCGTTTCTTTGAT 1080
Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1081 GAGGAATTTAATCACTGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATTCGTTAC 1140
Qy 381 GlySerPhePheIysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyIys 400
Db 1141 GGTAGTTTCTTTAAACATATTGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAA 1200
Qy 401 GluAsnGluThrAspArgGluAlaGlyIysAsnIleThrLeuAspIleMetArgGluIys 420
Db 1201 GAAAAATGAACCGATCGTGAACGGGAAAAAATATTTACGCTCGATATTATGAGAAAAAG 1260
Qy 421 ValProTyrIleTyrArgIysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db 1261 GTCCCTTATATCTATAGAAAATTTTACCATAGAGATTCGCATATCAATAGATACCT 1320
Qy 441 LeuValSerIleTyrIleProIleAlaAsnIleAsnTyrIleGlnArgCysValAsp 460
Db 1321 TTATGTTCAATTTATATCCAGCTTATTAATCTGCAAACTATATTCAAGCTTTCGCTAGAT 1380
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db 1381 AGTGACATGAATCAGACTGTGTTGATCTCGAGGTTTGTATTTGTAACGATGGTTCACAA 1440
Qy 481 AspAsnThrLeuGluValIleAsnIysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db 1441 GATAATACCTTGAAGTATCAATAAGCTTTATGTTAATAATCCCTAGGTTAGCATCATG 1500
Qy 501 SerIysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaIysGly 520
Db 1501 TCTAAACCAATGGCGAATAGCTCAGCATCAATGCAAGCCGCTTCTTTGCTAAGGT 1560
```

```
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrIleuGluProAspAlaValGluLeuCys 540
Db 1561 TATTACATTCGGCAGTTAGATTAGATTATCTTTCAGCCTGATGCGATTGAACTGTGT 1620
Qy 541 LeuIysGluPheLeuIysAspIysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db 1621 TTAAGAAGATTTTAAAGATATAAACCGCTAGCTTGTGTTTATACCATATATAGAAACGTC 1680
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluIys 580
Db 1681 AATCCGATGGTAGCTTAATCGCTAATGGTTTACAAATGGCCAGAAATTTTCACGAGAAAA 1740
Qy 581 LeuThrThrAlaMetIleAlaHisIlePheArgMetPheThrIleArgAlaTyrHisLeu 600
Db 1741 CTCACACGGCTATGATGCTCACCATTTAGAAATGTTTCAGGATTAGAGCTTGGCATTTA 1800
Qy 601 ThrAspGlyPheAsnGluIysIleGluAsnAlaValAspTyrAspMetPheLeuIysLeu 620
Db 1801 ACTGATGATTTCAATGAAGAAATTTGAANAATGCCGTAGACTATGACATGTTCTCAACTC 1860
Qy 621 SerGluValGlyIysPheIysHisLeuAsnIysIleCysTyrAsnArgValLeuHisGly 640
Db 1861 AGTCAAGTTGGAAAAATTTAAACATCTTAATAAATCTGTATAACCGTGTATTACATGCT 1920
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnIysLysAsnHisPheValValValAsn 660
Db 1921 GATAACACATCAATTAAGAACTTGGCATTTGCAATTCAAAAGAAAAAACCATTTTGTGTAGTCAAT 1980
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 1981 CAGTCATTAAATGACAGGCAATCACTTATTATTAATATGACGAATTTGATGATTTAGAT 2040
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu 700
Db 2041 GAAAGTAGAAGTATATTTTCATTAACCCCTGATATCAAGAAGAGATTGATATCTTA 2100
Qy 701 LysAspIle 703
Db 2101 AAAGATATT 2109
RESULT 15
AX698176 2058 bp DNA linear PAT 02-APR-2003
LOCUS Sequence 1 from Patent EP1283259.
DEFINITION AX698176
ACCESSION AX698176
VERSION AX698176.1 GI:29499185
KEYWORDS Escherichia coli
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Ninomiya, T., Sugiyama, N. and Kimata, K.
TITLE Chondroitin polymerase and DNA encoding the same
JOURNAL Patent: EP 1283259-A 1 12-FEB-2003;
Seikagaku Corporation (JP)
FEATURES
source
1..2058
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
CDS
1..>2058
/codon_start=1
/transl_table=11
/protein_id="CAD87418.1"
/db_xref="GI:29499186"
/translation="MSILNQAINLYKNRYKQALSLFEKVAEIVDSVWEANIKLCQT
ALNLSEEDVPLNRKAVIDIDATKIMCSNAKISLNEVEKNEIIISKYEITATKGSRA
ELKEVEPTKLDPSPDLTPPLPESTNDYVMAGRKELDDYPRKQLIIDGLSTVITPTN
RAKIUAITLACLNOKTYIDYEVIVADDSKENIEIIVREFESLNIKVRKDYKGYQ
LCAVNLGLRAKYNVAIILDCDMPNPLVQSYMWELLAHVDNDVALIGPRKIDTISKH
TYLDFLSQKSLINEIPEITINNQVAGKEQNKSVDMRIEHFKNTDLNLCNTLTPFRFFS
```

GGNVAFKKWLFRAQWDEEFTHWGGEDNEFGYLYREGCYFRSVEGAMAYHOEPBCK  
 ENETDRAAGKNIIVQLLOQKVPYPRKKEKESATILKRVPLSVIYIPAYNCNKIIVRC  
 VESALNQITIDLEVICDDGSDTDLRLQEHYANHRVRFISOKNGKIGSANTAVR  
 LCRFYQGDSDDFLEPDLCLDEFKRLSLACVYVTRNRI DREGNLSNGYNMP  
 IYREKLTSAI CHHFMFARAWNLTEGFNESTINAVDYMVLKLSVEGPPFKHINKI  
 CYNVLHGENTSIKLLDIQXENHFKVNESLSRLGIKKYKYSPLTNLNECKRYTWEKI  
 END"

## ORIGIN

## Alignment Scores:

Pred. No.: 7,68e-129 Length: 2058  
 Score: 2209.00 Matches: 412  
 Percent Similarity: 76.56% Conservative: 117  
 Best Local Similarity: 59.62% Mismatches: 150  
 Query Match: 43.25% Indels: 12  
 DB: 6 Gaps: 4

US-10-642-248-2 (1-972) x AK698176 (1-2058)

Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
 Db 1 ATGAGTATCTTATCAAGCAATAAATTTATATAAAACCAAAATATTCGCCAGCTTTA 60  
 Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
 Db 61 TCTCTTTTTCGAGAGGTGCTGAAATTTATGATGTTAGTTGGGTGCGAGCAATATATAA 120  
 Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
 Db 121 TTATGCCAAACCGCACATCAATCTTCTGAAGAAGTTGAT-----AAGTTAAAT 168  
 Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
 Db 169 CGTAAAGCTGTATTGATATT-----GATCGAGCAACAAAAAATAATGTGT 213  
 Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100  
 Db 214 TCTAACCCCAAGCAATTAGTCTGAACGAGTTGAAATAAATGAAATAAAGCAATAAT 273  
 Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
 Db 274 CGAGAAATACCGCAAGAAATCAGACGGCGGAGTTAAAGGAAGTCGAACCCATTCCT 333  
 Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisLevalAsnAspPheThr 140  
 Db 334 TTAGATTGGCCTAGTGAATTAACCTTTACCGCGCTTACCTGAGAGCACAAACGATATGTT 393  
 Qy 141 TptTyrLysLysAspGlyLysArgLeuGlyLysProGluHisGlnHisVal----- 158  
 Db 394 TGGCGGGGAAAGAAAGAG----CTTGATGATTATCAAGAAACAGATTAATCATTTGAC 450  
 Qy 159 GlyLeuSerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAla 178  
 Db 451 GGGCTTAGTATTGTAATTCCTACATATAATCGACCAAAATACITTCGAATTTACACTTGT 510  
 Qy 179 CysLeuValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySer 198  
 Db 511 TGTCTTTGTAAACCAAGACCATATACGACTATGAAGTTATTGTTGGCGATGATGGAAGT 570  
 Qy 199 GlnGluAspLeuSerProIleIleArgGlnTyrGlnAsnLysLeuAspIleArgTyrVal 218  
 Db 571 AAAGAAATATTGAAGAAATAGTAAGAGAAATTTGAAAGTTTATTAAATATAAAATATGTA 630  
 Qy 219 ArgGlnLysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAla 238  
 Db 631 CGTCAGAGGATTATGGATCAACTGTGTCTGTAGAAATCTTGGGCTTAGGGCTGCA 690  
 Qy 239 LysTyrAspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTptValHis 258  
 Db 691 AAGTATTAATTATGTTGCAATTTCTGGATTGTGATATGGCTCGCAACCCACTATGGGTTCA 750  
 Qy 259 SerTyrValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyr 278  
 Db 1831 AAACCTTAGTCAAGTTGGACCGTTCAAGCATATAAACAATAATTTGTTATATAATTCGGGTATTG 1890

Db 751 TCATATATGGAACCTATTAGCGGTGGACGATAATATGTTGCTTAATTTGGCCCTAGAAAAATAT 810  
 Qy 279 IleAspThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSer 298  
 Db 811 ATAGATACAGCAAGCATACATATTTAGATTTCTCTTTCCCAAAAATCACTAATAAATGAA 870  
 Qy 299 LeuProGluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeu 318  
 Db 871 ATTCTCGAATCATTTACTAATAATCAGTTTCAGGCAAGGTTCAGCAAAAACAATCAGTT 930  
 Qy 319 AspTptArgLeuGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPhe 338  
 Db 931 GACTGGCGAATAGACATTTCAAATAATCCGATAATCTAAGATTATGCAACACACCATTT 990  
 Qy 339 ArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLysTptLeuAsnLysSerGlyPhe 358  
 Db 991 CGATTTTTCAGCGAGGTAAATGTCGCTTTTCGAAAAAATGCGTTTCCGTGCGAGTGG 1050  
 Qy 359 PheAspGluGluPheAsnHisTptGlyGlyGluAspValGluPheGlyTyrArgLeuPhe 378  
 Db 1051 TTTGATGAAGAGTTTACGCATTCGGGGGGGAGGATAATGAGTTTGATATCGTCTCTAC 1110  
 Qy 379 ArgTyrGlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProPro 398  
 Db 1111 AGAGAAGGATGTTACTTTCGCTCTGTTGAAGGAGCAATGCATATCATCAAGAACCACCC 1170  
 Qy 399 GlyLysGluAsnGlnThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArg 418  
 Db 1171 GCGAAAGAAAACGAGACGGATCGTGGCGGAGGAAAAATATTACTGTTCATTTGTTACAG 1230  
 Qy 419 GluLysValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisLeuAsnArg 438  
 Db 1231 CAAAAGTTTCTTATTCTATATATATTCGGCGCTATAACTGCTCTAAATATATTGTTGTTGT 1290  
 Qy 439 ValProLeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCys 458  
 Db 1291 GTACCACTAGTATCTATATATATTCGGCGCTATAACTGCTCTAAATATATTGTTGTTGT 1350  
 Qy 459 ValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGly 478  
 Db 1351 GTTGAAGACGCCCTTAAATCAGACAAATCACTGATTGAAGTATGCATATCGATGATGTT 1410  
 Qy 479 SerTyrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArg 498  
 Db 1411 TCCACAGATGATACATTCGGGATTCCTCAGGACCATATGCAAAACCATCTCTCGATTCTGT 1470  
 Qy 499 IleMetSerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAla 518  
 Db 1471 TTTATTTCACAAAAAACAAGGAATTTGGTTTCAGCATCTAATACAGCAGTTAGATTCTGT 1530  
 Qy 519 LysGlyTyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGlu 538  
 Db 1531 CGGGGATTTCTATATAGTCAGTCTGATGACTCTGTGATGACTTCTTGAACCAAGATGCTGTTGAA 1590  
 Qy 539 LeuCysLeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArg 558  
 Db 1591 CTATGCTAGATGAATTTAGAAAGATCTATCAATGCGATGTTGATGATGTTTATACACTTAACCGT 1650  
 Qy 559 AsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTptProGluPheSerArg 578  
 Db 1651 AATATAGATCGTGAAGTAAATTTGATATCAATAGGCTATTAATTTGGCCCATTTATTTCGCA 1710  
 Qy 579 GluLysLeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTpt 598  
 Db 1711 GAAAAACTTACTAGTGAATGATGATGTCATCATTTCCAGGATGTTTCACAGCAAGACATGG 1770  
 Qy 599 HisLeuThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeu 618  
 Db 1771 AACCTAACTGAAGTTTCAACGAATCGATCGCAACCGAGTTGATTCAGATATGATATTA 1830  
 Qy 619 LysLeuSerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeu 638  
 Db 1831 AAACCTTAGTCAAGTTGGACCGTTCAAGCATATAAACAATAATTTGTTATATAATTCGGGTATTG 1890

Qy	639	HisGlyAspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValVal	658
Db	1891	CATGGTGAATAACGTCCTATATAAAGTTGGATATTCAAAAGGAAATCATTTTAAAGTT	1950
Qy	659	ValAsnGlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAsp	678
Db	1951	GTTAACGAATCATTAAAGTAGGCTAGGCATAAAAAATATAAATATTCACCATTAACTAAT	2010
Qy	679	LeuAspGluSerArgLysTyrIlePheAsnLys	689
Db	2011	TTGAATGAATGTAGAAATATACCTGGGAAAAA	2043

Search completed: January 8, 2006, 20:53:49  
 Job time : 10750 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 8, 2006, 17:28:01 ; Search time 400 Seconds  
(without alignments)  
4319.475 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAKGENIPVKNKFIINSITL 972

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool\_p/US10642248/runat\_06012006.125011.26887/app\_query.fasta\_1.1159  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=50  
-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10642248 @C@N\_1.1.290 @runat\_06012006.125011.26887 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*\*

1: /cgn2.6/prodata/1/ina/1 COMB.seq.\*  
2: /cgn2.6/prodata/1/ina/5 COMB.seq.\*  
3: /cgn2.6/prodata/1/ina/6A COMB.seq.\*  
4: /cgn2.6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2.6/prodata/1/ina/H COMB.seq.\*  
6: /cgn2.6/prodata/1/ina/PCTUS COMB.seq.\*  
7: /cgn2.6/prodata/1/ina/PP COMB.seq.\*  
8: /cgn2.6/prodata/1/ina/RE COMB.seq.\*  
9: /cgn2.6/prodata/1/ina/baCkfilese1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	2937	3	US-09-469-2008-8
2	5104	99.9	2937	3	US-10-172-527A-9
3	4490.5	87.9	2979	3	US-09-437-277-4
4	3693	72.3	2112	3	US-09-437-277-2
5	384.5	7.5	11474	3	US-09-495-406-1
6	384.5	7.5	11474	3	US-09-816-028A-1
7	384.5	7.5	11474	3	US-10-303-162-1
8	384.5	7.5	11474	3	US-10-303-134-1
9	384.5	7.5	11474	3	US-10-303-118-1

10	384.5	7.5	11474	3	US-10-303-128-1	Sequence 1, Appli
11	308	6.0	13825	3	US-09-634-238-29	Sequence 29, Appli
12	302.5	5.9	6865	3	US-09-900-038A-3	Sequence 3, Appli
13	301.5	5.9	2166	3	US-09-107-532A-3235	Sequence 3235, Ap
14	287.5	5.6	2529	3	US-09-134-000C-2344	Sequence 2344, Ap
15	281.5	5.5	32768	3	US-08-961-527-71	Sequence 71, Appli
16	264.5	5.2	1002	3	US-09-107-532A-1469	Sequence 1469, Ap
17	252	4.9	1602	3	US-09-134-000C-1682	Sequence 1682, Ap
18	251.5	4.9	14602	2	US-08-597-236-1	Sequence 1, Appli
19	251.5	4.9	14602	2	US-08-746-682A-1	Sequence 1, Appli
20	246.5	4.8	984	3	US-09-107-532A-2527	Sequence 2527, Ap
21	245	4.8	536165	3	US-09-214-808-1	Sequence 1, Appli
22	244	4.8	1830121	3	US-09-557-884-1	Sequence 1, Appli
23	244	4.8	1830121	3	US-09-643-990A-1	Sequence 1, Appli
24	244	4.8	1830121	3	US-10-158-865-1	Sequence 1, Appli
25	241.5	4.7	993	3	US-09-134-000C-2987	Sequence 2987, Ap
26	236.5	4.6	3171	3	US-09-134-000C-1681	Sequence 1681, Ap
27	235	4.6	1035	3	US-08-891-641-40	Sequence 40, Appli
28	231.5	4.5	2023	3	US-08-961-083-199	Sequence 199, App
29	231.5	4.5	2023	3	US-09-536-784-199	Sequence 199, App
30	231.5	4.5	2023	3	US-09-765-271-199	Sequence 199, App
31	231.5	4.5	2023	3	US-09-765-272A-199	Sequence 199, App
32	228.5	4.5	2184	3	US-09-134-001C-1230	Sequence 1230, Ap
33	223.5	4.4	11474	3	US-09-495-406-1	Sequence 1, Appli
34	223.5	4.4	11474	3	US-09-816-028A-1	Sequence 1, Appli
35	223.5	4.4	11474	3	US-10-303-162-1	Sequence 1, Appli
36	223.5	4.4	11474	3	US-10-303-134-1	Sequence 1, Appli
37	223.5	4.4	11474	3	US-10-303-118-1	Sequence 1, Appli
38	223.5	4.4	11474	3	US-10-303-128-1	Sequence 1, Appli
39	214.5	4.2	19390	3	US-08-961-527-86	Sequence 86, Appli
40	210.5	4.1	5859	2	US-08-312-387B-1	Sequence 1, Appli
41	210.5	4.1	5859	2	US-08-312-387B-7	Sequence 7, Appli
42	210.5	4.1	5859	2	US-08-683-426-1	Sequence 1, Appli
43	210.5	4.1	5859	2	US-08-683-426-7	Sequence 7, Appli
44	210.5	4.1	5859	2	US-08-683-458-1	Sequence 1, Appli
45	210.5	4.1	5859	2	US-08-683-458-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-469-2008-8  
; Sequence 8, Application US/09469200E  
; Patent No. 6833264  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kshama  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/09/469,200E  
; CURRENT FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pastuerella Multocida  
US-09-469-2008-8

Alignment Scores:  
Pred. No.: 0 Length: 2937  
Score: 5108.00 Matches: 972  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-642-248-2 (1-972) x US-09-469-2008-8 (1-2937)

Qy 1 MetAsnThrLeuSerGlnAlaIleIysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
Db 19 ATGAATACATTATCACAGCAATAAAGCATATATACAGCAATGACTATCAATTAGCACTC 78  
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
Db 79 AATATTATTTGAAAAGTCGGCCGGAATCTATCGACGGAAAATTTGTGAATTTCAAAATTACC 138  
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
Db 139 AAATGCAAGAAAAAATCTCAGCACATCTCTCTGTTAATTAGCACACATCTTCTGTGAAT 198  
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
Db 199 AAAGAAGAAAAAGTCAATGTTTGGATAGTCGGTTAGATATTGCAACACAACTGTTACTT 258  
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
Db 259 TCCAAACGTAAAAAAAATTAGTACTTCTGACTCGGNAAAAAACACAGTTAAAAAATAATGG 318  
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
Db 319 AAATTGCTCACTGAGAGAAATCTGMAAATCGCGAGGTAAAGCGCTCGCCCTTTGTACCA 378  
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
Db 379 AAAGATTTCCTCAAGAGATCTCGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACA 438  
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyLysProGluHisGlnHisValGlyLeu 160  
Db 439 TGGTACAAAAACGGAAAAAGACTTGGCAATAAACCCTGAAACATCAACATGTTGGTCTT 498  
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
Db 499 TCTATTATGCTTACAAACATCTCAATCGACCAACAAATTTTATCGATTACATTAGCTGTGTTA 558  
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
Db 559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTGACAGATGATGAGTAGCAGAA 618  
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
Db 619 GATCTATCACCGATCAATTCGCAATATGAAAATAAATTGGATATTTCGTACTGTCAGACAA 678  
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
Db 679 AAAGATAACCGTTTTCAAGCCAGTCCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 738  
Qy 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
Db 739 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTATGGGTTTCATCTTAT 798  
Qy 261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
Db 799 GTTCAGAGCTATTAGAAAGATGATGATTTAACATCATTTGTTCCAGNAATAATACATCGAT 858  
Qy 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300  
Db 859 ACACAACATAATTGACCCAAAAGACTTCTTAATAAACCGCGAGTTTGTCTTGAATCATTTACCA 918  
Qy 301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 919 GAAGTGAAAACCAATAATAGTGTTCGCCCAAAAGGGGAAGGAGGATTTCTCTCGGATTGG 978  
Qy 321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTAGAACAAATTCGAAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1038  
Qy 341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
Db 1039 TTTCCGGCGGGTAATGTTGCTTTCGCTAAAAAATGGCTAAATAAATCCGGTTTTCTTTGAT 1098

Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1099 GAGAAATTTTAATCCTGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTTCCGTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1159 GGTAGTTTCTTTAAAACTATTGATGCATTATGGCTACCATCAAGAGCCACCAGGTAAA 1218  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAAAATGAAACCGATCGTGAAGCGGAAAAAATAATTATTCGCTCGATATTATTAGAGAAAAAG 1278  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATTAGAAAACCTTTTACCAATAGAGATTTCGATATCAATAGATACCT 1338  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1399 AGTGCACATGAATCAGACTGTTGTGATCTCAGGTTTGTATTGTACGATGGTTCAACA 1458  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1459 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCTTAGGTACGATCATG 1518  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1519 TCTAAACCAAAATGGCGAATAGCCTCAGCATCAAAATGCAGCGTTCTTTTGTCTAAAGGT 1578  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTCGGCAGTTAGATTAGATGATTATCTTGAGCCTGATGCACTGGAATCTGT 1638  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560  
Db 1639 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTATTATACCCTAATATAGAAACGTC 1698  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1699 AATCCGAGTGGTAGCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCCAGCAGAAAAA 1758  
Qy 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1759 CTCACAACGCTATGATTTGCTCACCCTTTAGAAATGTTACGATTTAGAGCTTGGCATTTA 1818  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGGATTCAATGAAAAAATTTGAAAATGCGGTAGACTATGACATGTTCTCTCNAACCTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGTGTATTACATGGT 1938  
Qy 641 AspAsnThrSerLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660  
Db 1939 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACCACTTTTGTGTAGTCAT 1998  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680  
Db 1999 CAGTCATTAAATAGCAAGGCATAACTTATTATTAATATGACCAATTTTGATGATTTAGAT 2058  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeu 700  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTGATATCTTA 2118  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2119 AAAGATATTTAAATCATCCAGAAATAAAGATGCCAAAATCGCAGTCAGTATTTTTTATCCC 2178  
Qy 721 AsnThrLeuAsnGlyLeuValLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740



2179 AATACATTAACGGCTAGTGAAGAACTAAACAAATATTA TTGAATATAATAAAATATA 2238  
741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLeuGluIle 760  
2239 TTCGTTATGTGTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298  
761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358  
781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800  
2359 ACGAGTAATAGATTAATAAAACCTGAGCGCATTTAAGTAATATTAATAAAATTAAGTCAG 2418  
801 LeuAsnLeuAsnCysGluTyrIleLysPheAspAsnHisAspSerLeuPheValLysAsn 820  
2419 TTAATCTAAATTTGTGAATACATCATCTTTTGTATATCATGACAGCCTATTTCGTTAAAAAT 2478  
821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
2479 GACAGCTATGCTTATGAAAAAATATGATGTCGCATGAATTTCTCAGCATTAACACAT 2538  
841 AspTrpIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860  
2539 GATTCGATCGAGAAATCAATCGCATCCACCATTAAAAAGCTCATTTAAAACTTATTTT 2598  
861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880  
2599 AATGCAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGACG 2658  
881 TyrAlaLeuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSer 900  
2659 TATGCGCTAGCCGATGAGCTTCGAGATTTAAAGAGTATTAAGAGTATGTTTATGACG 2718  
901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
2719 ATTGATAGTGTCCAGATATTAACACTGAGGATATTGTTTCCAAATTTGCACTTTTAATC 2778  
921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
2779 TTAGAAAAAGAAACCGGCATGATTTTAAATAAACATCAGACCTGACCTTATATGCTTGG 2838  
941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGluAsnIle 960  
2839 GAACGAAATTAACAATGGAACAAATGAACAAATTTGAAAGTGAAGAGGAGGAGAAATATA 2898  
961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
2899 CCTGTTAACAGTTCAATTAATTAATAGTATACTCTA 2934

RESULT 2  
US-10-172-527A-9  
; Sequence 9, Application US/10172527A  
; Patent No. 6951743  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Kshama  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: HYALURONAN SYNTHASE GENES AND EXPRESSION THEREOF IN BACILLUS HOST  
; FILE REFERENCE: 3554.048  
; CURRENT APPLICATION NUMBER: US/10/172,527A  
; CURRENT FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: 60/297,788  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 60/297,744  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 09/469,200  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: pasteurella multocida  
US-10-172-527A-9  
Alignment Scores:  
Pred. No.: 0 Length: 2937  
Score: 5104.00 Matches: 971  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 99.92% Indels: 0  
DB: 3 Gaps: 0  
US-10-642-248-2 (1-972) x US-10-172-527A-9 (1-2937)  
QY 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20  
DB 19 ATGAATACATTTATCACAGCAATTAAGCATATTAACAGCATGACTATCAATTAGCACATC 78  
QY 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40  
DB 79 AAATTTATTTGAAAAGTCGGGGGAAATCTATGACGCGAAAAATTGTTGAATTTCAAAATACC 138  
QY 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60  
DB 139 AAATGCCCAAGAAAAAATCTCTCAGCACATCTTCTGTAAATTCAGCACATCTTCTGTGTAAT 198  
QY 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80  
DB 199 AAGAAGAAAAAAGTCAATGTTTGGATAGTCCGTTAGATATTTGCACCACTGTACTT 258  
QY 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTrp 100  
DB 259 TCCAACTGAAAAAATTAAGTACTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 318  
QY 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120  
DB 319 AAATGTCTCACTGAGAAGAAATCTGAAAATCGGAGGTAAAGAGCGGTCCGCTTGTACCA 378  
QY 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140  
DB 379 AAGAATTTTCCAAAGATCTGGTGTTCGCGCTTTTACCTGATCATGTTAATGATTTTACA 438  
QY 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160  
DB 439 TGGTACAAAAAGCGAAGAAAGACTTGGCATAAAACCTGAACATCAACATCTGTGCTTT 498  
QY 161 SerIleIleValThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180  
DB 499 TCTATTATCGTTACAAATTCATTCGACGAGCAATTTTATCGATTTACATTTAGCCTGTTTA 558  
QY 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200  
DB 559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTATTCAGAA 618  
QY 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220  
DB 619 GATCTATCACCGATCATTCGCCAATATGAAAATAAATTTGATATTCGCTACGTCAGACAA 678  
QY 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240  
DB 679 AAAGATAACGGTTTTTCAAGCCAGTCGCGCTCGGAATATGGGATATGGCTTAGCAAAATAT 738  
QY 241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTrpValHisSerTyr 260  
DB 739 GACTTTTATGGCTTACTCGACTGTGATATGGCGCAAAATCCCAATTTGGGTTTCACTTTAT 798  
QY 261 ValAlaGluLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280  
DB 799 GTTCAGAGACTATTAGAGATGATGATTTACAAATCATTTGGTCCAAAGAAAAATACATCGAT 858  
QY 281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300

Db 859 ACACACATATTGACCCCAAGACCTTCTTAATAAACCGGAGTTTGCTTGAATCAATTACCA 918  
Qy 301 GluVallyThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTrp 320  
Db 919 GMACTGAAACCAATAATAGTGTGTCGCGCAAAAGGGAAGAACAGTTTCTCTCGAATTGG 978  
Qy 321 ArgLeuGluInPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340  
Db 979 CGCTTTAGAACCAATTCGAAAAACAGAAATCTCGCTTATCCGATTCGCCTTTCCGTTTT 1038  
Qy 341 PheAlaLaGlyAsnValAlaPheAlaLysLysTrpLeuAsnLysSerGlyPhePheAsp 360  
Db 1039 TTTCCGCGGGTAATGTGCTTTTCCTAAAAAATGGCTAAATAATCCGGTTTCTTTGAT 1098  
Qy 361 GluGluPheAsnHisTrpGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380  
Db 1099 GAGGAAATTTAATCACTGGGGTGGAGAGATGTGGAATTTTGGATATCGCTTATTCGTTAC 1158  
Qy 381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400  
Db 1159 GGTAGTTTCTTTAAACCTATTGATGGCAATTATGGCTTACCATCAAGAGCCACCAAGTAAA 1218  
Qy 401 GluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArgGluLys 420  
Db 1219 GAAAAATGAAACCGATCGTGAACGGGAAAAAATAATTACGCTCGATATATTATGAGAGAAAAG 1278  
Qy 421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440  
Db 1279 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTTCGCATATCAATAGAGTACCT 1338  
Qy 441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460  
Db 1339 TTAGTTTCAATTTATATCCCACTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1398  
Qy 461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480  
Db 1399 AGTCACATGAATCAGACTGTGTGATCTCAGAGTTTGTATTGTACGATGGTTCAACA 1458  
Qy 481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500  
Db 1459 GATAATACCTTTAGAAGTGATCAATAAGCTTTATGGTAATAATCTCTAGGTCAGCATCATG 1518  
Qy 501 SerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520  
Db 1519 TCTAAACCAATGCGCGAATAGCCTCAGCATCAAAATGCAGCCGTTCTTTTGTCTAAAGGT 1578  
Qy 521 TyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGluLeuCys 540  
Db 1579 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCCTGATGCGTTGAACGTGTG 1638  
Qy 541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnVal 560  
Db 1639 TTAAAAAGAAATTTTAAAAAGATAAAAAAGCTAGCTTGTGTTTATACCACCTAATAGAAACGTC 1698  
Qy 561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLys 580  
Db 1699 AATCCGATGTTAGCTTAATCGCTAATGGTTTACAAATTTGGCCAGAAATTTTTCACGAGAAAAA 1758  
Qy 581 LeuThrThrAlaMetIleAlaHisIlePheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1759 CTCACACGGCTATGATTGCTCACACCTTTAGAATGTTTCAGATTAGAGCTTGGCATTTA 1818  
Qy 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620  
Db 1819 ACTGATGATTTCAATGAAAAAATTTGAAAAATTCGCGTAGCATATGACATGTTCTCTCAAACTC 1878  
Qy 621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640  
Db 1879 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAAAATCTGCTATAAACCGGTGATTACATGGT 1938  
Qy 641 AspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsn 660

Db 1939 GATAACACATCAATTAAGAAACTTGGCAATTCAAAAAGAAAAACCAATTTTGTGTAGTCAAT 1998  
Qy 661 GlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAsp 680  
Db 1999 CAGTCATTAATAAGCAAGGCATAACTTATTATTAATATGACGAATTTGATGATTTAGAT 2058  
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluLeuAspIleLeu 700  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATGATATCTTA 2118  
Qy 701 LysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720  
Db 2119 AAAGATATTAAATCATCCAGATAAAGATGCCAAAAATCGCAGTCAGTATTTTTTATCCC 2178  
Qy 721 AsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIle 740  
Db 2179 AATACATATTAAACGGCTAGTGAAAAAACTAAACAATATTATTGAATATATAAAAAATATA 2238  
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760  
Db 2239 TTCGTTATTGTTCTACATGTTGATAAGATCATCTTACACCATATCAAAAAAGAAATA 2298  
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780  
Db 2299 CTAGCCTTCTATCAAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2358  
Qy 781 ThrSerAsnArgLeuLeuLysThrGluAlaHisSerAsnIleAsnLysLeuSerGln 800  
Db 2359 ACGAGTAATAGATTAATAAAAACTGAGCGCATTTAAGTAATATTATAATAATTAAGTCAG 2418  
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820  
Db 2419 TTAATCTCAAAATGTGAATACATCATTTTGTGAATAATCATGACAGCCTATTCGTTAAAAAT 2478  
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840  
Db 2479 GACAGCTATGCTTATGAAAAAATATGATGTCGCGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 841 AspTrpIleGluLysIleAsnAlaHisProProPheLysLysLeuLeuLysThrTyrPhe 860  
Db 2539 GATTGGATCGAGAAAAATCAATGCGCATCCACCACTTTAAAAAGCTCATTTAAACCTTATTTT 2598  
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyValaSerGlnGlyMetPheMetThr 880  
Db 2599 AATGACAAATGACTTAAAAAGTATGAATGTGAAGGGGCATCACAGGTAIGTTTATGACG 2658  
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleIleLysGluValIleThrSerCysGlnSer 900  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTATTAAAGAGTCATCATCTTGCACGTCA 2718  
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920  
Db 2719 ATTGATAGTGTGCGAGAAATAACACTGAGGATATTTGGTTCCAATTTGCACCTTTTAATC 2778  
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTrp 940  
Db 2779 TTAGAAAAAGAAAAACCGGCCATGTATTATAAATAAACATCGACCTGACTTATATGCTCTGG 2838  
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960  
Db 2839 GAACGAAAAATTACATCGACCAATGAACAAATTTGAAAGTGCNAAGAGAGAGAGAAATATA 2898  
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972  
Db 2899 CCTGTTAAACAAGTTCATTATTAATAGTATAACTCTA 2934

## RESULT 3

US-09-437-277-4

; Sequence 4, Application US/09437277

; Patent No. 644447

; GENERAL INFORMATION:

; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA

; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES

FILE REFERENCE: 5820.551  
CURRENT APPLICATION NUMBER: US/09/437,277  
CURRENT FILING DATE: 1999-11-10  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: WordPerfect 8.0 (saved in ASCII format)  
SEQ ID NO 4

LENGTH: 2979  
TYPE: DNA  
ORGANISM: Pasteurella multocida  
US-09-437-277-4

## Alignment Scores:

Pred. No.:	0	Length:	2979
Score:	4490.50	Matches:	843
Percent Similarity:	93.11%	Conservative:	62
Best Local Similarity:	86.73%	Mismatches:	60
Query Match:	87.91%	Indels:	7
DB:	3	Gaps:	2

US-10-642-248-2 (1-972) x US-09-437-277-4 (1-2979)

```
Qy      1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db      61 ATGAATACATTATCACAGCAATAAAGCATATATAACAGCAATGACTATGAATTAGCACTC 120

Qy      21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db      121 AARTATTATTGAGAAGTCTGCTGAAACCTACCGGGCGGAAATTCGTTGAATTCCAATATATC 180

Qy      41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db      181 AATGTAAGGAAATCACTC-----TCGACCAATTC-----TATGTAAGT 219

Qy      61 LysGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db      220 GAAGATAAAAAACAGTGTTCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 279

Qy      81 SerAsnValLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db      280 TCCACAGTAAATAAATAAATCACTATCCGAATCAGAAAAAACAGTTTAAAAAATAAATGG 339

Qy      101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db      340 AATCTATCACTGGGAAAAAATCGAGAACGAGAAATCAGAAAGGTGGAACCTAGTACCC 399

Qy      121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db      400 AAGATTTTCTCTAAAGATCTTGTCTCTCCATTGCCAGATCATGTTAATGATTTTACA 459

Qy      141 TrpTyrLysLysArgLysLysArgLeuGlyLysIleLysProGluHisGlnHisValGlyLeu 160
Db      460 TGGTACAAAATCGAAAAAAGCTTAGGTATAAAGCCCTGTAAATGAAGATATCGGCTT 519

Qy      161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db      520 TCTATTATTTCCTACATTTAATCGTACCGGTATTTAGATATTAACGTTAGCCGTGTTG 579

Qy      181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db      580 GTCAATCGAAAAACAACATACCCTTTTGAAGTCGTTGTCAGATGATGCTAGTAGGAA 639

Qy      201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db      640 AACTTACTTACCATTTGTGCAAAATACGAAACAAATCTTGACATAAAGATATGTAGACAA 699

Qy      221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db      700 AAGATATTGGATATCAATGTGTGCGAGTCAGAAACTTAGTTAGTTAGTATGTAGACAA 759

Qy      241 AspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeuTyrValHisSerTyr 260
Db      760 GATTTGTCTCGATCTAGCTCGCATATGGCACCACCAACATTTATGGGTTCTATCTTAT 819
```

```
Qy      261 ValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyProArgLysTyrIleAsp 280
Db      820 CTTACAGAACTATTAGAACAAATGATATTGTTTAAATTTGGACCTAGAAAAATATGTGGAT 879

Qy      281 ThrGlnHisIleAspProLysAspPheLeuAsnAsnAlaSerLeuLeuGluSerLeuPro 300
Db      880 ACTATAAATATTACCGCAGAACCAATTCCTTAACGATCCATATTATTATAGAAATCACTACCT 939

Qy      301 GluValLysThrAsnAsnSerValAlaAlaLysGlyGluGlyThrValSerLeuAspTyr 320
Db      940 GAAACCCCTACAAATAACAAATCTTCGATTACATAAAGGAAATATATCGTTGGATTGG 999

Qy      321 ArgLeuGluGlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPhe 340
Db      1000 AGATTAGAACATTTCAAAAAAACCGATAATCTACGTCTATGTGATTCTCCGTTTCGTTAT 1059

Qy      341 PheAlaAlaGlyAsnValAlaPheAlaLysLysTyrLeuAsnLysSerGlyPhePheAsp 360
Db      1060 TTTGTTCCGGGTAAATGTTGCATTTTCTAAGAATGGCTAATAAAGTAGGTGGTTCGAT 1119

Qy      361 GluGluPheAsnHisTyrGlyGlyGluAspValGluPheGlyTyrArgLeuPheArgTyr 380
Db      1120 GAAGAATTTAATCATTCGGGGGCGGAGAGTAGAATTTTGGTTACAGATTATTTCGCCAA 1179

Qy      381 GlySerPhePheLysThrIleAspGlyIleMetAlaTyrHisGlnGluProProGlyLys 400
Db      1180 GGCTGTTTTTTCAGAGTAATTCAGCGCGGAATTCATCAAGAACCCACCTGGGTAAA 1239

Qy      401 GluAsnGluThrAspArgGluAlaGlyAsnIleThrLeuAspIleMetArgGluLys 420
Db      1240 GAAATGAAACAGAACCGGAGCTGGTAAAGTATTACGCTTAAATTTGTGAAGAAAAG 1299

Qy      421 ValProTyrIleTyrArgLysLeuLeuProIleGluAspSerHisIleAsnArgValPro 440
Db      1300 GTACTTACATCTATAGAAAGCTTTTACCAATAGAGATTCACATATTTCATAGAATACCT 1359

Qy      441 LeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAsp 460
Db      1360 TTAGTTTCTATTATATATCCCGCTTATAACTGTGCAAAATATATATTCAAAGATGTGTAGAT 1419

Qy      461 SerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAspGlySerThr 480
Db      1420 AGTCCTCTTAATCAAACTGTTGTCGATCTCGAGTTTGTATTGTTAAGATGTTTCAACA 1479

Qy      481 AspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMet 500
Db      1480 GATTAATACCTTAGAAGTGATCAATAAGCTTTATCGTAATAATCTAGGAGTACGCATCATG 1539

Qy      501 SerLysProAsnGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGly 520
Db      1540 TCTAAACCAATGCGGAATAGCCTCAGCATCAAAATGCGCCGTTTCTTTTGTCTAAAGGT 1599

Qy      521 TyrTyrIleGlyGlnLeuAspSerAspAspTyrIleGluProAspAlaValGluLeuCys 540
Db      1600 TATTACATGCGCAGTTAGATTTCAGATGATTATCTTAGCCTGATGCGAGTTGAACGTGT 1659

Qy      541 LeuLysGluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsnVal 560
Db      1660 TTAAAGAAATTTTAAAGATATAAACGCTAGCTGTGTGTTTATACCACATAATAGAAACGTC 1719

Qy      561 AsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTyrProGluPheSerArgGluLys 580
Db      1720 AATCCGGATGTAGCTTAATCGCTAAATCGTTTACAAATGCGCAGAAATTTTTCAGAGAAAA 1779

Qy      581 LeuThrThrAlaMetIleAlaHisHisPheArgMetPheThrIleArgAlaTyrHisLeu 600
Db      1780 CTCACACCGCTATGATTCCTCACCATTATTAGAAATGTTTACGATTAGAGCTTGGCATTTA 1839

Qy      601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeu 620
Db      1840 ACGGATGATGATTAAACGAAATATTGAAACCCCGGTGATATGACATGTTCTCTTAAACCTC 1899

Qy      621 SerGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGly 640
```

```
Db 1900 AGTCAAGTGGAAAAATTAAACATCTTAATAAATCTGCTATAACCGGTATTACATGGT 1959
Qy 641 AsnAsnThrSerLeuLysLeuGlyLeuGlnLysAsnHisPheValValAsn 660
Db 1960 GATAACACATCCATTAGAAATCGGCATTCAAAAGAAAAACCACTTTGTGTAGTCAAT 2019
Qy 661 GluSerLeuAsnArgGlnGlyLeuThrTyrTyrAsnTyrAspGluPheAspAspLeuAsp 680
Db 2020 CAGTCATTAAATAGCAAGGCATCAATATTATTAATATTGACAAATTTGATGATTTAGAT 2079
Qy 681 GluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeu 700
Db 2080 GAAAGTAGAAGATATATCTCAATAAACCCTGAATATCAAGAGAAATGGATATGTTA 2139
Qy 701 LysAspIleLysIleLeuGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrPro 720
Db 2140 AAAGATCTTAACACTCAATCAAAATAAAGATGCCAAATCGCAGTCAGTATTTCTATCCC 2199
Qy 721 AsnThrLeuAsnGlyLeuValLysLeuAsnAsnIleLeuGluTyrAsnLysAsnIle 740
Db 2200 AATACATTAACCGCTTAGTGAAAAAATAAACAATATTATTGAATATATAAATAATATA 2259
Qy 741 PheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGluIle 760
Db 2260 TTGCTTATTATCTACATGTTGATAGAAATCATCTTACACGACATCAAAAAGAAATA 2319
Qy 761 LeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSerTyrTyr 780
Db 2320 TTGGCTTTCTATCATAGCACCAAGTCGAATATTTTACTAATAATGACATCTCATATTAC 2379
Qy 781 ThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGln 800
Db 2380 ACGAGTAAATGACTAATAAATAAAGCTGAGCGCATTTAAGTAAATATAAATAAATTAAGTCAG 2439
Qy 801 LeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsn 820
Db 2440 TTAAATCTAAATTTGTGAATACATCATTTTGTGATTAATCATGACAGCCATTCGTTAAANAAT 2499
Qy 821 AspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHis 840
Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGCATGAATTTCTCAGCATTAACACAT 2559
Qy 841 AspTyrIleGluLysIleAsnAlaHisProPheLysLysLeuIleLysThrTyrPhe 860
Db 2560 GATTGGATCGAGAAAAATCAATGCGCATCCACCATTTAAAAAGCTGATTAACACCTATTTT 2619
Qy 861 AsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThr 880
Db 2620 AATGACAAATGACTTAAGAGATATGATGTGAAGGGGCATCAAGAGTATGTTTATGAAG 2679
Qy 881 TyrAlaLeuAlaHisGluLeuLeuThrIleLeuLysGluValIleThrSerCysGlnSer 900
Db 2680 TATCGCTACCGCATGAGCTTCTCAGCATTTAAGAGAGTCATCAATCCTCGCAATCA 2739
Qy 901 IleAspSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIle 920
Db 2740 ATTGATAGTGGCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAAATC 2799
Qy 921 LeuGluLysLysThrGlyHisValPheAsnLysThrSerThrLeuThrTyrMetProTyr 940
Db 2800 TTAGAAAGAAACCGGCATGATTTTAAATAAACATCGACCCCTGACTTATATGCCCTGG 2859
Qy 941 GluArgLysLeuGlnTrpThrAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIle 960
Db 2860 GAACGAAAAATTACAAATGGACAAATGAACAAATTCAAAGTGCAAAAAAGGCGAAATATC 2919
Qy 961 ProValAsnLysPheIleIleAsnSerIleThrLeu 972
Db 2920 CCGGTTAAACAGTTTCAATTTAATAGTATATAACGCTA 2955
```

RESULT 4

US-09-437-277-2

```
; Sequence 2, Application US/09437277
; Patent No. 644447
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCES: 5820.551
; CURRENT APPLICATION NUMBER: US/09/437,277
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 2
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; US-09-437-277-2
```

```
Alignment Scores:
Pred. No.: 0 Length: 2112
Score: 3693.00 Matches: 702
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.86% Mismatches: 0
Query Match: 72.30% Indels: 0
DB: Gaps: 0
```

US-10-642-248-2 (1-972) x US-09-437-277-2 (1-2112)

```
Qy 1 MetAsnThrLeuSerGlnAlaIleLysAlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu 20
Db 1 ATGAATACATTTATCACAGCAATATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
Qy 21 LysLeuPheGluLysSerAlaGluIleTyrGlyArgLysIleValGluPheGlnIleThr 40
Db 61 AAATTTATTTGAAAAGTCGGCGGAAATCTATGACGGAATAATGTTGAAATTTCAAAATACC 120
Qy 41 LysCysLysGluLysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsn 60
Db 121 AAATGCCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTAAT 180
Qy 61 LysGluGluLysValAsnValCysAspSerProLeuAspIleAlaThrGlnLeuLeuLeu 80
Db 181 AAAGAAAGAAAAAGTCAATGTTTCGATAGTCGCTTAGATATTGCAACACAACTGTTACTT 240
Qy 81 SerAsnValLysLysLeuValLeuSerAspSerGluLysAsnThrLeuLysAsnLysTyr 100
Db 241 TCCACAGTAAAAAAATTAGTACTTTCTGACTCGAAAAAACAACACGTTTAAAAAATTAATGG 300
Qy 101 LysLeuLeuThrGluLysLysSerGluAsnAlaGluValArgAlaValAlaLeuValPro 120
Db 301 AAATTCCTCACTCAGAAAGAAATCTGAAAAATGCGAGGTAAGAGCGGTGCGCCTTGTTACCA 360
Qy 121 LysAspPheProLysAspLeuValLeuAlaProLeuProAspHisValAsnAspPheThr 140
Db 361 AAAGATTTTCCCAAGATCTGTTTTTAGCGCCTTTTACCTGATCATGTATATGATTTTACA 420
Qy 141 TrpTyrLysLysArgLysLysArgLeuGlyIleLysProGluHisGlnHisValGlyLeu 160
Db 421 TGTACAAAAAGCGAAAGAAAGACCTGGCATAAAACTGCAACATCAACATGTTGGTCTT 480
Qy 161 SerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCysLeu 180
Db 481 TCTATTATCGTTACAAACATTTCAATCGACCAGCAATTTTATCGATTACATTTAGCGCTGTTA 540
Qy 181 ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGlySerGlnGlu 200
Db 541 GTAACCAAAAAACACATTAACCGCTTGAAGTTTATCGTGACAGATGATGTTAGTCAGGAA 600
Qy 201 AspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIleArgTyrValArgGln 220
Db 601 GATCTATACCGATCAITTCGCCAATATGAANAATTAATTTGGATATTTCGTACTACGTACAGCAA 660
Qy 221 LysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeuAlaLysTyr 240
Db 661 AAAGATAACGGTTTTCAAGCCAGTCGCGCTCGGAATATGGATTACGCTTAGCAANAATAT 720
```

```
Qy 241 AspPheileGlyLeuLeuAaspCyaspMetAlaproAenProLeuTtpValHisSerTyr 260
Db 721 GACTTTATGGCTTACTCGACTGTGATGATGGCCAAATCCATATATGGGTTCTTCTTAT 780
Qy 261 ValAlaGluLeuLeuGluAaspAaspLeuThrileileGlyProArgLysTyrileAasp 280
Db 781 GTTCAGAGCTATTAGAAGATGATGATTTAAACATCATTTGGTCCAGAAAAATACATCGAT 840
Qy 281 ThrGlnHisileAaspProLysAaspPheLeuAenAenAlaserLeuLeuGluSerLeuPro 300
Db 841 ACACAACATATTGACCCAAAAGACTTCTTAATAAACGCGAGTTTGTCTGAATCATACCA 900
Qy 301 GluValLysThrAenAenSerValAlaAlaLysGlyGluGlyThrValSerLeuAaspTirp 320
Db 901 GAAGTGAAACCAATAATAGTTGTGGCCCAAAAGGGAGGAGACAGTTCTCTGGATGG 960
Qy 321 ArgLeuGluGlnPheGluLysThrGluAenLeuArgLeuSerAaspSerProPheArgPhe 340
Db 961 CGCTTAGACAAATTCGAAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTT 1020
Qy 341 PheAlaAlaGlyAenValAlaPheAlaLysLysTrpLeuAenLysSerGlyPheAasp 360
Db 1021 TTTGCGCGGTAATTTGCTTTCGCTAAAAAATGGCTAAATAAATCCGGTTTCTTTGAT 1080
Qy 361 GluGluPheAenHisTtrpGlyGlyLysValGluPheGlyTyrArgLeuPheArgTyr 380
Db 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGTTAC 1140
Qy 381 GlySerPhePheLysThrileAaspGlyileMetAlaTyrHisGlnGluProProGlyLys 400
Db 1141 GGTAGTTTCTTTAAACTATTGATGGCATTTATGGCTACCATCAAGACCCACAGGTAAA 1200
Qy 401 GluAenGluThrAaspArgGluAlaGlyLysAenlleThrLeuAaspilleMetArgGlyLys 420
Db 1201 GAAATGAAACCGATCGTGAACGGGAAAAAATATTACGCTCGATATTATGAGAGAAAG 1260
Qy 421 ValProTyrilleTyrArgLysLeuLeuProilleGluAaspSerHisleAenArgValPro 440
Db 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTGCGATCAATAGAGTACT 1320
Qy 441 LeuValSerilleTyrileProAlaTyrAenCyAlaAenTyrilleGlnArgCysValAasp 460
Db 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAAGTTGCGTAGAT 1380
Qy 461 SerAlaLeuAenGlnThrValValAaspLeuGluValCysilleCysAenAaspGlySerThr 480
Db 1381 AGTGCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAGCATGGTTCAACA 1440
Qy 481 AaspAenThrLeuGluValilleAenLysLysTyrGlyAenAenProArgValArgileMet 500
Db 1441 GATAATACCTTAGAAGTGATCAATTAAGCTTTATGTTAATAATCCTAGGGTACGCATATG 1500
Qy 501 SerLysProAenGlyGlyileAlaSerAlaSerAenAlaAlaValSerPheAlaLysGly 520
Db 1501 TCTAAACCAATGCGGGAATACGCTCAGCATCAATATGACGCGGTTCTTTGCTTAAGGT 1560
Qy 521 TyrTyrilleGlyGlnLeuAaspSerAaspTyrLeuGluProAaspAlaValGluLeuCys 540
Db 1561 TATTACATTTGGCAGTTAGATTAGATGATTTATCTTGAAGCTGATGCGAGTTCAACTGTGT 1620
Qy 541 LeuLysGluPheLeuLysAaspLysThrLeuAlaCysValTyrThrAenArgAenVal 560
Db 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAACGTC 1680
Qy 561 AenProAaspGlySerLeuileAlaAenGlyTyrAenTirpProGluPheSerArgGlyLys 580
Db 1681 AATCCGGATGGTAGCTTAATCGCTAATGTTACATTTGCCAGAAATTTTCACAGAGAAA 1740
Qy 581 LeuThrThrAlaMetilleAlaHisPheArgMetPheThrilleArgAlaTirpHisLeu 600
Db 1741 CTCACACCGCTATGATTGCTCACCACTTTAGAAATGTTTACCGATTAGAGCTTGGCATTTA 1800
```

```
Qy 601 ThrAaspGlyPheAenGluLysilleGluAenAlaValAaspTyrAaspMetPheLeuLysLeu 620
Db 1801 ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCAAACTC 1860
Qy 621 SerGluValGlyLysPheLysHisLeuAenLysileCysTyrAenArgValLeuHisGly 640
Db 1861 AGTGAAGTTGGAAATTTTAAACATCTTNAATCTGCTATTAACCGTGTATTACATGGT 1920
Qy 641 AaspAenThrSerilleLysLysLeuGlyilleGlnLysLysAenHisPheValValAen 660
Db 1921 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980
Qy 661 GlnSerLeuAenArgGlnGlyilleThrTyrTyrAenTyrAaspGluPheAaspLeuAasp 680
Db 1981 CAGTCATTAATAGACAGGCATAAATTTATTAATTTATGACGAATTTGATGATTTAGAT 2040
Qy 681 GluSerArgLysTyrillePheAenLysThrAlaGluTyrGlnGluGluilleAaspilleLeu 700
Db 2041 GAAAGTAGAAGTATATTTTCAATTAACCCGCTGAATATCAAGNAGAGATTTGATATCTTA 2100
Qy 701 LysAaspille 703
Db 2101 AAAGATATT 2109

RESULT 5
US-09-495-406-1
; Sequence 1, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11474
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384
; OTHER INFORMATION: including LOS biosynthesis locus
US-09-495-406-1

Alignment Scores:
Pred. No.: 1,24e-30 Length: 11474
Score: 384.50 Matches: 243
Percent Similarity: 35.71% Conservative: 163
Best Local Similarity: 21.37% Mismatches: 337
Query Match: 7.53% Indels: 394
DB: 3 Gaps: 52

US-10-642-248-2 (1-972) x US-09-495-406-1 (1-11474)
Qy 10 AlaTyrAenSerAenAaspTyrGlnLeuAlaLeu-----LysLeuPheGluLysSer 26
Db 1459 AGTTATGCAAAAAATGATTGGATTTTAAGCATTTGATGCTGATGAAGTCTTGAAATGAG 1518
Qy 27 Ala-----GluilleTyrGlyArgLysileValGluPheGlnilleThrLysCysLysGlu 44
Db 1519 TGTATTAAAGAGCTTAAAAAATTTAAACTTCAAGAGATAATATTCATCGCATTAGCCGT 1578
Qy 45 LysLeuSerAlaHisProSerValAenSerAlaHisLeuSerValAenLysGluLys 64
Db 1579 AAA-----AATCTCTATAAAGCGCAATGG 1602
Qy 65 ValAenValCys-----AaspSerProLeuAaspilleAlaThrGln----- 77
```





```
QY 719 rProAsnThrLeuAenGlyLeuValLysLeuAenAsnIleleGluTyrAsnLysAs 739
Db 3421 TAGAGATATTTCTTTTGA-----TGGATCGATGATGATTTAT----- 3463
QY 739 nIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGlu 759
Db 3464 -----TTTAAAGCAAT 3477
QY 759 uIleLeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAenAspIleSer-- 778
Db 3478 TAAACTTAATTT-----ATAAATTTTATTCATCAATGAAGATATACACTT 3522
QY 779 -----TyrTyrThrSerAsnArgLysLeuLysThrGluAlaHisLeuSerAs 794
Db 3523 TGGGATAATTTTGTGTAGTGTCTAATAAATTTATGTT-----TTATCACA 3570
QY 794 nIleAsnLysLeuSerGlnLeuAsnLeuAsnCysGluTyrIlelePheAspAsnHisAs 814
Db 3571 AAAGTTGATTTGTGCTGCTTTAAGAGCAACAGT-----ATATCAATCATGA 3618
QY 814 pSerLeuPheValLysAsnAspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAs 834
Db 3619 T-----AAGAAG----- 3625
QY 834 nPheSerAlaLeuThrHisAspTyrIleGluLysIleAsnAlaHisProPheLysLys 854
Db 3626 -----ATTACAAAGCAATGTGTCAGAGTATTTTAAAGA 3660
QY 854 sLeuIleLysThrTyrPheAsnAspAsnAspLeuLysSerMetAsnValLysGlyAlaSe 874
Db 3661 TATATATGAACT--TTTCGGGAAACGCTAAGGAGCAAAATTTTAAAGCAGC 3717
QY 874 rGlnGlyMetPheMetThrTyrAlaLeu-----AlaHisGluLe 887
Db 3718 AAGCAGGGTTATACTGCTTTTAAATTTGATAGAATTTTAAAGATCAAAACGAAAA 3777
QY 887 uLeuThrIleleLysGluValIleThrSerCys----- 898
Db 3778 TGCACCTGCTATAAAGAAACATATTTTACCTTGCTATGCCAAAAAGCTTTAATGATTAA 3837
QY 899 -----GlnSerIleAspSerValProGluTyr 907
Db 3838 AAAATTTAAAGATCCTTTAAATTTAAAGGAACAATTTAGTTTAAATTAACCTTTTAT 3897
QY 907 rAsnThrGlu-----AspIleTyr 913
Db 3898 TCAACAAACAACTCCTTATGATATTTGGAAATTTTGGCAAAAAATAAAAAATATTAAATA 3957
QY 913 ----- 913
Db 3958 ATAAAAATAAAAAATTAATTAATTTTAGGTATTAATCACTATTAATTAGGAGAAAT 4017
QY 914 -----PheGln-----PheAlaLeuLeuIleLeuGluLys 923
Db 4018 ATTTTATATGCTATTTCAATCATACTTTGTGAAATAATTTGCTTATTCATCCTTTTAG 4077
QY 923 sLysThrGlyHisValPheAsnLysThrSerThrLeu----- 935
Db 4078 AAAAATTAGACATAAAATAAAAAACATTTTACTAAAAAACATACACGAGATAAAAT 4137
QY 936 -----ThrTyrMetProTyrGluArgLysLeuGln-----TrpThrAsnGlnIle 951
Db 4138 CGAATCTTATTTACCAAAAAAACTCTGTGCAATTAATAATAACACATGAAGATT 4197
QY 951 eGluSerAlaLysArgGlyGluAsnIleProValAsnLysPheIleIle 967
Db 4198 A-----ATTAACTTAATAAGCTATTATA 4222
```

## RESULT 6

US-09-816-028A-1

; Sequence 1, Application US/09816028A

; Patent No. 6699705

## GENERAL INFORMATION:

```
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11474
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384
; OTHER INFORMATION: including LOS biosynthesis locus
US-09-816-028A-1
```

## Alignment Scores:

Pred. No.:	1.24e-30	Length:	11474
Score:	384.50	Matches:	243
Percent Similarity:	35.71%	Conservative:	163
Best Local Similarity:	21.37%	Mismatches:	337
Query Match:	7.53%	Indels:	394
DB:	3	Gaps:	52

US-10-642-248-2 (1-972) x US-09-816-028A-1 (1-11474)

```
QY 10 AlaTyrAsnSerAsnAspTyrGlnLeuAlaLeu-----LysLeuPheGluLysSer 26
Db 1459 AGTTATGCAAAAATGATTTAGCATTTTAACTTCAAGAGATAATATCATCGCACTTAGCGGT 1518
QY 27 Ala-----GluIleTyrGlyArgLysIleValGluPheGlnIleThrLysCysLysGlu 44
Db 1519 TGTATTAAAGAGCTTAAAAATTTAAACTTCAAGAGATAATATCATCGCACTTAGCGGT 1578
QY 45 LysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsnLysGluLys 64
Db 1579 AAA-----AATCTCTATANAAGCGCAATGG 1602
QY 65 ValAsnValCys-----AspSerProLeuAspIleAlaThrGln----- 77
Db 1603 ATAAAGGCATGTGGTGTGGCTGCTATGTTTGGAGATTTTAAATAAAATTTCACT 1662
QY 78 -----LeuLeuLeuSerAsnValLysLysLeu 86
Db 1663 CGTTTAAATGATAATTTAGTACATCAAGCCTTGTTTTGGCAAGTAAATGCTAAAAAATT 1722
QY 87 ValLeuSerAspSerGluLysAsnThrLeuLys----- 97
Db 1723 TATCTT-----AAAAATCGATTGAAGCATTTATCTTTAAGGATATCTCTCAC 1770
QY 98 -----AsnLysTyr-----LysLeuLeuThrGluLysLys 107
Db 1771 TTAATTCAAAAATCGAGTACTACTCAAGCTCTTTGGGCAAAACAAAAATATACACAAAAA 1830
QY 108 SerGlu-----AsnAlaGluValArgAlaValAlaLeuValProLysAspPhe----- 123
Db 1831 AGTGTGTTTAAAGCAAAATTTAGAGCTTTTGGACTTTTGGACTTTTGGAGAAATTTATTTTA 1890
QY 124 -----ProLysAspLeuValLeuAlaProLeuProAspHisVal 136
Db 1891 AAAAATGCTTTTATATGTTTAAAGGTTTATAATTAGC-----GTTTGTCTCGATTG 1947
QY 137 AsnAspPheThrTyrTyrLysLysArgLysLysArgLeuGlyLysProGluHisGln 156
Db 1948 GGAACATTTTAAATATATGAAATTTATATGAACCTTCAAGACAAAAACCAAAA----- 2001
```





Qy 262 -----AlaGluLeuLeuGluAspLeuThrIleIle 273  
Db 2353 GTAATTTTAAATAAAGAAAGCAAGATTTTAAACAAAGATGATTCGCATAAAT 2412  
Qy 274 GlyProArgLysTyrIleAspThrGlnHisIleAspProLysAspPheLeuAsnAla 293  
Db 2413 -----TTTAATAAATAAAGATTTTAAAGT- 2436  
Qy 294 SerLeuLeuGluSerLeuProGluValLysThrAsnAsnValAlaAlaLysGlyGlu 313  
Db 2437 -----TCTAAATAATCTCTTTTGTAGCTAAA- 2460  
Qy 314 GlyThrValSerLeuAspTrpArgLeuGlnPheGluLysThrGluAsnLeuArgLeu 333  
Db 2461 -----ATATTTTACAGCTTTTCAAAA-AAAAGATGAAAAATCTT- 2502  
Qy 334 SerAspSerProPhe-ArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLysTrpLe 353  
Db 2503 AAAACCACTCTTATTAAGGTATTAGGGTGGCAATATGAGTGTTTTAAACTGATTT 2562  
Qy 353 uAsnLysSerGlyPheAspGluGluPheAsnHisIleTrpGlyGlyGluAspValGluPh 373  
Db 2563 TGATGAACCTTGATGGTTTAAATGAAATTTTATTGGTTGGGTAGAGAAGATAGTAAT 2622  
Qy 373 eGlyTyrArg--LeuPheArgTyrGlySerPhe-----PheLysThrIleAs 388  
Db 2623 TGTTCGTAGATTTTATTTAATAAAGGCATTTTTCAGACGATTAATAATTTAAAGCTATT- 2680  
Qy 388 pGlyIleMeAlaTyrHisGlnGluProGlyLysGluAsnGluThrAspArgGluAl 408  
Db 2681 -GCTATCATATTTATCACAAAGAAATAGCAAAAATGCTTGAAGCAATCATCAA- 2737  
Qy 408 aGlyLysAsnIleThrLeuAspIleMetArgGluLysValProTyrIleTyrArgLysLe 428  
Db 2738 -----ATTATTATAGATACATCAAAAATAA- 2764  
Qy 428 uLeuProIleGluAspSerHisIleAsnArgValProLeuValSerIleTyrIleProAl 448  
Db 2765 -----AAGATTTCTGGAGATAAAACATGAAGAAATAATAGTGTAGTTATACCAAT 2814  
Qy 448 aTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGlnThrVal 468  
Db 2815 CTATATGTAGAAAAATATTAGAGAGATGTTTATAGATAGCGTTATCAATCAAACTTATAC 2874  
Qy 468 lAspLeuGluValCysIleCysAsnAspGlySerThrAsp---AsnThrLeuGluValIl 487  
Db 2875 TAACTTAGAATATCACTTGTCAATGATGGTAGCACAGATGAACACTCACTCAATATTGC 2934  
Qy 487 eAsnLysLeuTyrGlyAsnAsnProArgValArgIleMetSerLysProAsnGlyGlyIl 507  
Db 2935 AAAAGAATATACCTTAAAGAGATAAAGAAATAACTCTTTTGTATGAAGAAATGCGGGTTT 2994  
Qy 507 eAlaSerAlaSerAsnAlaValSerPheAlaLysGlyTyrTyrIleGlyGlnLeuAs 527  
Db 2995 AAGTTCAGCTAGAATATATAGGTATAGAAATCTTTAGCGGGGAATAT- 3040  
Qy 527 pSerAspAspTyrLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLysAs 547  
Db 3041 -----AAATTAATAAAA 3051  
Qy 547 pLysThrLeuAlaCysValTyrThrThrAsnArgAsnValAsnProAspGlySerLeuIl 567  
Db 3052 CAAAACCTCAACATATAAAGAAAAATCTTTAATAGAATTTCAATTTGGATGGTAAT- 3106  
Qy 567 eAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLysLeuThrThrAlaMetIleAl 587  
Db 3107 -----AATCCTTATAAT- 3118  
Qy 587 aHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPheAsnGluLys 607  
Db 3119 -----ATATATAAGCATATAAAGACTCTCAAGCTTTTATAATAGA 3159

Qy 607 sIleGlu-----AsnAlaValAspTyrAspMetPheLeuLysLeuSe 621  
Db 3160 AAAAGATTTAAACCAATTTTACTTACCCTAGTATAGATATTATTATTATCTTACATAGTGA 3219  
Qy 621 rGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAs 641  
Db 3220 TAATTATTGGAACATA- 3235  
Qy 641 pAsnThrSerIleLysLeuGlyIleGlnLysLysAsnHisPheValValValAsnGl 661  
Db 3236 -----AACTGCATAGAAATGCGTTATAAGATGAAAAAT- 3271  
Qy 661 nSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAsp---GluPheAspAspLeuAs 680  
Db 3272 -----GTGGATGATTGGTGTTCACCATGATTGCACCTATGAAGAC- 3313  
Qy 680 pGluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIle---AspIl 699  
Db 3314 -----AATATAAATAAATAAGCACAAAAAACAGGATGGAATTTTGTATTT 3360  
Qy 699 eLeuLysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTy 719  
Db 3361 TAAAAAAGAATGATATATCACTCCAAAAGAATATGCAAAATCGAGCATTAAGTGTAGATC 3420  
Qy 719 rProAsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAs 739  
Db 3421 TAGAGATATTTCTTTTGGG------TGAATGGAATGATTGATTTTAAT- 3463  
Qy 739 nIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGl 759  
Db 3464 -----TTTTAAAGCAAAAT 3477  
Qy 759 uIleLeuAlaPheTyHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSer-- 778  
Db 3478 TAAACTTAAATTT-----ATAAATTTTATTATCAATCAAGATATACACTT 3522  
Qy 779 -----TyrTyrThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAs 794  
Db 3523 TGGGATAATTTGTTTGTAGTGTCTAATAAATTTATGTT-----TTATCACA 3570  
Qy 794 nIleAsnLysLeuSerGlnLeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAs 814  
Db 3571 AAAGTTGTTATTTGTCGTCGTTTAAGACAAACAGT-----ATATCAAAATCATGA 3618  
Qy 814 pSerLeuPheValLysAsnAspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAs 834  
Db 3619 T-----AAGAAG----- 3625  
Qy 834 nPheSerAlaLeuThrHisAspTrpIleGluLysIleAsnAlaHisProProPheLysLy 854  
Db 3626 -----ATTACAAAGCAAAATGTGTACAGATATTTTAAGA 3660  
Qy 854 sLeuIleLysThrTyrPheAsnAspAsnLeuLysSerMetAsnValLysGlyAlaSe 874  
Db 3661 TATATATGAACCT---TTCGGGAAACCGCTAAGGAAGCAAAAATATTATTAAAGCAGC 3717  
Qy 874 rGlnGlyMetPheMetThrTyrAlaLeu-----AlaHisGluLe 887  
Db 3718 AAGCAGGGTTATACTGCTTTAAATTTGATAGAATTTTAAAGATCAAAAAAACGAAAA 3777  
Qy 887 uLeuThrIleLysGluValIleThrSerCys----- 898  
Db 3778 TGCACCTTGCTATAAAGAAACATTTTACCTTCTGTATGCCAAAAAGCTTTAATGATTAA 3837  
Qy 899 -----GlnSerIleAspSerValProGluTy 907  
Db 3838 AAAATTTAAAAAGATCCTTTAAATTTAAAGGAACAATTAGTTTAAATTAACCTTTAT 3897  
Qy 907 rAsnThrGlu-----AspIleTrp----- 913  
Db 3898 TCAACAAACAAACTTCTCTTATGATATTGGAATTTTGGCAAAAAATAAAAAATATTTAATA 3957  
Qy 913 ----- 913

Db	3958	ATAAAAATATAAAAAATTAAATTAATTTTGGTGATTAATCACTATAAATTTAGGAGAAAAT	4017
Qy	914	-----PheGln-----PheAlaLeuLeuIleLeuGluLy	923
Db	4018	ATTTTATATGCTATTTCACATCATACTTTGTGAAAAATAATTTGCTTATTCATCCCTTTTAG	4077
Qy	923	sLyThrGlyHisValPheAsnIysThrSerThrLeu	935
Db	4078	AAAAATTAGACATATAAAATAAAAAAAACATTTTCTATAAAAAACATACACGAGATAAAAT	4137
Qy	936	-----ThrTyrMetProTrpGluArgLysLeuGln-----TrpThrAsnGluGlnI	951
Db	4138	CGATTCTTATTATACCAAAAAAACTCTGTGCAAAATTAATAAATCAACAATGAAGATT	4197
Qy	951	eGluSerAlaLysArgGlyGluAsnIleProValAsnLysPheIleIle	967
Db	4198	-----ATTAACTTTAATAAAGCTATTATA	4232

## RESULT 8

```

US-10-303-134-1
; Sequence 1, Application US/10303134
; Patent No. 6825019
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,134
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11474
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384
; OTHER INFORMATION: including LOS biosynthesis locus

```

Alignment Scores:	
Pred. No.:	1,24e-30
Score:	384.50
Length:	11474
Matches:	243
Conservative:	163
Mismatches:	337
Best Local Similarity:	21.37%
Query Match:	7.53%
Indels:	394
Gaps:	52
DB:	3

US-10-642-248-2 (1-972) x US-10-303-134-1 (1-11474)

Qy	10	AlaTyrAenSerAsnAspTyrGlnLeuAlaLeu-----LysLeuPheGluLysSer	26
Dd	1459	AGTTATGCACAAAATGATTGGATTTTAAGCATTCATCTCATGAGTGCTTGAATAATGAG	1518
Qy	27	Ala-----GluIleTyrGlyArgGlysIleValGluPheGlnIleThrLysCysLysGlu	44
Dd	1519	TGTATTAAGAAGCTTAAATAATTTAAACTCAAGAACATAATATCATCGCACITTAGCCGT	1578
Qy	45	LysLeuSerAlaHisProSerValAsnSerAlaHisLeuSerValAsnLysGluLys	64
Dd	1579	AAA-----AATCTCTATAAAGCGAATGG	1602
Qy	65	ValAsnValCys-----AspSerProLeuAspIleAlaThrGln-----	77

Qy 373 eGlytyrArg---LeupheargtyrGlyserPhe-----PheylsThrileAs 388  
Db 2623 TGTTCAGATATTTTATTAATAAAGGCATTTTTCAGCGATTAATAATTTAAAGCTATT-- 2680  
Qy 388 pGlyleMetAlaTyrrHisGlnGluProProGlyLysGluAsnGluThrAspArgGluAl 408  
Db 2681 -GCTTATCATATTTATCACAAGAAATAATAGCAAAATAAGCTTGAAGCAATCATCAA-- 2737  
Qy 408 aGlyLysAsnIleThrLeuAspIleMetArgGluLysValProTyrrileTyrrArgLysLe 428  
Db 2738 -----ATTATTTATAGATACATCAAAATAA-- 2764  
Qy 428 uLeuProIleGluAspSerHisIleAsnArgValProLeuValSerileTyrrileProAl 448  
Db 2765 -----AAGATTTCTTCGAGATAAACAAGAAATAAGCTTAGTATACCAAT 2814  
Qy 448 aTyrrAsnCyseAlaAsnTyrrileGlnArgCyseValAspSerAlaLeuAsnGlnThrValVa 468  
Db 2815 CTATATGTAGAAAATAATTTAAGAGAATGTTTAGATAGCGTTATCAATCAACTTATAC 2874  
Qy 468 lAspLeuGluValCysIleCyseAsnAspGlySerThrAsp---AsnThrLeuGluValIl 487  
Db 2875 TAACCTAGAAATCATACTTGTCAATGATGTTAGTACACAGATGAACACTCACTCAATATTC 2934  
Qy 487 eAsnLysLeuTyrrGlyAsnAsnProArgValArgIleMetSerLysProAsnGlyGlyIl 507  
Db 2935 AAAAGAATATACCTTAAAGAGATAAAGAATAAATCTTTTTCGATAAGAAAAATGGGGTTT 2994  
Qy 507 eAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGlyTyrrileGlyGlnLeuAs 527  
Db 2995 AAGTTCAGCTAGAAATATATAGTATAGATATCTTTAGCGGGGAATAT-- 3040  
Qy 527 pSerAspAspTyrrLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLysAs 547  
Db 3041 -----AAATTAATAAAA 3051  
Qy 547 pLysThrLeuAlaCysValTyrrThrThrAsnArgAsnValAsnProAspGlySerLeuIl 567  
Db 3052 CAAAACTCAACATATAAAGAAAAATCTTTTAATAGAATTTTCAATTTGGATGGTAAT----- 3106  
Qy 567 eAlaAsnGlyTyrrAsnTrpProGluPheSerArgGluLysLeuThrThrAlaMetIleAl 587  
Db 3107 -----AATCCTTATAAT-- 3118  
Qy 587 aHisGlePheargMetPheThrIleArgAlaTrpHisLeuThrAspGlyPheAsnGluLy 607  
Db 3119 -----ATATATAAGCATATAAAGACTCTCAAGCTTTTATAATAATGA 3159  
Qy 607 sIleGlu-----AsnAlaValAspTyrrAspMetPheLeuLysLeuSe 621  
Db 3160 AAAAGATTTAAACCAATTTTACTTACCCTAGTATAGATTTATATATTTCTTAGATAGTA 3219  
Qy 621 rGluValGlyLysPheLysHisLeuAsnLysIleCysTyrrAsnArgValLeuHisGlyAs 641  
Db 3220 TAATTTTGGAACTA----- 3235  
Qy 641 pAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValValAsnGl 661  
Db 3236 -----AACTGCATAGAGAATCGTTATAAGAATGAAAAAT-- 3271  
Qy 661 nSerLeuAsnArgGlnGlyIleThrTyrrAsnTyrrAsp---GluPheAspAspLeuAs 680  
Db 3272 -----GTGGATGTATTGTGGTTTGCACCATGATTCACCTATGAAGAC----- 3313  
Qy 680 pGluSerArgLysTyrrilePheAsnLysThrAlaGluTyrrGlnGluIle---AspIl 699  
Db 3314 -----AATATAAATAATAGCACAAAAAACAAGGATGGAATTTTGTATT 3360  
Qy 699 eLeuLysAspIleLysIleGlnAsnLysAspAlaLysIleAlaValSerilePheTy 719  
Db 3361 TAAAAAAGAATGATATAATCACTCCAAAAGAATATGCAAAATCGACATTAAGTGTAGGATC 3420

Qy 719 rProAsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrrAsnLysAs 739  
Db 3421 TAGAGATATTTCTTTTGG-----TCGAATGGAATGATTTGATTTTAAT-- 3463  
Qy 739 nIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGl 759  
Db 3464 -----TTTTTAAAGCAAT 3477  
Qy 759 uIleLeuAlaPheTyrrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSer-- 778  
Db 3478 TAAACTTAATTTT-----ATAAATTTTATATCAATCAAGATATACACTT 3522  
Qy 779 -----TyrrTyrrThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAs 794  
Db 3523 TGGGATAATTTTCTTCTAGTCTGCTAATAAATTTATGTT-----TTATCACA 3570  
Qy 794 nIleAsnLysLeuSerGlnLeuAsnLeuAsnCyseGluTyrrileIlePheAspAsnHisAs 814  
Db 3571 AAAGTTGTTATTTGTCGCTTTAAGACAAACAGT-----ATATCAAAATCATGA 3618  
Qy 814 pSerLeuPheValLysAsnAspSerTyrrAlaTyrrMetLysLysTyrrAspValGlyMetAs 834  
Db 3619 T-----AAGAAG----- 3625  
Qy 834 nPheSerAlaLeuThrHisAspTrpIleGluLysIleAsnAlaHisProProPheLysLy 854  
Db 3626 -----ATTACAAAAGCAATGTCGACAGATTTTAAAGA 3660  
Qy 854 sLeuIleLysTyrrThrPheAsnAspAspLeuLysSerMetAsnValLysGlyAlase 874  
Db 3661 TATATATGAAACT---TTGGGGAAAAACGCTAAGGAAGCAAAAATATTTTAAAGCAGC 3717  
Qy 874 rGlnGlyMetPheMetThrTyrrAlaLeu-----AlaHisGluLe 887  
Db 3718 AAGCAGGTATTAACCTGCTTTAAATTTGATAGAAATTTTAAAGATCAAAAAAACGAAA 3777  
Qy 887 uLeuThrIleLysGluValIleThrSerCys----- 898  
Db 3778 TGCACCTGCTATTAAGAAACATTTTACCTGCTGATGCCAAAAAGCTTTAATGATTAA 3837  
Qy 899 -----GlnSerIleAspSerValProGluTy 907  
Db 3838 AAAATTTAAAAAAGATCCTTTAAATTTTAAAGGAACAATTAGTTTAAATTAACCTTTAT 3897  
Qy 907 rAsnThrGlu-----AspIleTrp----- 913  
Db 3898 TCAAACAAAACTTCTTATGATATTTGGAAATTTTGGCAAAAAATAAAAAATATTTAATA 3957  
Qy 913 ----- 913  
Db 3958 ATAAAAATATAAAAAATTAATTTTAGGTATTAATCACTATATATATAGGAGAAAAT 4017  
Qy 914 -----PheGln-----PheAlaLeuLeuIleLeuGluLy 923  
Db 4018 ATTTTATATGCTATTTCAATCATACTTTGTGAAAAATAATTTGCTTATTCATCCCTTTAG 4077  
Qy 923 sLysThrGlyHisValPheAsnLysThrSerThrLeu----- 935  
Db 4078 AAAAATTTAGACATAAAAAATAAAAAAACATTTTACTAAAAAACATACACAGATAAAAT 4137  
Qy 936 -----ThrTyrrMetProTrpGluArgLysLeuGln-----TiphThrAsnGluGlnIl 951  
Db 4138 CGATTCCTTATTTACCAAAAAAAACTCTGTGGCAAAATTAATAATACAACTGAGAGTTT 4197  
Qy 951 eGluSerAlaLysArgGlyGluAsnIleProValAsnLysPheIleIle 967  
Db 4198 A-----ATTAAACTTAATAAAGCTATTATA 4222

## RESULT 9

US-10-303-118-1

; Sequence 1, Application US/10303118

; Patent No. 6905867

; GENERAL INFORMATION:





```
Qy 487 eAsnLysLeuTyrGlyAsnAsnProArgValArgIleMetSerLysProAsnGlyGlyI1 507
Db 2935 AAAAGAAATATACCTTAAAGAGATAAAGAAATACCTTTTGTATAGAAAATGGGGTGT 2994
Qy 507 eAlaSerAlaSerAsnAlaValSerPheAlaLysGlyTyrTyrIleGlyGlnLeuAs 527
Db 2995 AAGTTAGCTAGAAATATAGTATAGAACTACTTTAGCGGGGAATAT----- 3040
Qy 527 pSerAspTyrLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLysAs 547
Db 3041 -----AAATTAAGAAA 3051
Qy 547 pLysThrLeuAlaCysValTyrThrThrAsnArgAsnValAsnProAspGlySerLeuI1 567
Db 3052 CAAAACTCAACATATAAAGAAAATCTTTTAATAGAATTTCAATGGATGGTAAT----- 3106
Qy 567 eAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLysLeuThrAlaMetIleAl 587
Db 3107 ----AATCCTTATAT----- 3118
Qy 587 aHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPheAsnGluLy 607
Db 3119 -----ATATATAAGCATATAAAGAGCTCTCAAGCTTTTAATAATGA 3159
Qy 607 sIleGlu-----AsnAlaValAspTyrAspMetPheLeuLysLeuSe 621
Db 3160 AAAAGATTTAACCAATTTTACTTACCCTGATGATATATATATATCTTTAGATAGTGA 3219
Qy 621 rGluValGlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAs 641
Db 3220 TAATTATGGAACTA----- 3235
Qy 641 pAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheValValAsnGl 661
Db 3236 ----AACTGCATAGAAGATCGTTATAAGAAATGAAAAAT----- 3271
Qy 661 nSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTyrAsp---GluPheAspAspLeuAs 680
Db 3272 -----GTGGATGTATTGTGTTTGGACCATGATGTCACCTTGAAGAC----- 3313
Qy 680 pGluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIle---AspI1 699
Db 3314 -----AATATAAATAATAGCACAAAAAACAAGGATGGAATTTTGATTT 3360
Qy 699 eLeuLysAspIleLysIleIleGlnAsnLysAlaLysIleAlaValSerIlePheTy 719
Db 3361 TAAAAAAGATGTATATACCTCCAAAAGAATATGCAATCGAGCATTAAGTGATGATC 3420
Qy 719 rProAsnThrLeuAsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAs 739
Db 3421 TAGAGATATTCTTTTGG-----TGAATGGAATGATGATTTAAT----- 3463
Qy 739 nIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLysLysGl 759
Db 3464 -----TTTTTAAGCAAT 3477
Qy 759 uIleLeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAsnAspIleSer-- 778
Db 3478 TAAACTTAAATTT-----ATAAATTTTATATCAATGAAGATATACACTT 3522
Qy 779 -----TyrTyrThrSerAsnArgLeuIleLysThrGluAlaHisLeuSerAs 794
Db 3523 TGGGATAATTTGTGCTAGTGTGTAATAAATTTATGTT-----TTATCACA 3570
Qy 794 nIleAsnLysLeuSerGlnLeuAsnLeuAsnCysGluTyrIleIlePheAspAsnHisAs 814
Db 3571 AAAGTTGATTGTGCTGTTTAAGAGCAACAGT-----ATATCAATCATGA 3618
Qy 814 pSerLeuPheValLysAsnAspSerTyrAlaTyrMetLysLysTyrAspValGlyMetAs 834
Db 3619 T-----AAGAA----- 3625
```

```
Qy 834 nPheSerAlaLeuThrHisAspTrpIleGluLysIleAsnAlaHisProProPheLysLy 854
Db 3626 -----ATTACAAAAGCAATGTGTACAGATATTTTAAAGA 3660
Qy 854 sLeuIleLysThrTyrPheAsnAspLeuLysSerMetAsnValLysGlyAlaSe 874
Db 3661 TATATATGAACT---TTCGGGAAACCGCTAAGGAAGCAAAAAATTTATTTAAAGCAGC 3717
Qy 874 rGlnGlyMetPheMetThrTyrAlaLeu-----AlaHisGluLe 887
Db 3718 AAGCAGGTATTAACCTTTAAATTTAGATAATTTTAAAGATCAAAAAACGAAAA 3777
Qy 887 uLeuThrIleLysGluValIleThrSerCys----- 898
Db 3778 TGCACCTTGCTATAAAGAAACATTTTACCTGCTATGCCAAAAAGCTTTAATGATTAA 3837
Qy 899 -----GlnSerIleAspSerValProGluLy 907
Db 3838 AAAATTTAAAAAGATCCTTTAAATTTAAAGGAACAATAGTTTAAATTAACCTTTTAT 3897
Qy 907 rAsnThrGlu-----AspIleTrp----- 913
Db 3898 TCAACACAAACTTCTTATGATATTTGGAAATTTTGGCAAAATTTTGCACAAAAATATTTAATA 3957
Qy 913 ----- 913
Db 3958 ATAAAAATATAAAAAATTAATTAATTTTAGGTATATCACTATATATATAGGAGAAAT 4017
Qy 914 -----PheGln-----PheAlaLeuLeuIleLeuGluLy 923
Db 4018 ATTTTATATGCTATTTCAATCATCATCTTTGTGAAAAATAATTTGCTTATTCATCCCTTTTAG 4077
Qy 923 sLysThrGlyHisValPheAsnLysThrSerThrLeu----- 935
Db 4078 AAAAATTTAGACATAAAATAAAAAACATTTTACTAAAAAACATACACAGAGATAAAAT 4137
Qy 936 ----ThrTyrMetProTrpGluArgLysLeuGln-----TyrThrAsnGluGlnI1 951
Db 4138 CGATTTCTATTACCAAAAAAAACTCTGTGCAAAATTAATAATACAAATGAAGATTT 4197
Qy 951 eGluSerAlaLysArgGlyGluAsnIleProValAsnLysPheIleIle 967
Db 4198 A-----ATTAACTTAATAAAGCTATTATA 4222

RESULT 10
US-10-303-128-1
; Sequence 1, Application US/10303128
; Patent No. 6911337
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,128
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11474
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384
; OTHER INFORMATION: including LOS biosynthesis locus
US-10-303-128-1
```





```
QY 519 LysGlyTyrTyrIleGlyGlnLeuAspSerAspTyrLeuGluProAspAlaValGlu 538
Db 11634 CGGGCAATGATATCATTTGTTGATCCCGCATGATATGGATCCAGATATATTGAG 11575
QY 539 -LeuCysLeuLysGlnPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnAr 558
Db 11574 TATCTGTATGTCATCTGTTAAGA--GCAATGCTACCATGTCTATC-TGTCAACACCG 11519
QY 558 gAsnValAsnProAspGlySerLeuIleAlaAsnGlyTyrAsnTrpProGlu----- 575
Db 11518 AAACGTTTACAAAATGCAAAATTCAGCAAACTTGTATGAAGACCGCTGCTTGA 11459
QY 576 -----PheSerArgGluLysLeuLysThrAlaMetIleAl 587
Db 11458 TTCGCATCTGCTGTTAAGCGTTATTGTACATGACCAAAATTGATCTTCAGTCTGGC 11399
QY 587 aHisHisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGly---PheAsnGl 606
Db 11398 GAAATTGTTATCCCGCTGGCTTCCAAAAAATTCATTTTCCAAAGCGCTTATTGTA 11339
QY 606 uLysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeuSerGluVal----- 623
Db 11338 AGACATC-----GCCGCAACATATAAGACGTTTCTGCGCTCGGACGATATTGCTGTGG 11285
QY 624 -GlyLysPheLysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAspAsnTh 643
Db 11284 TTCAGAAGCAAGTAGTATTATTCATTCAGATATAACTCGATTGTGAAT---GACCAATT 11228
QY 643 rSerIleLysLysLeuGlyIle-----GlnLysLys 653
Db 11227 TTCCTTTCACAGTTGGACTTAATTGATATGACAGACAGATGCGATGGAAGTTAAAAA 11168
QY 653 sAsnHisPheValValValAsnGlnSerLeuAsnArgGlnGlyIleThrTyrTyrAsnTy 673
Db 11167 A-----GTTTTCGGATCTTCAAAATCGCTTCTCAACGCTCGAGTGTATATGCATA 11117
QY 673 r-----AspGluPheAspLeuAspGluSerArgLysTyrIle 686
Db 11116 CATCAGTACCTTAAATCATGATGCAAAATGTTGCTATCAAGAAATTAAGAACAGCT 11057
QY 686 ePheAsnLysThrAlaGluTyrGlnGluIleAspIleLeuLysAspIleLysIle-- 705
Db 11056 AATTTCAAAATTAAGAGTTCCGAAA-----CCAGTTTGAAGATCATAAAGCGCC 11003
QY 706 -IleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrProAsnThrLeuAsnGl 725
Db 11002 TATACGAGATAAAGTAGCAATTTGTTAATTGGTTTGTAGTTATCCG----- 10957
QY 725 yLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIlePheValIleVal 745
Db 10956 -----ATATATAGAAAAGCTTGGAAATTTATCT 10928
QY 745 uHisValAspLysAsnHisLeuThrProAspIleLysLysGluIleLeuAlaPheTyrHi 765
Db 10927 TAAGATTAAAGAGGT-----GAGGAAGTATCGCTAATACTT 10889
QY 765 sLysHisGlnVal-----AsnIleLeuLeuAsnAsnAspIleSerTyrTy 780
Db 10888 TAAATGGTTTGGTTAAGATTGTTAAGATGCTCTG-----GATATATCTGTATTA 10838
QY 780 r-----ThrSerAsnArgLeuIleLysThrGluAlaHi 791
Db 10837 CCTTATGTATTCGAATTCGAAGGGAGTATTTCTGTCTCGTTATCAAAACAGGTGAAAA 10778
QY 791 sLeuSerAsnIleAsnLysLeuSerGlnLeuAsnLeuAsnCysGluTyrIleIlePheAs 811
Db 10777 AGCAAGTGGTTATGCAAA-----CACTTGAATAAACACATTTCTCACGTTCTTTT-- 10726
QY 811 pAsnHisAspSerLeuPheValLysAsnAspSerTyr 823
Db 10725 -TAAATAAATGCATATGATTTTCAACCCCAAGTTT 10690
```

```
RESULT 12
US-09-900-038A-3
; Sequence 3, Application US/099000038A
; Patent No. 6828128
; GENERAL INFORMATION:
; APPLICANT: Miyake, Katsuhide
; APPLICANT: Watanabe, Masaki
; APPLICANT: Iijima, Shinji
; TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
; FILE REFERENCE: 766.53
; CURRENT APPLICATION NUMBER: US/09/900,038A
; PRIOR FILING DATE: 2001-09-21
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6865
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae type Ib
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (617)..(1789)
; NAME/KEY: CDS
; LOCATION: (1816)..(2262)
; NAME/KEY: CDS
; LOCATION: (2265)..(2744)
; NAME/KEY: CDS
; LOCATION: (2843)..(3979)
; NAME/KEY: CDS
; LOCATION: (3982)..(4953)
; NAME/KEY: CDS
; LOCATION: (5009)..(5947)
US-09-900-038A-3
Alignment Scores:
Pred. No.: 6,21e-22 Length: 6865
Score: 302.50 Matches: 215
Percent Similarity: 38.02% Conservative: 158
Best Local Similarity: 21.92% Mismatches: 341
Query Match: 5.92% Indels: 267
DB: 3 Gaps: 45
US-10-642-248-2 (1-972) x US-09-900-038A-3 (1-6865)
QY 160 LeuSerIleIleValThrThrPheAsnArgProAlaIleLeuSerIleThrLeuAlaCys 179
Db 4000 GTTCTCATCTGTTATACCTTATATACACTCGGAAGCATATCTTAAA-----CAATGC 4050
QY 180 Leu-----ValAsnGlnLysThrHisTyrProPheGluValIleValThrAspAspGly 197
Db 4031 GTGCATTCGCTCTACACAGACTCATTCATTGATAGAAGTTATCTGATTAAATGATGGA 4110
QY 198 SerGlnGluAspLeuSerProIleArgGlnTyrGluAsnLysLeuAspIleArgTyr 217
Db 4111 TCCACTGATAATAGTGGAGAAATTTGTGATAATTTATCTCAAAAAGACGATCCGATACCT 4170
QY 218 ValArgGlnLysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeuArgLeu 237
Db 4171 GTATTTCATAAAAAAATTTGGA---GGGGTATCTTCGGCAAGGAACCTAGTCTTTGATAAA 4227
QY 238 AlaLysTyrAspPheIleGlyLeuLeuAspCysAsp-----MetAlaProAsnProLeu 255
Db 4228 TCCACAGCGGAATTCATTAACGTTTGTAGATGATGATTTTGTAGCACCAGATATAAT 4287
QY 256 TrpValHisSerTyrValAlaGluLeuLeuGluAspAsp-----Asp 269
Db 4288 GAAATA-----ATGTTAAAAAATTTAATCACTAGGATGCTGATATAGCAGAGTAGAT 4341
QY 270 LeuThrIleIleGlyProArgLysTyrIleAspThrGlnHisIleAsp---ProLysAsp 288
Db 4342 TTTGATATTTCCGAATGAGAGAGATTATAGAAAAAAGAAACGAAACCTTTTATAGGTC 4401
```

Qy 289 PheLeuAsnAenAlaSerLeuLeuGluSerLeuProGluValLysThrAsnAsnSerVal 308  
Dy 4402 TTTTAAAAACAATAATCTTTTAAAGAAATTTTATCAGGTAAATAGAGTGGAAATATTTGTT 4461  
Qy 309 AlaAlaLysGlyGlu-----GlyThrValSerLeuAspTrpArgLeuGlu 323  
Dy 4462 TGTACAAAAATATATATAAAAAAGTATAATTCGTAACTTGAGGTTTGAT----- 4509  
Qy 324 GlnPheGluLysThrGluAsnLeuArgLeuSerAspSerProPheArgPheAlaAla 343  
Dy 4510 -----GAGAAATTTAAAAATTTGGTGAG----- 4530  
Qy 344 GlyAsnValAlaPheAlaLysLysTrpLeu----- 353  
Dy 4531 ---GATTTTACTTTTAAATTTGTAATAATTTTATGTCAGAGCACTGCATAGTCGTAGATACG 4597  
Qy 354 -----AsnLysSerGlyPhePheAspGluGluPheAsn 364  
Dy 4598 ACTTCTTCCTTGACACCTATCGCATCGTAAAGACTTCTGCAATGAATCAGGAGTTCAC 4647  
Qy 365 His----- 365  
Dy 4648 GAAAAATTCATTAGATTTTATAACAATTTTAAATGAAATAAGCAGTATTTGTTCTCGCAAAA 4707  
Qy 366 -----TrpGlyGlyGluAspValGluPheGlyTyArgLeu 377  
Dy 4708 TTACGTAATTAATGTTGAAGCGAAATTTTAAAGAGAAAGGTAAAGTGCTCCGAAAAATG 4767  
Qy 378 PheArgTyArgLys-----PhePheLys 385  
Dy 4768 TTTGAATTAGCTAGTAAATATTGACAGTAAATCAAATTTACAACGAGAGATTTTTCACAA 4827  
Qy 386 ThrIleAspGlyIleMetAlaTyHisGlnGluProGlyLysGluAsnGluThrAsp 405  
Dy 4828 GATGTAATTAATACCTTTCTAT----- 4851  
Qy 406 ArgGluAlaGlyLysAsnIleThrLeuAsp-----IleMetArgGluLys 420  
Dy 4852 ---AAAGCGGTAAAGTACTTATCAATTAAGGGATTTAGATATTTTCAATGAAATGT 4908  
Qy 421 ValProTyIleTyArgLysLeuLeuPro-----IleGluAspSer 434  
Dy 4909 TCACCCATCTGTATATAAATTTATATCAGAGTTTCAAAAACAGTAAGTAATCAAAAAT 4968  
Qy 435 HisIleAsnArgValProLeu-----ValSerIleTyI 446  
Dy 4969 TAAATTAACCTCAATTAACCTTTTAAATTTATAGGAGTTGAAAAATGAATATAGTATCAT 5028  
Qy 446 eProAlaTyArgAsn---CysAlaAsnTyIleGlnArgCysValAspSerAlaLeuAsnG 465  
Dy 5029 GTCGGTATATAATGAGCCTTTAAATTTATGTGAGAGATTCAGTAGAATCTATATTAAATCA 5088  
Qy 465 nThrValValAspLeuValCysIleCysAsnAspGlySerThrAspAsnThrLeuG 485  
Dy 5089 AACCGCTTACTGATTTTGATTCATAATTTGTCATTTGATATCAATCAAGTAGAGTGATTTAA 5148  
Qy 485 uValIleAsnLysLeuTyArgLys---AsnAsnProArgValArgIle---MetSerLysPr 503  
Dy 5149 GCAATTCCTAACAGAAATATTCAGTTGTAGATAATAGATAAATAAATCTTGTCTAATGAAGA 5208  
Qy 503 oAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPheAlaLysGlyTyTyI 523  
Dy 5209 AAATATTGGTTTATGATCACTCAAGTTTGAACAAAGCGGTGAAATTTCTTAAGGGAATATAT 5268  
Qy 523 eGlyGlnLeuAspSerAspTyArgLeuGluProAspAlaValGluLeuCysLysLeuG 543  
Dy 5269 TTTTGAATGATGCTGATGATATTTTATATCCAGTAGATTTGTAAGCAAAATTCGT-- 5326  
Qy 543 uPheLeuLysAspLysThrLeuAlaCysValTyThrThrAsnArgAsnValAsnProAs 563  
Dy 5327 -TTTATGAGGAAAAATTCATTTGGATTTTCTCAGCAACTCTAATAGAAATTTGATAGACCAAAA 5385  
Qy 563 pGlySerLeuIleAlaAsnGlyTyArgAsnTrpProGluPheSerArgGluLysLeuThrTh 583

Dy 5386 AGGAATTTAGTA-----TATAAACAACGAGAAAGTATAATAATATATACTTAACATA 5436  
Qy 583 r-----AlaMetIleAlaHisIlePheArgMetPheTh 594  
Dy 5437 TGATATACGGAAGATGTTATTGAATAGATCTATACTTGCACCCACCAACGTCGGTGGTAA 5496  
Qy 594 rIleArgAlaTrpHisLeuThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTy 614  
Dy 5497 AAAGAAAGTTTTCGATAAGTTAATGGATATAGAGATTTAGTACCT---GTTGAAGATTA 5553  
Qy 614 rAspMetPheLeuLeuSerGluValGlyLysPheLysHisLeuAsnLysIleCysTy 634  
Dy 5554 TGATTTTGCAATAGA---GGACTCTGGCTGATTTC----- 5587  
Qy 634 rAsnArgValLeuHisGlyAspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAs 654  
Dy 5588 -----AAATCGGCTTACTCAATAAA-- 5608  
Qy 654 nHisPheValValAsnGlnSerLeuAsnArgGlnGlyIleThrTyTyArgAsn---Ty 673  
Dy 5609 ---GTACTTTTACAGTATAGATTAAACGAGAATGGAATATCAAAACCAATAAGTT 5661  
Qy 673 rAspGluPhe-----AspAspLeuAspGluSerArgLysTyIle-- 686  
Dy 5662 TAAGCAATATATTACTCAGCTATTTTACAAGATTTTATAAGAAAAAATCTTATATGA 5721  
Qy 687 -PheAsnLysThrAlaGluTyArgGlnGluIleAspIle----- 699  
Dy 5722 TATCACAAAAATTTACTAATTTACTTTCAAGAGTAGTGTGATAAAGAAACGCTATACTCAGCA 5781  
Qy 700 -----LeuLysAspIleLysIleIleGlnAsnLysAspAlaL 712  
Dy 5782 AGAGCTCTCTAAATATTTTGAGCTAAATCTACCCCTAGTATTACTATTAGAAAACTATA 5841  
Qy 712 sIleAlaValSerIlePheTyProAsnThrLeuAsnGlyLeuValLysLysLeu---- 730  
Dy 5842 TATTTGTTTATATTATATCTTTAAGTCTCCC-----TTGGTTAGGAGTTTATTAAT 5892  
Qy 731 -AsnAsnIleIleGluTyArgLysAsnLysAsnIlePheValIleValLeuHis-ValAspLysA 750  
Dy 5893 AAATGATATT-----AATATTTTAGTACTGAAATTTGTTGGAGGAGAGAA 5937  
Qy 750 snHisLeuThrProAspIleLysLysGluIleLeuAlaPheTyHisLysHisGlnValA 770  
Dy 5938 ACAAGTGACT-----AATAGAAAAATTTATGTATGTCATCTCTTTTATCATTTAT 5988  
Qy 770 snIleLeuLeuAsnAsnAspIleSerTyTyThrSerAsnArgLeuIleLysThrGluA 790  
Dy 5989 TGATTTGTTTATATAAGAGAGATATAT-----TCAATTTTAGAAATTTATCTCTCT 6042  
Qy 790 laHisLeuSerAsnIleAsn-----LysLeuSerGlnLeuAsnLeuAsnCysG 806  
Dy 6043 CTCTCTCTCTGATGTTGATAATTTAGAGAAAAAATAAATAAATAAATAAATAATATAC 6102  
Qy 806 luTyIleIlePheAspAsnHisAspSerLeuPheValLysAsnAspSerTyArgLysM 826  
Dy 6103 ATATTTTA-----GAAGAACTCTAGTCGTGAAAGTGAAGATTTATTCAGTAC 6150  
Qy 826 etLysLysTyArgValGlyMetAsnPheSerAlaLeuThrHisAspTrpIleGluLysI 846  
Dy 6151 TTTAAA-----GATCTGGTCTAAGTTATAGTAGTTGATAGTAAATTTGTTTATTTTA 6204  
Qy 846 leAsnAlaHisProPheLysLysLeuLys-----ThrTyPheAsn-----A 862  
Dy 6205 ATGATGCAACGCTTATTTGGGAGGACACTAATAAAGCATGTTATTTTATATAATCTAAT 6264  
Qy 862 spAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMet----- 877  
Dy 6265 AAGATGGTTTAAATGTTGTTTACTTACTTATATTAGTCAAAACCTTTGGAGGTATTATG 6324  
Qy 878 -----PheMetThrTyArgAlaLeuAlaH 885



Db 6325 TAAAAAATATATTCTTCACAAAATTCAGCCACATGGATTTTCACGATATTGTTTGGGA 6384  
Qy 885 isGluLeuThrIleile----- 891  
Db 6385 TTGAAGTTAATCAATTAGTTAATTGGCAAGGATCCGCTTATAAAAAATTTATTGAAG 6444  
Qy 892 -----LysGluValIleThrSerCysGlnSerIleAspSerValProGluTyrAsnT 909  
Db 6445 TCCCTAGGAAGAACTT-----TTTGACAATGTAACGAATATCAAA 6486  
Qy 909 hrGluAspIleTrpPheGlnPheAlaLeuLeuIleLeuGluLysThrClyHisValP 929  
Db 6487 AAGAAATGGCAATAAATCTTTTGGAGCAGTAAGAGTTAGTATTAAATCACTTCAGTAC 6546  
Qy 929 heAsnLysThrSerThrLeuThr-----TyrMetProTIPGluArgLysLeuG 945  
Db 6547 TAGTATTAAACCGACCTCTACTATAGATAAAGAGTTTATGAGTTATAACAAATAGATAG 6606  
Qy 945 InTTrpAsnGluGlnIleGluSerAlaLysArgGlyGluAsnIleProValAsnLys 964  
Db 6607 AAACGTCGAGAACAAATTTAATTTTATAAATCAATAGTCAATGAATATATAATAAA 6665  
RESULT 13  
US-09-107-532A-3235  
; Sequence 3235, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD/ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Deneka  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 3235:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2166 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...2166  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

## US-09-107-532A-3235

Alignment Scores:  
Pred. No.: 1.19e-22 Length: 2166  
Score: 301.50 Matches: 153  
Percent Similarity: 38.06% Conservative: 121  
Best Local Similarity: 21.25% Mismatches: 259  
Query Match: 5.90% Indels: 187  
DB: 3 Gaps: 28

## US-10-642-248-2 (1-972) x US-09-107-532A-3235 (1-2166)

Qy 269 AspLeuThrIleIleGly-----ProArgLysTyrIleAspThrGlnHis 283  
Db 88 GATTTCGTTATTGTCGGCTCGGCAATTGATGAAGTGACCAAGAAATCCCTACGATAAAG 147  
Qy 284 IleAspProLysAspPheLeuAsnAlaSerLeuLeuGluSerLeuPro----- 300  
Db 148 GTAGAAAAGAAATGATGATTGCTGAAGCAACACATGTCGTAGATTGGATATCAATCAT 207  
Qy 301 -----GluValLysThrAsnAsnSer-----ValAlaLysGly 312  
Db 208 TTATATAATCTTGATGTTAGACCCAAAGCGGTTTTAAGGTACGTTTATCAGGAAATG 267  
Qy 313 GluGlyThrValSerLeuAspTrpArgLeuGluGlnPheGluLysThrGluAsnLeuArg 332  
Db 268 AGAGGAAAAGCAATCTTTAGACTTCCAAACACAGCAACATCAAAATGGCATAGCTGTGAAA 327  
Qy 333 LeuSerAspSer---ProPheArgPhePheAlaAlaGlyAsnValAlaPheAlaLysLys 351  
Db 328 TTAACCGTAAATATCCTTAT-----GATGACGGCATTTGAATCTTCA 369  
Qy 352 TrpLeuAsnLysSerGlyPhePheAspGluGluPheAsnHisTrpGlyGlyGluAspVal 371  
Db 370 TGGGAAAAGAAAAGATTACTGAAAAAGGGATAAATTATGCAAGGACTCATGGCGTA 429  
Qy 372 GluPheGlyTyrArgLeuPheArgTyrGlySerPhePheLysThrIleAspGlyIle--- 390  
Db 430 AAAAAAGCAATCCCGCGGTCAAACTGGAATTGAAACCCAGGATCGATGTCAGAG 489  
Qy 391 ---MetAlaTyrHisGlnGluProGlyLysGluAsnGluThrAspArgGluAlaGly 409  
Db 490 TGGATCAGTCGTCATGAGAAACCTGATCTGAAAGAGCAAGG----- 531  
Qy 410 LysAsnIleThrLeuAspIleMetArgGluLysValProTyrIleTyrArgLysLeuLeu 429  
Db 532 -----AAAGAAGTCAACAGGATTTGCCTACCGC----- 558  
Qy 430 ProIleGluAspSerHisIleAsnArgValProLeuValSerIleTyrIleProAlaTyr 449  
Db 559 -----CCATTGATTTCCATATCTTATGCTGCTCAT 588  
Qy 450 AsnCys---AlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGlnThrValVal 468  
Db 589 AACGTTGAAATCAAAATGGCTCGAAAATGCAATTGATTCGGTACTTGATCAAAAGTATGAT 648  
Qy 469 AspLeuGluValCysIleCysAsnAspGlySerThrAspAsnThrLeu---GluValIle 487  
Db 649 CACTGGGAACATATGATCATGATGATGCTTCTACTGATCCAGCTATCCGAAAGTCTTA 708  
Qy 488 AsnLysLeuTyrGlyAsnAsnProArgValArgIleMet---SerLysProAsnGlyGly 506  
Db 709 GAATCCTATCAAGCAAAAGATGATAGATAATAAGTCGTTTTCCGACAAAGAAATGGACAC 768  
Qy 507 IleAlaSerAlaSerAsnAlaValSerPheAlaLysGlyTyrIleGlyGlnLeu 526  
Db 769 ATCAGTCTGGCAACTAATTCTGCATTGGAAATGGCAGAGGAGAGATTATACCGCTCTTA 828  
Qy 527 AspSerAspAspTyrLeuGluProAspAlaValGluLeuCysLeuLysGluPheLeuLys 546  
Db 829 GATAATGATGACGAATTACCTCCATTTGCCTTATATGAAGTGGCAAAAGTGTAAACGTA 888  
Qy 547 AspLysThrLeuAlaCysValTyrThrAsnArgAsnValAsnProAspGlySerLeu 566

```

Db      889  CATCCAGAACTGGATTGATCTACAGTCAGCAAGATATAATCGATCGAGATGGGAATCGC 948
Qy      567  IleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLysLeuThrThrAlaMetIle 586
Db      949  TTTGACCGGCACTTCAAA---GCAGACTGGTCTCCCGATACATTGATGGGAAATAATTAT 1005
Qy      587  AlahisPheArgMetPheThrIleArgAlaTrpHisLeuThrAspGlyPheAsnGlu 606
Db      1006  ATCTCTCACTTAGCGGTATATCGGACCAAGCATTTGTTAAGGAACCTTGGCGGTTTCCGTA 1065
Qy      607  LysIleGluAsnAlaValAspTyrAspMetPheLeuLysLeuSerGluValGlyLysPhe 626
Db      1066  GGATATGAGGCTCTCAAGATTATGATTTGGTCTTCTGTGACAGAACAAATTCCTGCA 1125
Qy      627  LysHisLeuAsnLysIleCysTyrAsnArgValLeuHisGlyAspAsnThrSerIleLys 646
Db      1126  GAACACATTTACCACATT-----GACGCTGCTCTGTAT----- 1158
Qy      647  LysLeuGlyIleGlnLysLysAsnHisPheValValValAsnGlnSerLeuAsnArgGln 666
Db      1159  -----CAITGGCGGACGATCCCGGATCAACTGCAAGCAAT 1194
Qy      667  GlyIleThrTyrTyrAsnTyrAspGluPheAspLeuAspGluSerArgLysTyrIle 686
Db      1195  GGA-----GAAGCTAAAGCTCATC 1215
Qy      687  PheAsnLysThrAlaGluTyrGlnGluIleAspIleLeuLysAspIleLysIleIle 706
Db      1216  -----TATGATCTCGGATGAAAGCATTTGACAGATGCTCTATCTAGA 1257
Qy      707  GlnAsnLysAspAlaLysIle-----AlaValSerIlePheTyrProAsnThrLeu 723
Db      1258  AGAAATATCAAGGGAAGCGTACATCTCGGCAAGAAATTTCTGGTTTTATGAATCACTTAT 1317
Qy      724  AsnGlyLeuValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsnIlePhe----- 741
Db      1318  GATGTTTTCGAAGAAGACTTGGTCGTGTGATCATTCCAACTAAGATGGCTATGAAGAT 1377
Qy      742  -----ValIle-----ValLeu 745
Db      1378  CTAAAAAATTGTTGGATTGTCATCATCGAAAAACGCTTTATCCAAATATTAGAAATCAT 1437
Qy      746  HisValAspLysAsnHisLeuThrProAspIleLysLysGluIleLeuAlaPheTyrHis 765
Db      1438  ATTGCAGATATGAAGTACAGATCCTAAAAATG---CAAGAATATTATTGCAAGATAC--- 1491
Qy      766  LysHisGlnValAsn-----IleLeuLeuAsnAsnAspIleSerTyrTyrThrSer 782
Db      1492  AAGCATCAGCTGAAAGACCGATTATCGTC----- 1521
Qy      783  AsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGlnLeuAsn 802
Db      1522  ---GAATTAATTGACATTTCCATTCATTTATTCAGTATCAACATCTGGCAGCAGAAAAA 1578
Qy      803  LeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsnAsp--- 821
Db      1579  GCAAAACGGCAAAATACTTTTATTTCTGAATTAACGATACAGAAGTGATTTGAACCTGCT 1638
Qy      822  -----SerTyrAlaTyr----- 825
Db      1639  ATGACAGGATGGTTTCTTATGCAAGTTTGATCGAATCGGCTGTGTAGGAGCAAAATTA 1698
Qy      825  ----- 825
Db      1699  TTTTATCCGGATGATACACCGCAGCATCGAGGTGATTATTATAGGATCGTGGCGTTGCA 1758
Qy      826  -----MetLysLysTyrAsp-----Val 831
Db      1759  GGACATGCATTTGAATAACTATGATCGAACAATTTGGTGTACTTTGGCCGATTTGGTCATT 1818
Qy      832  GlyMetAsnPheSerAlaLeuThrHisAspTrpIle-----GluLysIleAsn 847

```

```

Db      1819  GACGTCATTTACTTAGCAGTCACCTGAGCTTGTATGATGTCAGGCAAGCAGCTGACTTCAAT 1878
Qy      848  AlahisPheProPheLysLysLeuIleLysThrTyrPheAsnAspAsnAspLeuLysSer 867
Db      1879  GCTGTCAATGGAATTTGATGAATATTAGAAAGTAGCATTCAACGATGTTGACTTG----- 1932
Qy      868  MetAsnValLysGlyAlaSerGlnGlyMetPheMetThrTyrAlaLeuAlaHisGluLeu 887
Db      1933  ---TGCTTGAAGTTTATGAATCGGTGCTTACAAATGCTATGCACATCAAGCAGAAATTG 1989

RESULT 14
US-09-134-000C-2344
; Sequence 2344, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2344
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2344

Alignment Scores:
Pred. No.: 5,42e-21 Length: 2529
Score: 287.50 Matches: 189
Percent Similarity: 36.25% Conservative: 151
Best Local Similarity: 20.15% Mismatches: 298
Query Match: 5.63% Indels: 300
DB: 3 Gaps: 43

US-10-642-248-2 (1-972) x US-09-134-000C-2344 (1-2529)
Qy      156  GlnHisValGlyLeuSerIleIleValThrPheAsnArgProAlaIleLeuSerIle 175
Db      22  GAAATGTGAAGTGTCAGTCATTCCTGATACCCGCTATTAACGTAGAACCTATTAGAAGAG 81
Qy      176  ThrLeuAlaCysLeuValAsnGlnLysThrHisTyrProPheGluValIleValThrAsp 195
Db      82  GCATTAATGAGTTTGAAGAAACCAA---ACATTGAAGAAATTCGAATTCCTTAATTTAAT 138
Qy      196  AspGlySerGlnGluAspLeuSerProIleIleArgGlnTyrGluAsnLysLeuAspIle 215
Db      139  GATGGCTCTACTGATTAATAGTCAAAAATTTATTGAAGAA----- 177
Qy      216  ArgTyrValArgGlnLysAspAsnGlyPheGlnAlaSerAlaAlaArgAsnMetGlyLeu 235
Db      178  -----ATTCCACAAGATGATCCACGTTTCGGGTTTCAATGTTAAANATGGGGA--- 228
Qy      236  ArgLeuAlaLysTyrAspPheIleGlyLeuLeuAspCysAspMetAlaProAsnProLeu 255
Db      229  ---ATTGAAAGAGCCTTAACTTTGGGTGTTTCAGAGCAAAA----- 267
Qy      256  TrpValHisSerTyrValAlaGluLeuLeuGluAspAspLeuThrIleIleGlyPro 275
Db      268  -----GGTGAGTATATTGCTGAATTTGAAAGTGACGATGATGATGATGATGATGATG 321
Qy      276  ArgLysTyrIleAspThr-----GlnHisIleAspProLysAspPheLeuAsnAsn 292
Db      322  GAGGTTTATCAATACCGGCTAAAGTCATCATCGCAT----- 360
Qy      293  AlaSerLeuLeuGluSerLeuProGluValLysThrAsnAsnSerValAlaAlaLysGly 312
Db      361  -----GTTGTCGCTGTAATTTGGGTTGAATTTCTTCT 393

```

QY 313 GluGlyThrValSerLeuAsp-----TyrArgLeu-----GluGlnPheGluLeuThrGlu 329  
Db 394 GAAGAGAGGTGGAGGAGATATATTATGGCAATATCCGATAAATCAATCAATTTGATT 453  
QY 330 AsnLeuArgLeuSerAspSerProPheArgPhePheAlaAlaGlyAsnValAlaPheAla 349  
Db 454 GACTTAAACCGAGGATTTAATTGATCAAGTTTAT---CCATGGAATGCCATTTATATAA 510  
QY 350 LysLysTrpLeuAsnLysSerGlyPhe---PheAspGluGluPheAsnHisTyrGlyGly 368  
Db 511 AAAAGTAGTGTGAGAGAAACGTAACCTAGGATGAGGAATATAAAGTTATGGGAC 570  
QY 369 GluAspValGluPheGlyTyrArgLeuPheArgTyrGlySerPhePheLys----- 385  
Db 571 ACT-----GGTCTATTGTGGAATAATCAATTCA 597  
QY 386 -----ThrLeuAspGlyLeuMetAlaTyrHisGlnGluProPro 398  
Db 598 GCATCTCAGAATGTTATTTTATTAAAGATTGTTGTTATTTTATAGACAAGACACCCA 657  
QY 399 GlyLysGluAsnGluThrAspArgGluAlaGlyLysAsnIleThrLeuAspIleMetArg 418  
Db 658 -----AATCGCAGATAAATAATGTGGCA 681  
QY 419 GluLysValProTyrIleTyrArg----- 426  
Db 682 ACAAGGTTCCCTTCTGTTTCAACAATTTAACTAAATTCGTTCAAAATTTAAATGAACAA 741  
QY 426 ----- 426  
Db 742 AATAAATTTGAACGCTACAAAGTTATTTTATATAACAAATGTTGCAAAAAATACTTTGG 801  
QY 427 -----LysLeuLeuProIleGluAsp----- 433  
Db 802 GCGATTGAAATAATTAACCAATTTACGTGTGATGAGTCGGTTTATGAAGTGAATCAAAAGTG 861  
QY 433 ----- 433  
Db 862 CGAGTAGATTTTAGACAAGCTTTAGAACAGACGACGAGTGAATGATATCGATTTTGAATAC 921  
QY 434 -----SerHisIleAsn 437  
Db 922 ATCAACAATTTTATCAAAATTCGAAATGATCCAGCAGCTTATTATGAGGACTACTTGAAA 981  
QY 438 ArgValProLeuValSerIleTyrIleProAlaTyrAsnCysAlaAsnTyrIleGlnArg 457  
Db 982 AATCTGATAAAGTTAGTGTCTGTCGCGATTCACAATGCTTCAAAATATATTNAGACAA 1041  
QY 458 CysValAspSerAlaLeuAsnGlnThrValValAspLeuGluValCysIleCysAsnAsp 477  
Db 1042 ACATTAGAAACTGTTTGTGAGCAGTCTTTTACGTGAGATTGAATCATTTTAGTAGAAT 1101  
QY 478 GlySerThrAspAsnThrLeuGluValIleAsnLysLeuTyrGlyAsnAsnProArgVal 497  
Db 1102 GGCCTACAGATAATACCATGATGATATTATTAACGAATTTGCGAGTAAAGATCCGAGAATT 1161  
QY 498 ArgIleMetSerLysProAsnGlyGlyIleAlaSerAlaSerAsnAlaAlaValSerPhe 517  
Db 1162 ACGGGATTTCTATTGGCAAAAGTAACTCTGACACGCAAGAAATGTGGGCATTTTCGATG 1221  
QY 518 AlaLysGlyTyrTyrIleGlyGlnLeuAspSerAspAspTyrLeuGlu----- 533  
Db 1222 GCACGAGGACGGTATTTTGCATTTCTCGGATGCGATGATCATTTTGGACCGAATTTATTA 1281  
QY 534 -----ProAspAlaValGluLeuCysLeuLys 542  
Db 1282 CAAGACGCTTATTCGTGCATATGATAGTAGCAACAGATATCTGTTATTTCGCATGAAA 1341  
QY 543 GluPheLeuLysAspLysThrLeuAlaCysValTyrThrThrAsnArgAsnValAsnPro 562  
Db 1342 GAAAGTTACCAATGGAGAGTGCACGTTGTTTCAC-----AATCCA 1383  
QY 563 AspGlySerLeuIleAlaAsnGly-----TyrAsnTrpProGluPheSerArgGluLys 580

Db 1384 -----TTACTAATAATGCGGACGATGCTCGTGAAGAAATTTTATTGGATGAA 1434  
QY 581 LeuThrThrAlaMetIleAlaHisPheArgMetPheThrIleArgAlaTrpHisLeu 600  
Db 1435 GTAACCCCTTATTATATGATAAATATTTTATTAGAAATACATCAAGAAATAACTTG 1494  
QY 601 ThrAspGlyPheAsnGluLysIleGluAsnAlaValAspTyrAspMetPheLeu----- 618  
Db 1495 GTAAAC-----TTAGAACAAATTTGTTGCGGAGGATGCTTATTTCCACTTAT 1539  
QY 619 ---LysLeuSerGluValGlyLysPheLysHisIleuAsnLysIleCysTyrAsnArgVal 637  
Db 1540 ACAGCATTTATAGTACGAAATAATTTGTCACATCAACAAATATTTGCTGCACAGCAATC 1599  
QY 638 LeuHisGlyAspAsnThrSerIleLysLysLeuGlyIleGlnLysLysAsnHisPheVal 657  
Db 1600 GTTAGACAAGATGCTTG---ATGCTCAGTATCGAATGAATTTATCGTGATGATGTTCAAT 1656  
QY 658 ValValAsnGlnSerLeu-----AsnArg----- 665  
Db 1657 TTACATGACAAATGTTGGAGTACTTAAACAACATGCTCCAATTCGAATTTGAAGCATPAT 1716  
QY 666 ---GlnGlyIleThrTyrTyrAsnTyrAspGluPheAsp-----AspLeuAspGlu 681  
Db 1717 CGGTAAATAATTTAATACATTAATTAACCTGGTTTATTTTATGATATGAATCGTGTGATCNA 1776  
QY 682 SerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluGluIleAspIleLeuLys 701  
Db 1777 GCATTTAAAGACGTTTC-----TATCAAGAA-----TTAAAA 1809  
QY 702 AspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIlePheTyrProAsn 721  
Db 1810 GAG---AAATACATCCAACAATTTAGGGCTAGACTTAGTGAATAAAGAAATATTTCTAAT 1866  
QY 722 ThrLeuAsnGlyLeu-----ValLysLysLeuAsnAsnIleIleGluTyrAsnLysAsn 739  
Db 1867 GATCAGAACAAAGTAGAGCGTATCACAGCAATCCAAATATTTTACAATACATCATAGAA 1926  
QY 740 IlePheValIleVal-----LeuHisValAspLysAsnHisLeuThrProAspIle 756  
Db 1927 ATATATCAAAATATTTATAAGATTTTGGGATGAATAAACCTTTATTTATTCGGAATGTT 1986  
QY 757 Lys-----LysGluIleLeuAlaPheTyrHisLysHisGlnValAsn--- 770  
Db 1987 CATATTCAGAGCGTGGAGGTAAAGTAATTTTGGACAAGAGAGACCCAGGGAATGG 2046  
QY 771 -----IleLeuLeuAsnAsnAspIleSerTyrTyrThrSer 782  
Db 2047 ACGCAATTTGAAATGTTTTCATTTATTTATTCAGATAACGAT-----ACAAGC 2094  
QY 783 AsnArgLeuIleLysThrGluAlaHisLeuSerAsnIleAsnLysLeuSerGlnLeuAsn 802  
Db 2095 AAT-----GCCAGCGAGTATGATTTGTTTATATGCGT 2130  
QY 803 LeuAsnCysGluTyrIleIlePheAspAsnHisAspSerLeuPheValLysAsnAspSer 822  
Db 2131 GACATACAAAAATAAT-----CATGATAGTTTATTAGTATCT----- 2169  
QY 823 TyrAlaTyrMetLysLysTyrAspValGlyMetAsnPheSerAlaLeuThrHisAspTrp 842  
Db 2170 ---TTATTAAATTAATAAAGAGGTACTACTTTTAAATCGATTTGTTTACACCGCAGTGG 2226  
QY 843 IleGluLysIleAsnAlaHis-ProProPheLysLysLeuIleLysThrTyrPheAsnAs 862  
Db 2227 ---GAAAAA-----GGCTATACCTTACTTACAGAAATAATGATATATA----- 2266  
QY 862 pAsnAspLeuLysSerMetAsnValLysGlyAlaSerGlnGlyMetPheMetThrTyrAl 882  
Db 2267 -----CTTTCGTAGACAATGTTTTTACAAATTTGG 2295  
QY 882 aleuAlaHisGluLeuLeuThrIleLysGluValIleThrSerCysGlnSerIleAs 902

Db 2296 GCGGCT-----ATACTCAAAATATGCACATTTGATTACA----- 2332  
Qy 902 pSerValProGluTyrAsnThrGluAspIleTrpPheGlnPheAlaLeuLeuIleLeuG1 922  
Db 2333 -----ATGTCGAATTTTGACTTCTC----- 2353  
Qy 922 uLysLysThrGlyHisVal-----PheAsnLysThrSerThrLeuThr 936  
Db 2354 -GAGAAAGGGGAAACACATTTTAGTGTCTGACAAAACCAAGGCTATATCC 2404  
RESULT 15  
US-08-961-527-71  
; Sequence 71, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Dikette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32768 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-961-527-71  
Alignment Scores:  
Pred. No.: 1,74e-18 Length: 32768  
Score: 281.50 Matches: 113  
Percent Similarity: 38.31% Conservative: 87  
Best Local Similarity: 21.65% Mismatches: 173  
Query Match: 5.51% Indels: 149  
DB: 3 Gaps: 19  
US-10-642-248-2 (1-972) x US-08-961-527-71 (1-32768)  
Qy 426 ArgLysLeuLeuProIleGluAspSerHisIleAsnArgValProLeuValSerIleTyr 445  
Db 6166 AGAAATTTGCTA---GTGGATGATAAA-----ATAACAGTCATT 6201  
Qy 446 IleProAlaTyrAsnCysAlaAsnTyrIleGlnArgCysValAspSerAlaLeuAsnGln 465  
Db 6202 GTACCGATATACAAATGTGGAAATCTATCTGAGGAAGTCCTAGATAGTATTATTACTCAA 6261  
Qy 466 ThrValValAspLeuGluValCysIleCysAsnAspGlySerThrAspAsnThrLeuGlu 485  
Db 6262 ACATATAAAATATTGAGATTGTGTCGTTAATGATGGTCTACGGATGCTTCAGGTGAA 6321

Qy 486 ValIleAsnLysLeuTyrGlyAsnAsnProArgValArgIleMetSerLysProAsnGly 505  
Db 6322 ATTTGTAAGAATTTTCAGAAATGGATCACCGAATTTCTATATAGAACACAGAAATGCT 6381  
Qy 506 GlyIleAlaSerAlaSerAsnAlaValSerPheAlaLysGlyTyrTyrIleGlyGln 525  
Db 6382 GGTCTTTTCGCCACGAAACACCGGTCTGANAATATATGTCGGAATATATGTGACCTTT 6441  
Qy 526 LeuAspSerAspAspTyrLeuGluProAspAlaValGluLeuCysLeuLys----- 542  
Db 6442 GTGGACTCGGATGATTGGATTGAGCAAGATTATGTAGAACTCTATATAAAAAATAGTA 6501  
Qy 543 GluPheLeuLysAspLysThrLeuAlaCysValTyrThrAsnArgAsn----- 559  
Db 6502 GAGTATCAGGCTGATATTGAGTTGGTAATATTATTCTTTCACGAAGATGAAGGAATG 6561  
Qy 560 -----ValAsnProAspGlySerLeu 566  
Db 6562 TTCTACTTTTCATATATTGGAGACTCTCTATTATGAGAAAGTATATGATATGTTCTATC 6621  
Qy 567 IleAlaAsnGlyTyrAsnTrpProGluPheSerArgGluLysLeuThrAlaMetIle 586  
Db 6622 TTTGAGAACTTGTATGAA-----ACTCAAGAAATGAAGAGTTTGTCTTGATA 6669  
Qy 587 AlaHisPheArgMetPheThrIleArgAlaTrpHisLeu----- 600  
Db 6670 TCTGCTGGGGTAAACTCTATAGGCAAGATTGTTGAGCAGTTGCGCTTTTGACATAGGT 6729  
Qy 601 -----ThrAspGlyPhe---AsnGluLysIleGluAsnAlaValAspTyrAspMet 616  
Db 6730 AATTAGGAGAGATGTTACTCTCAATCAAAAGGTA----- 6765  
Qy 617 PheLeuLysLeuSerGluValGlyLysPheLysHisLeuAsnLysIleCysTyr---Asn 635  
Db 6766 ---TATTATTATCAGAA-----AAGGTAATTTATTAATAAAGTCTTTATGCTTAT 6816  
Qy 636 ArgValLeuHisGlyAsp----- 641  
Db 6817 CGGATTAGAAAAGGTAGTTTATCAAGAGTTTGGACAGAAAGTGGATGCACGCTTAGTT 6876  
Qy 642 -----AsnThrSerIleLysLeuGlyIleGlnLysLysAsnHis 655  
Db 6877 GATGCTATGCTGAACGTATTACGCTACTAGCTAATATGGGTTATCTCTAGAGAACAC 6936  
Qy 656 PheValValValAsnGlnSerLeu-----AsnArgGlnGly----- 667  
Db 6937 TTGGCAGTTTATCGTCAGATGTTTGGAAAGTCAGTCTCGCCAAACGGTCAAGCTAGTGGTTA 6996  
Qy 668 -----IleThrTyrTyrAsnTyrAsp-----GluPheAsp 677  
Db 6997 TCTGACACAGCAACGTATAAGAGTTTGAANAAGGCTTTTAATACAGCTATCG 7056  
Qy 678 AspLeuAspGluSerArgLysTyrIlePheAsnLysThrAlaGluTyrGlnGluIle 697  
Db 7057 AGACAGAGGAAAGTGAAGAAAGCCATTGCTCTCGCAACAACTATGGCTATGTAGAC 7116  
Qy 698 AspIleLeuLysAspIleLysIleIleGlnAsnLysAspAlaLysIleAlaValSerIle 717  
Db 7117 CAAGTTTAAACGACAACTCAAGTCTATTGTTATCATAACTCGTTCGATTCTTTTATCTG 7176  
Qy 718 PheTyrProAsnThrLeuAsnGlyLeuValLysLeuAsnAsnIleIleGluTyrAsn 737  
Db 7177 ATTATAGCGATTTTCCAAATGAATGAATTAAGCAATTAATAAGCGCTTAGAG----- 7230  
Qy 738 LysAsnIlePheValIleValLeuHisValAspLysAsnHisLeuThrProAspIleLys 757  
Db 7231 -----AGTTTGATCTCAGAAATTAATTAATTCGCGGTAAC 7266  
Qy 758 LysGluIleLeuAlaPheTyrHisLysHisGlnValAsnIleLeuLeuAsnAspIle 777  
Db 7267 TCTGAGCAAAATTTTCATGTTAT-----AAATCGGATATT 7299



**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:05:28 ; Search time 30 Seconds  
(without alignments)

274.974 Million cell updates/sec

Title: US-10-642-248-2

Perfect score: 5108

Sequence: 1 MNTLSQAIKAYNSNDYQLAL.....SAGRGENIPWKNFIINSITL 972

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	972	US-11-172-145-2	Sequence 2, Appli
2	5104	99.9	972	US-11-124-215-1	Sequence 1, Appli
3	5104	99.9	972	US-11-120-422-10	Sequence 10, Appli
4	4733	92.7	972	US-11-124-215-7	Sequence 7, Appli
5	4511	88.3	972	US-11-124-215-3	Sequence 3, Appli
6	4502.5	88.1	965	US-11-172-145-4	Sequence 4, Appli
7	3697	72.4	703	US-11-124-215-17	Sequence 12, Appli
8	3697	72.4	703	US-11-172-145-12	Sequence 21, Appli
9	3687	72.2	703	US-11-172-145-21	Sequence 22, Appli
10	3687	72.2	703	US-11-172-145-22	Sequence 25, Appli
11	3151.5	61.7	704	US-11-172-145-25	Sequence 8, Appli
12	529	10.4	101	US-11-124-215-8	Sequence 9, Appli
13	223	4.4	101	US-11-124-215-9	Sequence 10, Appli
14	212	4.2	99	US-11-124-215-10	Sequence 10, Appli
15	210	4.1	651	US-11-172-145-10	Sequence 14, Appli
16	209	4.1	37	US-11-124-215-14	Sequence 5, Appli
17	209	4.1	337	US-11-102-497-5	Sequence 12, Appli
18	209	4.1	337	US-11-102-497-12	Sequence 3, Appli
19	208.5	4.1	348	US-11-102-497-3	Sequence 11, Appli
20	208.5	4.1	348	US-11-102-497-11	Sequence 104, App
21	202	4.0	252	US-10-510-386-104	Sequence 8, Appli
22	193.5	3.8	617	US-11-172-145-8	Sequence 11, Appli
23	192.5	3.8	101	US-11-124-215-11	Sequence 41, Appli
24	184	3.6	2710	US-11-051-453-41	Sequence 6, Appli
25	180.5	3.5	615	US-11-172-145-6	

Sequence 1318, Ap  
Sequence 145, App  
Sequence 144, App  
Sequence 154, App  
Sequence 196, App  
Sequence 2408, Ap  
Sequence 285, App  
Sequence 214, App  
Sequence 121, App  
Sequence 215, App  
Sequence 339, App  
Sequence 5, Appli  
Sequence 2864, Ap  
Sequence 1432, Ap  
Sequence 3, Appli  
Sequence 42, Appli  
Sequence 87, Appli  
Sequence 110, App  
Sequence 43, Appli

26 161.5 3.2 306 6 US-10-467-657-1318  
27 155 3.0 1613 6 US-10-055-877-145  
28 153 3.0 1637 6 US-10-055-877-144  
29 150.5 2.9 1006 6 US-10-793-626-154  
30 149 2.9 552 6 US-10-131-826A-196  
31 148.5 2.9 327 6 US-10-467-657-2408  
32 145.5 2.8 412 6 US-10-485-517-285  
33 142.5 2.8 2665 7 US-11-124-368A-214  
34 142 2.8 1167 7 US-11-052-554A-121  
35 141 2.8 2668 7 US-11-124-368A-215  
36 140.5 2.8 588 7 US-11-052-554A-339  
37 134.5 2.6 1147 6 US-10-815-668-5  
38 132.5 2.6 5024 6 US-10-793-626-2964  
39 132 2.6 1145 6 US-10-793-626-1432  
40 131.5 2.6 1067 7 US-11/062  
41 131.5 2.6 1092 7 US-11/062  
42 131 2.6 2367 7 US-11-051-453-42  
43 130 2.5 179 6 US-10-873-528-87  
44 125 2.4 1420 7 US-11-077-550-110  
45 124 2.4 603 7 US-11-134-241-43

## ALIGNMENTS

### RESULT 1

US-11-172-145-2  
; Sequence 2, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172.145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 2  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-11-172-145-2

Query Match 100.0%; Score 5108; DB 7; Length 972;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTLSQAIKAYNSNDYQLALFKSAIYGRKIVEFOITCKEKLSAHPSVNSAHL5VN 60  
DB 1 MNTLSQAIKAYNSNDYQLALFKSAIYGRKIVEFOITCKEKLSAHPSVNSAHL5VN 60

```
Qy 61 KEEKVNVCDSPDLATQALLSNVKKLVLSDEKNTLKNKWKLLTEKKSNAEVAVALVP 120
Db 61 KEEKVNVCDSPDLATQALLSNVKKLVLSDEKNTLKNKWKLLTEKKSNAEVAVALVP 120
Qy 121 KDFPKDLVLAPLPDHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTFNRPAILSIITLACL 180
Db 121 KDFPKDLVLAPLPDHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTFNRPAILSIITLACL 180
Qy 181 VNOKTHYPFVIVTDDGSDQLSPIIRQYENKLDIRYVRQKONGFOASARNMGLRLAKY 240
Db 181 VNOKTHYPFVIVTDDGSDQLSPIIRQYENKLDIRYVRQKONGFOASARNMGLRLAKY 240
Qy 241 DFIGLDDCMAPNPLVHVSVAELLEDDDLTIIGPKYIDTQHDIDPKDFLNNASLLESPL 300
Db 241 DFIGLDDCMAPNPLVHVSVAELLEDDDLTIIGPKYIDTQHDIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGEGTWSLDRLEQFEKTENLRSDSPFRFAAGNVAFAKKWLNKSGFFD 360
Db 301 EVKTNNSVAAKGEGTWSLDRLEQFEKTENLRSDSPFRFAAGNVAFAKKWLNKSGFFD 360
Qy 361 EEFNHGGEDVEFGYRLFYSGSFKTIIDGIMAYHQBPFGKENETDREAGNIITLDMREK 420
Db 361 EEFNHGGEDVEFGYRLFYSGSFKTIIDGIMAYHQBPFGKENETDREAGNIITLDMREK 420
Qy 421 VPYIYRKLLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPNRVRIMSKPNGGIASNAAVSPAKGYIIGQLSDDDYDLEPDAVELC 540
Db 481 DNTLEVINKLYGNPNRVRIMSKPNGGIASNAAVSPAKGYIIGQLSDDDYDLEPDAVELC 540
Qy 541 LKEFLKDKTLACVYTNTRNVPDGSIIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLACVYTNTRNVPDGSIIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIENAVDYDMFLKLSSEVGKFKHLNKI CYNRVLHGDNTSIKKLGIOKKNHFFVFN 660
Db 601 TDGFNEKIENAVDYDMFLKLSSEVGKFKHLNKI CYNRVLHGDNTSIKKLGIOKKNHFFVFN 660
Qy 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEQEEIDILKDIKIQNKDAKIAVSIFYP 720
Db 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEQEEIDILKDIKIQNKDAKIAVSIFYP 720
Qy 721 NTNLGLVKLNNIIEYNKNI FVILVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
Db 721 NTNLGLVKLNNIIEYNKNI FVILVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIPDNHDSLFPVKNDSYAYMKKYDVGWNFSAETH 840
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIPDNHDSLFPVKNDSYAYMKKYDVGWNFSAETH 840
Qy 841 DWLEKINAHPPFKKLIKTYFNDNDLSKMNKVASQGMFTYALAHELLTTIIEKVIITSCQS 900
Db 841 DWLEKINAHPPFKKLIKTYFNDNDLSKMNKVASQGMFTYALAHELLTTIIEKVIITSCQS 900
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLQWMTNEQIESAKGENI 960
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLQWMTNEQIESAKGENI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
```

RESULT 2

```
US-11-124-215-1
; Sequence 1, Application US/11124215
; Publication No. US20050266460A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND
; TITLE OF INVENTION: USBS THEREOF
```

```
; FILE REFERENCE: 35541.101
; CURRENT APPLICATION NUMBER: US/11/124,215
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,951
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-124-215-1
```

```
Query Match 99.9%; Score 5104; DB 7; Length 972;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALAKLFEKSABEYGRKI VEFQITKCKEKL SAHPSVNSAHL SVN 60
Db 1 MNTLSQAIKAYNSNDYQALAKLFEKSABEYGRKI VEFQITKCKEKL SAHPSVNSAHL SVN 60
Qy 61 KEEKVNVCDSPDLATQALLSNVKKLVLSDEKNTLKNKWKLLTEKKSNAEVAVALVP 120
Db 61 KEEKVNVCDSPDLATQALLSNVKKLVLSDEKNTLKNKWKLLTEKKSNAEVAVALVP 120
Qy 121 KDFPKDLVLAPLPDHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTFNRPAILSIITLACL 180
Db 121 KDFPKDLVLAPLPDHVNDFTWYKKRKRGLGKPEHQHVGLSIIVTFNRPAILSIITLACL 180
Qy 181 VNOKTHYPFVIVTDDGSDQLSPIIRQYENKLDIRYVRQKONGFOASARNMGLRLAKY 240
Db 181 VNOKTHYPFVIVTDDGSDQLSPIIRQYENKLDIRYVRQKONGFOASARNMGLRLAKY 240
Qy 241 DFIGLDDCMAPNPLVHVSVAELLEDDDLTIIGPKYIDTQHDIDPKDFLNNASLLESPL 300
Db 241 DFIGLDDCMAPNPLVHVSVAELLEDDDLTIIGPKYIDTQHDIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGEGTWSLDRLEQFEKTENLRSDSPFRFAAGNVAFAKKWLNKSGFFD 360
Db 301 EVKTNNSVAAKGEGTWSLDRLEQFEKTENLRSDSPFRFAAGNVAFAKKWLNKSGFFD 360
Qy 361 EEFNHGGEDVEFGYRLFYSGSFKTIIDGIMAYHQBPFGKENETDREAGNIITLDMREK 420
Db 361 EEFNHGGEDVEFGYRLFYSGSFKTIIDGIMAYHQBPFGKENETDREAGNIITLDMREK 420
Qy 421 VPYIYRKLLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPNRVRIMSKPNGGIASNAAVSPAKGYIIGQLSDDDYDLEPDAVELC 540
Db 481 DNTLEVINKLYGNPNRVRIMSKPNGGIASNAAVSPAKGYIIGQLSDDDYDLEPDAVELC 540
Qy 541 LKEFLKDKTLACVYTNTRNVPDGSIIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLACVYTNTRNVPDGSIIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIENAVDYDMFLKLSSEVGKFKHLNKI CYNRVLHGDNTSIKKLGIOKKNHFFVFN 660
Db 601 TDGFNEKIENAVDYDMFLKLSSEVGKFKHLNKI CYNRVLHGDNTSIKKLGIOKKNHFFVFN 660
Qy 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEQEEIDILKDIKIQNKDAKIAVSIFYP 720
Db 661 QSLNRQGITYYNDEFDLDESRYIFNKTAEQEEIDILKDIKIQNKDAKIAVSIFYP 720
Qy 721 NTNLGLVKLNNIIEYNKNI FVILVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
Db 721 NTNLGLVKLNNIIEYNKNI FVILVHVDKNHLPDIKKEILAFYKHQVNNILNNDISYY 780
```

```

Db 721 NTNLGLVKLNIIIEYNKNIFVIVLVHVDKNHLPDICKETLAFVHKHVNILLNNDISYY 780
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIDFNHDSLFVKUDSYAYMKKYDVGWNSALH 840
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIDFNHDSLFVKUDSYAYMKKYDVGWNSALH 840
Qy 841 DWIEKINAHPPFKKLKITYFENDNDLKSNNVKGASQGMFTYALAHALLTTIIKEVITSQS 900
Db 841 DWIEKINAHPPFKKLKITYFENDNDLKSNNVKGASQGMFTYALAHALLTTIIKEVITSQS 900
Qy 901 IDSVPEYNTEDIMFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGENI 960
Db 901 IDSVPEYNTEDIMFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGENI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972

RESULT 3
US-11-120-422-10
; Sequence 10, Application US/11120422
; Publication No. US20050287646A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kshana
; APPLICANT: Deangelis, Paul
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION
; TITLE OF INVENTION: IN BACILLUS SUBTILIS
; FILE REFERENCE: 3554.049
; CURRENT APPLICATION NUMBER: US/11/120,422
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/09/879,959
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 972
; TYPE: PRF
; ORGANISM: pasteurella multocida
US-11-120-422-10

Query Match 99.9%; Score 5104; DB 7; Length 972;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALALFKESABIYGRKIVEFOITCKEKLSAHPSVNSAHLNV 60
Db 1 MNTLSQAIKAYNSNDYQALALFKESABIYGRKIVEFOITCKEKLSAHPSVNSAHLNV 60
Qy 61 KEEKVNVCDSPDIATOLLNVKLVLSDEKNTLKNWKLITBKKSENAEVRVALVP 120
Db 61 KEEKVNVCDSPDIATOLLNVKLVLSDEKNTLKNWKLITBKKSENAEVRVALVP 120
Qy 121 KDFPKDLVLPDHPNDFTWYKKRKLGLIKPEHQHVGSLSIIVTTFNRPAILSLITLACL 180
Db 121 KDFPKDLVLPDHPNDFTWYKKRKLGLIKPEHQHVGSLSIIVTTFNRPAILSLITLACL 180
Qy 181 VNQKTHYPPEVITDDGSOEDLSPIIROYENKLDIRYVRQKNDGQASAAARMGLRLAKY 240
Db 181 VNQKTHYPPEVITDDGSOEDLSPIIROYENKLDIRYVRQKNDGQASAAARMGLRLAKY 240
Qy 241 DFIGLLDCDMPNPLVHVSVAELLEDLDTIIGPRKVIDTOHIDPKDFLNNASLESPL 300
Db 241 DFIGLLDCDMPNPLVHVSVAELLEDLDTIIGPRKVIDTOHIDPKDFLNNASLESPL 300
Qy 301 EVKTNNSVAAKGGTGVSLDWRLDLEQEKTEENLRSLDSPFRFFAAGNVFAKKWLKSGPFD 360
Db 301 EVKTNNSVAAKGGTGVSLDWRLDLEQEKTEENLRSLDSPFRFFAAGNVFAKKWLKSGPFD 360

```

```

Qy 361 EEFNHWGGBDVEGYRLFRYGSFPFKTIDGIMAYHQBPCKENETDREAGNITLDMIREK 420
Db 361 EEFNHWGGBDVEGYRLFRYGSFPFKTIDGIMAYHQBPCKENETDREAGNITLDMIREK 420
Qy 421 VPIYIRKLLPIEDSHINRVLPSIYIPAYNCANYIORCVDLSALNOTVVDLEVCICNDGST 480
Db 421 VPIYIRKLLPIEDSHINRVLPSIYIPAYNCANYIORCVDLSALNOTVVDLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPNVRIMSKPNKGIGIASASNAVAFKAGYIICQLDSDDDYLEPDAYELC 540
Db 481 DNTLEVINKLYGNPNVRIMSKPNKGIGIASASNAVAFKAGYIICQLDSDDDYLEPDAYELC 540
Qy 541 LKEFLKDKTKLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTKLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIEANVDYDMFLKLSEVKGPKHLNKICYNRVLHGDNTSIKKGIOKKNHFVVVN 660
Db 601 TDGFNEKIEANVDYDMFLKLSEVKGPKHLNKICYNRVLHGDNTSIKKGIOKKNHFVVVN 660
Qy 661 QSLNRQGITYYNDEPDLDDESRYIFNKTABYQEEIDILDKIKIIONKDAKIAVSIFYP 720
Db 661 QSLNRQGITYYNDEPDLDDESRYIFNKTABYQEEIDILDKIKIIONKDAKIAVSIFYP 720
Qy 721 NTNLGLVKLNIIIEYNKNIFVIVLVHVDKNHLPDICKETLAFVHKHVNILLNNDISYY 780
Db 721 NTNLGLVKLNIIIEYNKNIFVIVLVHVDKNHLPDICKETLAFVHKHVNILLNNDISYY 780
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIDFNHDSLFVKUDSYAYMKKYDVGWNSALH 840
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIDFNHDSLFVKUDSYAYMKKYDVGWNSALH 840
Qy 841 DWIEKINAHPPFKKLKITYFENDNDLKSNNVKGASQGMFTYALAHALLTTIIKEVITSQS 900
Db 841 DWIEKINAHPPFKKLKITYFENDNDLKSNNVKGASQGMFTYALAHALLTTIIKEVITSQS 900
Qy 901 IDSVPEYNTEDIMFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGENI 960
Db 901 IDSVPEYNTEDIMFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGENI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972

```

```

RESULT 4
US-11-124-215-7
; Sequence 7, Application US/11124215
; Publication No. US20050266460A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 3554.101
; CURRENT APPLICATION NUMBER: US/11/124,215
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 972
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus of alignment of SEQ ID NOS:1 and 3

```

```
/ NAME/KEY: MISC FEATURE
/ LOCATION: (17)..(17)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (62)..(62)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (90)..(90)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (113)..(113)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (158)..(158)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (164)..(164)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (192)..(192)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (201)..(201)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (206)..(206)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (211)..(211)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (225)..(225)
/ OTHER INFORMATION: Phe or Tyr
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (233)..(233)
/ OTHER INFORMATION: Met or Leu
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (243)..(243)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (253)..(253)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (279)..(279)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (288)..(288)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (292)..(292)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (316)..(316)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
```

```
/ NAME/KEY: MISC FEATURE
/ LOCATION: (329)..(329)
/ OTHER INFORMATION: Phe or Tyr
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (340)..(340)
/ OTHER INFORMATION: Phe or Tyr
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (405)..(405)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (439)..(439)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (744)..(744)
/ OTHER INFORMATION: Ile or Val
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (952)..(952)
/ OTHER INFORMATION: Asn, Asp, Glu or Gln
/ US-11-124-215-7
```

```
Query Match 92.7%; Score 4733; DB 7; Length 972;
Best Local Similarity 92.7%; Pred. No. 1.4e-299;
Matches 901; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALAKLFEKSAEYGRKIVFQITKCKEKLSAHPSVNSAHLVSN 60
Db 1 MNTLSQAIKAYNCNDYXALAKLFEKSAEYGRKIVFQIICKOEKLSANPSVNEANLSVN 60

Qy 61 KEEKNVVCDSPDLATQLLLSNVKGLVLSDSSEKNTLKNWKLTLEKKSNAEYRAVALVP 120
Db 61 EXEKNVCDSPDLATQLLLSNVKLTLSXSEKSLKNWKLTLEKKSNAEYRAVALVP 120

Qy 121 KOPPKDLVLAPLDHVNDFWYKKRKRIGIKPEHGHVGLSIIIVTFNRPAILSITLACL 180
Db 121 KOPPKDLVLAPLDHVNDFWYKKRKRIGIKPENQNXGLSIIIXPTFNRPAILDITLACL 180

Qy 181 VNOKTHYFPEVITDDGSQEDLSPIIQOYENKLDIRYVKQKONGFOASAARNMGLRLAKY 240
Db 181 VNOKTNYPEVXVADDSQEXLLPIXROYEXKLDIRYVKQKONGXQACAARNMGLRLAKY 240

Qy 241 DFITGLDCDMPNPLMWHYSYVAELLEDDLTITIGPRKYIDTOHIDPKOFNNASLESPL 300
Db 241 DFXGILDCDMPXQLMWHYSYLAELLEDDDTITIGPRKYDTONIDAEXFLNXASLESPL 300

Qy 301 EVKTNNSVAAKGGTYSLDWRLEQPEKTENLRSLSDSPFRFAAGNVAFKAKWLKSGFFD 360
Db 301 ETATNNPAKGGGNKSLDWRLEQFEKTXNRLCDSPPFRXFAAGNVAFKAKWLKSGFFD 360

Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQBPPEGKNETDREAGNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFRKGCFFRTIDGMAYHQBPPEGKNETXREAGNITLDMREK 420

Qy 421 VPIYIRKLLPIEDSHINRVLPSIYIPAYNCANYIQCVDLSALNQTVDLEVCINCNGST 480
Db 421 VPIYIRKLLPIEDSHINRXLPSIYIPAYNCANYIQCVDLSALNQTVDLEVCINCNGST 480

Qy 481 DNTLEVINKLYGNPRVRIMSKPENGASASNAVSFAKGYIIGQDSDDDYLPDAVELC 540
Db 481 DNTIEVINKLYGNPRVRIMSKPENGASASNAVSFAKGYIIGQDSDDDYLPDAVELC 540

Qy 541 LKEFLKDKTTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMETIRAWHL 600
Db 541 LKEFLKDKTTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMETIRAWHL 600

Qy 601 TDGFNEKIENAVDYMFLKLSVGVKPKHLNKI CYNRVLHGDNTSIIKGLGIQKQHFVVVN 660
Db 601 TDGFNEKIENAVDYMFLKLSVGVKPKHLNKI CYNRVLHGDNTSIIKGLGIQKQHFVVVN 660
```

```
Qy 661 QSLNRQGIYYNYDEFDLDESRYIFNKTAEOEEIILKDIKIQNDKAKIAVSIFYP 720
Db 661 QSLNRQGIYYNYDEFDLDESRYIFNKTAEOEEIILKDIKIQNDKAKIAVSIFYP 720
Qy 721 NTNLGLVKLNIIIEYKNKIFVILVHDVKNHLPDIIKKEILAFYHKGQVNLNNDISYY 780
Db 721 NTNLGLVKLNIIIEYKNKIFVILVHDVKNHLPDIIKKEILAFYHKGQVNLNNDISYY 780
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAETH 840
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAETH 840
Qy 841 DWIEKINAHPPFKLIKITYFNDNDLKSNNVKGASQGMFMTYALAHELLITIIKEVITSQS 900
Db 841 DWIEKINAHPPFKLIKITYFNDNDLKSNNVKGASQGMFMTYALAHELLITIIKEVITSQS 900
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGNI 960
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGNI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
```

## RESULT 5

```
US-11-124-215-3
; Sequence 3, Application US/11124215
; Publication No. US20050266460A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 35541.101
; CURRENT APPLICATION NUMBER: US/11/124,215
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 3
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-124-215-3
```

```
Query Match 88.3%; Score 4511; DB 7; Length 972;
Best Local Similarity 86.7%; Pred. No. 3.4e-285;
Matches 843; Conservative 64; Mismatches 65; Indels 0; Gaps 0;
```

```
Qy 1 MNTLSQAIKAYNSNDYQALALFEKSAEYGRKIVFEQITCKEKLKSAHPSVNSHLVSN 60
Db 1 MNTLSQAIKAYNSNDYQALALFEKSAEYGRKIVFEQITCKEKLKSTNSYVSEDNSYVS 60
Qy 61 KEEKVNCDSPLDIATQALLSNVKKLVLSDEKNTLKNKKLLTEKKSNAEVRVALVP 120
Db 61 EDKKNSVCDSSLDIATQALLSNVKKLVLSSEKSNLKNKKWSITGKKSNAEIRKVELVP 120
Qy 121 KDFPKDLVLAPDHDVNDFTWYKKKQKGLGKPEHQHVGSLSIIVTFNRPAILSLITLACL 180
Db 121 KDFPKDLVLAPDHDVNDFTWYKRNKKSGLKIPVKNKGLSIIITFNRSRILDTLACL 180
Qy 181 VNQKTHYPPEVITVDGSGQEDLSPRIQYENKLDIRYVRQKXNGFQASARNMGLRLAKY 240
Db 181 VNQKTHYPPEVIVVADGSKENLLTIVQYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY 240
Qy 241 DFIGLDCDMAPNLVWHSYAEELLEDDEDDLLTIIGRPKVIDTQHDIPKOPLNNASLESILP 300
```

## RESULT 6

```
US-11-172-145-4
; Sequence 4, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; FILE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
```

```
/ PRIOR APPLICATION NUMBER: 10/195,908
/ PRIOR FILING DATE: 2002-07-15
/ PRIOR FILING DATE: 2002-07-15
/ PRIOR APPLICATION NUMBER: 09/437,277
/ PRIOR FILING DATE: 1999-11-01
/ PRIOR APPLICATION NUMBER: 60/107,929
/ PRIOR FILING DATE: 1998-11-11
/ PRIOR APPLICATION NUMBER: 09/283,402
/ PRIOR FILING DATE: 1999-04-01
/ PRIOR APPLICATION NUMBER: 60/080,414
/ PRIOR FILING DATE: 1998-04-02
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 4
/ LENGTH: 965
/ TYPE: PRT
/ ORGANISM: Pasteurella multocida
US-11-172-145-4

Query Match      88.1%; Score 4502.5; DB 7; Length 965;
Best Local Similarity 86.9%; Pred. No. 1.4e-284;
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

QY 1 MNTLSQAIKAYNSNDYQLALKLFKESAEIYGRKIVFQITKCKEKLKSAHPSVNSAHLNVN 60
DB 1 MNTLSQAIKAYNSNDYELALKLFKESAEIYGRKIVFQITKCKEKLKSAHPSVNSAHLNVN 53
QY 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLNKWKLLTEKKSENAEVRVALVP 120
DB 54 EDKNSVCSSLDIATQALLSNVKKLVLSSEKNTLNKWKLLTEKKSENAEVRVALVP 113
QY 121 KOPPKDLVAPLPHDNDFTWYKRRKGLGKPEHQHVGSLIIVTFNRPAILSLTACL 180
DB 114 KOPPKDLVAPLPHDNDFTWYKRRKGLGKPVNKNIGLSIIPFNRSRIIDLITACL 173
QY 181 VNQKTHYPEVITDDGSOEDLSPIIROYENKLDIRVROKNGFQASAAARNMGLSLAKY 240
DB 174 VNQKTHYPEVIVVADGSKENLTIIVQYEQKLDIKVROKDYGYQLCAVRNGLTAKY 233
QY 241 DFTGLDCCMAPNPLVHVSVAELLEDLDTIIGPKRYIDTOHIDPKDFLNNASLESPL 300
DB 234 DFVSLDCCMAPQQLVHVSVAELLEDNDIVLIGPKRYVDTHNITAEQFLNDPYLESPL 293
QY 301 EVKTNNSVAAKGEGTVSLDWRLQPEKTENLRSLSDSPFRFAAGNVAFACKWLNKSGFFD 360
DB 294 ETATNNPSITSGNISLWRLHFKKTDNRLCDSPPFRYFCGNVAFSEKWLNVKGFWD 353
QY 361 EEFNHWGGEDVEFGYRLFRYGSFFKTDIGIMAYHQBPFGKENETDREAGNITLDMREK 420
DB 354 EEFNHWGGEDVEFGYRLFAKGCFFRVIDGMAVHQBPFGKENETDREAGKSIILKIVKEK 413
QY 421 VPIYIRKLLPIEDSHINRPLVSIYIIPAYNCANYIORCVDSALNQTVDLVLCINDGST 480
DB 414 VPIYIRKLLPIEDSHIRPLVSIYIIPAYNCANYIORCVDSALNQTVDLVLCINDGST 473
QY 481 DNTLEVINKLYGNPNVRIMSKNGGITASASNAAVSFAGKGYIGQLSDSDYLEPDAVELC 540
DB 474 DNTLEVINKLYGNPNVRIMSKNGGITASASNAAVSFAGKGYIGQLSDSDYLEPDAVELC 533
QY 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTATTAHAFHFMFTIRAWHL 600
DB 534 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTATTAHAFHFMFTIRAWHL 593
QY 601 TDGFNKEINADVDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIGKQKNHFWVN 660
DB 594 TDGFNKEINADVDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIGKQKNHFWVN 653
QY 661 QSLNRQGIITYNVDDEDDDESRYFNKTAEOEIEDILDKIITONKDAKIAVSIFYP 720
DB 654 QSLNRQGIINYNDKFDDEDDDESRYIFNKTAEOEEMDILKOLKILQNKDAKIAVSIFYP 713
QY 721 NTLNGLVKKLNNIIEYKNIFVILVHVDKNHLPDIIKKEILAFYKHQVNNLLNNDISYY 780
DB 714 NTLNGLVKKLNNIIEYKNIFVILVHVDKNHLPDIIKKEILAFYKHQVNNLLNNDISYY 773
```

```
DB 714 NTLNGLVKKLNNIIEYKNIFVILVHVDKNHLPDIIKKEILAFYKHQVNNLLNNDISYY 773
QY 781 TSNRLIKTEAHLNSINIKLSQNLNCEYIIIFDNHDSLFVKNDSYAYNKKYDVGKNFSALTH 840
DB 774 TSNRLIKTEAHLNSINIKLSQNLNCEYIIIFDNHDSLFVKNDSYAYNKKYDVGKNFSALTH 833
QY 841 DMIEKINAHPPPKKLIKTYFNDNDLKSMMVKGASQGMFTYALAHELLTTIKKIVITSCQS 900
DB 834 DMIEKINAHPPPKKLIKTYFNDNDLKSMMVKGASQGMFTYALAHELLTTIKKIVITSCQS 893
QY 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPMERKLOMTNEQIESAKRGENI 960
DB 894 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPMERKLOMTNEQIQSAKUGENI 953
QY 961 PVNKFINSITL 972
DB 954 PVNKFINSITL 965

RESULT 7
US-11-124-215-17
/ Sequence 17, Application US/11124215
/ Publication No. US20050266460A1
/ GENERAL INFORMATION:
/ APPLICANT: DEANGELIS, PAUL
/ TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: 35541.101
/ CURRENT APPLICATION NUMBER: US/11/124,215
/ CURRENT FILING DATE: 2005-05-09
/ PRIOR APPLICATION NUMBER: 10/217,613
/ PRIOR FILING DATE: 2002-08-12
/ PRIOR APPLICATION NUMBER: 09/283,402
/ PRIOR FILING DATE: 1999-04-01
/ PRIOR APPLICATION NUMBER: 60/080,414
/ PRIOR FILING DATE: 1998-04-02
/ PRIOR APPLICATION NUMBER: 09/178,851
/ PRIOR FILING DATE: 1998-10-26
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 17
/ LENGTH: 703
/ TYPE: PRT
/ ORGANISM: Pasteurella multocida
US-11-124-215-17

Query Match      72.4%; Score 3697; DB 7; Length 703;
Best Local Similarity 100.0%; Pred. No. 1.4e-232;
Matches 703; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTLSQAIKAYNSNDYQLALKLFKESAEIYGRKIVFQITKCKEKLKSAHPSVNSAHLNVN 60
DB 1 MNTLSQAIKAYNSNDYQLALKLFKESAEIYGRKIVFQITKCKEKLKSAHPSVNSAHLNVN 60
QY 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLNKWKLLTEKKSENAEVRVALVP 120
DB 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLNKWKLLTEKKSENAEVRVALVP 120
QY 121 KOPPKDLVAPLPHDNDFTWYKRRKGLGKPEHQHVGSLIIVTFNRPAILSLTACL 180
DB 121 KOPPKDLVAPLPHDNDFTWYKRRKGLGKPEHQHVGSLIIVTFNRPAILSLTACL 180
QY 181 VNQKTHYPEVITDDGSOEDLSPIIROYENKLDIRVROKNGFQASAAARNMGLSLAKY 240
DB 181 VNQKTHYPEVITDDGSOEDLSPIIROYENKLDIRVROKNGFQASAAARNMGLSLAKY 240
QY 241 DFTGLDCCMAPNPLVHVSVAELLEDLDTIIGPKRYIDTOHIDPKDFLNNASLESPL 300
DB 241 DFTGLDCCMAPNPLVHVSVAELLEDLDTIIGPKRYIDTOHIDPKDFLNNASLESPL 300
QY 301 EVKTNNSVAAKGEGTVSLDWRLQPEKTENLRSLSDSPFRFAAGNVAFACKWLNKSGFFD 360
DB 301 EVKTNNSVAAKGEGTVSLDWRLQPEKTENLRSLSDSPFRFAAGNVAFACKWLNKSGFFD 360
```



```
QY 361 EEFNHGGEDVEFGYRLFRYGSFFKTIIDGIMAHQBPPGKENETDREAGKNIITLIDIMREK 420
DB 361 EEFNHGGEDVEFGYRLFRYGSFFKTIIDGIMAHQBPPGKENETDREAGKNIITLIDIMREK 420
QY 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQCVDLSALNQTVVDLEVCICNDGST 480
DB 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQCVDLSALNQTVVDLEVCICNDGST 480
QY 481 DNTLEVINKLYGNPNRVRIMSKPNGGIASASNAAVSPAKGYIYGOLDSDDDYLEPDAVELC 540
DB 481 DNTLEVINKLYGNPNRVRIMSKPNGGIASASNAAVSPAKGYIYGOLDSDDDYLEPDAVELC 540
QY 541 LKBEFLKDKTKLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHHFRMFTIRAWHL 600
DB 541 LKBEFLKDKTKLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHHFRMFTIRAWHL 600
QY 601 TDGFNEKIEANAVDYDMFLKLSVKGKFKHLNKCYNRVLHGDNTSIKGLGIQKKNHFVVVN 660
DB 601 TDGFNEKIEANAVDYDMFLKLSVKGKFKHLNKCYNRVLHGDNTSIKGLGIQKKNHFVVVN 660
QY 661 QSLNRQGITYYNYDEFDLDESRYIIFNKTAEOEEIDILKDI 703
DB 661 QSLNRQGITYYNYDEFDLDESRYIIFNKTAEOEEIDILKDI 703

RESULT 8
US-11-172-145-12
; Sequence 12, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-172-145-12

Query Match 72.4%; Score 3697; DB 7: Length 703;
Best Local Similarity 100.0%; Pred. No. 1.4e-232; Indels 0; Gaps 0;
Matches 703; Conservative 0; Mismatches 0;

QY 1 MNTLSQAIKAYNSNDYQLALKLFKSAEYIGRKIVFEQITCKEKLSAHPSVNSAHSV 60
DB 1 MNTLSQAIKAYNSNDYQLALKLFKSAEYIGRKIVFEQITCKEKLSAHPSVNSAHSV 60
```



```
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 21
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-172-145-21

Query Match      72.2%; Score 3687; DB 7; Length 703;
Best Local Similarity 99.7%; Pred. No. 6e-232;
Matches 701; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQLAKLFEKSAEYIGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Db 1 MNTLSQAIKAYNSNDYQLAKLFEKSAEYIGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Qy 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLKNKKWLLTEKKSENAEVRVALVP 120
Db 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLKNKKWLLTEKKSENAEVRVALVP 120
Qy 121 KDFPKDLVLAPLDPDHVNDFTWYKKRKLGIKPEHQHVGLSIIIVTTFNRPAILSIITLACL 180
Db 121 KDFPKDLVLAPLDPDHVNDFTWYKKRKLGIKPEHQHVGLSIIIVTTFNRPAILSIITLACL 180
Qy 181 VNQKTHYPPEVIIVTDDGSQEDLSPIIRQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240
Db 181 VNQKTHYPPEVIIVTDDGSQEDLSPIIRQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240
Qy 241 DFTGLLDCMAPLWVHSYVAELLEDLTIIGPKYIDTQHIDPKDFLNNASLLESPL 300
Db 241 DFTGLLDCMAPLWVHSYVAELLEDLTIIGPKYIDTQHIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFKAKWLNKSGFFD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFKAKWLNKSGFFD 360
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGPKENETDREAGKNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGPKENETDREAGKNITLDMREK 420
Qy 421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Db 421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPNRVRIMSKPENGASASNAVSAFAGYIYIGQLDSDDYLEDPAVELC 540
Db 481 DNTLEVINKLYGNPNRVRIMSKPENGASASNAVSAFAGYIYIGQLDSDDYLEDPAVELC 540
Qy 661 QSLNRQGITVYNYDEFDLDESRYIFNKTAEQEIDILKDI 703
Db 661 QSLNRQGITVYNYDEFDLDESRYIFNKTAEQEIDILKDI 703
```

## RESULT 10

```
US-11-172-145-22
; Sequence 22, Application US/11172145
; Publication No. US2005027269A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
```

```
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 22
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-172-145-22
```

```
Query Match      72.2%; Score 3687; DB 7; Length 703;
Best Local Similarity 99.7%; Pred. No. 6e-232;
Matches 701; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQLAKLFEKSAEYIGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Db 1 MNTLSQAIKAYNSNDYQLAKLFEKSAEYIGRKIVFEQITKCKEKLSAHPSVNSAHLNVN 60
Qy 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLKNKKWLLTEKKSENAEVRVALVP 120
Db 61 KEEKVNVCDSPDIATQALLSNVKKLVLSSEKNTLKNKKWLLTEKKSENAEVRVALVP 120
Qy 121 KDFPKDLVLAPLDPDHVNDFTWYKKRKLGIKPEHQHVGLSIIIVTTFNRPAILSIITLACL 180
Db 121 KDFPKDLVLAPLDPDHVNDFTWYKKRKLGIKPEHQHVGLSIIIVTTFNRPAILSIITLACL 180
Qy 181 VNQKTHYPPEVIIVTDDGSQEDLSPIIRQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240
Db 181 VNQKTHYPPEVIIVTDDGSQEDLSPIIRQYENKLDIRYVRQKNGFQASARNMGLRLAKY 240
Qy 241 DFTGLLDCMAPLWVHSYVAELLEDLTIIGPKYIDTQHIDPKDFLNNASLLESPL 300
Db 241 DFTGLLDCMAPLWVHSYVAELLEDLTIIGPKYIDTQHIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFKAKWLNKSGFFD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFKAKWLNKSGFFD 360
Qy 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGPKENETDREAGKNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFRYGSFFKTIIDGIMAYHQEPGPKENETDREAGKNITLDMREK 420
Qy 421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Db 421 VPYIYRKLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPNRVRIMSKPENGASASNAVSAFAGYIYIGQLDSDDYLEDPAVELC 540
Db 481 DNTLEVINKLYGNPNRVRIMSKPENGASASNAVSAFAGYIYIGQLDSDDYLEDPAVELC 540
```

```
Qy 541 LKEFLDKDTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHHFPMFTIRAWHL 600
Db 541 LKEFLDKDTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHHFPMFTIRAWHL 600
Qy 601 TDGFNEKIENAVDYDMFLKJSEVGKFKHLNKKICYNRVLHGDNSTIKKLGIOKQNHFFVYVN 660
Db 601 TDGFNEKIENAVDYDMFLKJSEVGKFKHLNKKICYNRVLHGDNSTIKKLGIOKQNHFFVYVN 660
Qy 661 QSLNRQGITYYNDEFDLDESRYKIFNKTAEOEIDILKDI 703
Db 661 QSLNRQGITYYNDEFDLDESRYKIFNKTAEOEIDILKDI 703

RESULT 11
US-11-172-145-25
; Sequence 25, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172.145
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 704
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-172-145-25

Query Match 61.7%; Score 3151.5; DB 7; Length 704;
Best Local Similarity 83.0%; Pred. No. 3.3e-197;
Matches 590; Conservative 57; Mismatches 57; Indels 7; Gaps 2;

Qy 1 MNTLSQAIKAYNSDYQALAKLFEKSAEYGRKIVEPQITCKEKLKLSAHPNSVNSAHSVN 60
Db 1 MNTLSQAIKAYNSDYQALAKLFEKSAEYGRKIVEPQITCKEKLKLSAHPNSVNSAHSVN 60
Qy 61 KEKKNVCDSPDIATQALLSNVKKLVLDSEKNTLKNKKWLLTEKKSNAEVRVALVP 120
Db 54 EDKNSVCDSSDDIATQALLSNVKKLVLDSEKNSLKNKKWKSITGKKSNAEIRKVELVP 113
Qy 121 KDFPKDLVLAPLDPHVDNFTWYKRRKRGKIGKPEHGVGLSIIVTTFNRPALISITLACL 180
Db 114 KDFPKDLVLAPLDPHVDNFTWYKRRKKSIGKIPVKNIGLSIIITFNRSRILDTLACL 173
Qy 181 VNQKTHYPEVITVDGSGQEDLSPIROYENKLDIYRVQKONGFQASARNNGRLAKY 240
Db 174 VNQKTYPEVIVVADGSGKENLLTIQVQEQLDKIKYVRQKDYQOLCAVRNLGLRTAKY 233
```

```
Qy 241 DFTGLDCDMPNPLVHVSIVVAELLEDDDLTTITGPRKYIDTQHDPKDFLNNASLLESPL 300
Db 234 DFVSLDCDMPQQLVHVSILYLTTELLEDNDIVLIGPRKYVDTHNTABQFLNDPYLESLP 293
Qy 301 EVKTNNSVAAKGEGTUSLDWRLRQFEKTEENLRLSDSPRPFPAAGNVAFPAKWLKNSGPF 360
Db 294 ETATNNPSTTSKGNISLDWRLRHFHFKKTNDLRLCDSFRIYFCGNVAFSKEWLNKVGWFD 353
Qy 361 EEFNHWGGEDEVFGYRLFRYGSFPFKTTIDIGIMAYHQBPPEKNETDREAGKNITLDMREK 420
Db 354 EEFNHWGGEDEVFGYRLFAKGCFFRVIDGGMAYHQBPPEKNETDREAGKSITLKIVKEK 413
Qy 421 VPIYIRKLLPIEDSHINRVPLVSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGST 480
Db 414 VPIYIRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGST 473
Qy 481 DNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYIIGQLSDDDYLEPDAVELC 540
Db 474 DNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYIIGQLSDDDYLEPDAVELC 533
Qy 541 LKEFLDKDTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHHFPMFTIRAWHL 600
Db 534 LKEFLDKDTLACVYTTNRNPNPDGSLIANGYNWPEFSREKLTAMIAHHFPMFTIRAWHL 593
Qy 601 TDGFNEKIENAVDYDMFLKJSEVGKFKHLNKKICYNRVLHGDNSTIKKLGIOKQNHFFVYVN 660
Db 594 TDGFNEKIENAVDYDMFLKJSEVGKFKHLNKKICYNRVLHGDNSTIKKLGIOKQNHFFVYVN 653
Qy 661 QSLNRQGITYYNDEFDLDESRYKIFNKTAEOEIDILKDIQNKDA 711
Db 654 QSLNRQGITYYNDEFDLDESRYKIFNKTAEOEIDILKDIQNKDA 704

RESULT 12
US-11-124-215-8
; Sequence 8, Application US/11124215
; Publication No. US20050266460A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL
; TITLE OF INVENTION: DNA ENCODING HVALURONAN SYNTHASE FROM PASTEURELLA MULTOCIDA AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 35541.101
; CURRENT APPLICATION NUMBER: US/11/124.215
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: 10/217,613
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-124-215-8

Query Match 10.4%; Score 529; DB 7; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 436 INRVPLVSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTDTNTLEVINKLYGNNP 495
Db 1 INRVPLVSIYIPAYNCANYIQRCDVSALNQTVDVLEVCICNDGSTDTNTLEVINKLYGNNP 60
Qy 496 RVRIMSKPNGGIASASNAAVSFAKGYIIGQLSDDDYLEPDA 536
Db 61 RVRIMSKPNGGIASASNAAVSFAKGYIIGQLSDDDYLEPDA 101
```



Db 409 RIIGILKQCQDHPHIIYLDGYEIPDFIKNLGNKATVVHCKDKONSIRDNGKFILLBELIE 468  
Qy 716 -----SIFYPNT-INGLVKGLNNIIIEYNKNI FVIVLH--VDKNHLPDIKKE- 759  
Db 469 KNQDGYIITCDDDIYPSDYINTMIKGLN---EYDDKA-VIGLHGILFPSRMTKYFSADR 524  
Qy 760 -ILAFYHKHQ-----VNILLANDISYTS--NRLIK---TEAHLNSI-----NKLSQL 801  
Db 525 LVYSFYKPLEKDKAVNVLGTGTVSFRVSLFNQFSLSDFTHSGMADIYFSLCKKGNILQI 584  
Qy 802 NLN--CEYIIFDNHDS-----LFVKNDSYAYMKKYDVGMNFSALTHDWI 843  
Db 585 CISRPANWLTEDNEDSETLYHQYEDNDEQQTOLIMENGPWGYSSIIYPLVKN----- 635  
Qy 844 EKINAHPPFKKLI 856  
Db 636 -----HPKFTDLI 643

Search completed: January 6, 2006, 16:16:51  
Job time : 32 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 05:19:53 ; Search time 14204 Seconds  
(without alignments)

11685.643 Million cell updates/sec

Title: US-10-642-248-1

Perfect score: 2920

Sequence: 1 atgaatacattatcacagc.....taatagataactctataaa 2920

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.hcg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2920	100.0	2920	1	AF036004
2	2919	100.0	2937	6	AR616925
3	2917.4	99.9	2919	1	AF237926
4	2917.4	99.9	2937	6	BD087261
5	2917.4	99.9	2937	6	BD205371
6	2913.6	99.8	16727	1	AF067175
7	2271.2	77.8	2979	6	BD228712
8	2271.2	77.8	2979	6	AR225814
9	2266.4	77.6	2979	1	AF195517
10	2108.8	72.2	2112	6	BD228711
11	2108.8	72.2	2112	6	AR225813
12	2066.4	70.8	11885	1	AE006116
13	2064.8	70.7	3156	1	AF604234
14	2063.2	70.7	8838	1	AF302467
15	765.8	26.2	14483	1	AB079602
16	765.8	26.2	14483	1	AX698178
17	760.6	26.0	2058	6	AX698176
18	747	25.6	998	1	AY225345

19	719.4	24.6	907	1	AY225347
20	652.4	22.3	864	1	AY225346
c 21	112	3.8	110000	14	CT009752_3
22	110.8	3.8	110000	14	CT009752_4
23	110.8	3.8	110000	14	CT009752_5
c 24	108.8	3.7	155204	14	AC007926_5
25	108.2	3.7	115990	5	EX890614
26	106.8	3.7	155885	14	CR848672
c 27	105.4	3.6	176147	5	AL929105
28	105.4	3.6	226847	14	EX664721
29	105.2	3.6	154561	5	CR391989
30	102.2	3.5	168212	5	CR352223
31	101.6	3.5	79882	14	EX908758_5
c 32	101.6	3.5	191146	5	EX530070
33	99	3.4	144604	14	EX899179
34	99	3.4	145553	5	AL935272
35	98.6	3.4	34340	14	EX957360
c 36	97.8	3.3	163843	5	EX510939
37	97.6	3.3	194784	5	EX890608
c 38	96.6	3.3	144375	14	CR354586
39	96.6	3.3	250029	2	AE014820
40	96	3.3	157544	5	CR762435
41	93.8	3.2	225581	14	EX537105
42	93.4	3.2	139980	14	CR855330
43	92.8	3.2	154071	2	AC115598
c 44	92.6	3.2	110000	14	AL954295_2
c 45	92.6	3.2	125031	5	EX248494

## ALIGNMENTS

RESULT 1	AF036004	Pasteurella multocida hyaluronan synthase (PmHAS) gene, complete cds.	2920 bp	DNA	linear	BCT 04-MAR-2004
LOCUS	AF036004	Pasteurella multocida				
DEFINITION	AF036004.2	GI:44986831				
ACCESSION	AF036004	Pasteurella multocida				
VERSION	AF036004.2	GI:44986831				
KEYWORDS		Pasteurella multocida				
SOURCE		Pasteurella multocida				
ORGANISM		Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.				
REFERENCE		1 (bases 1 to 2920)				
AUTHORS		DeAngelis, P.L., Jing, W., Drake, R.R. and Achuthan, A.M.				
TITLE		Identification and molecular cloning of a unique hyaluronan synthase from Pasteurella multocida				
JOURNAL		J. Biol. Chem. 273 (14), 8454-8458 (1998)				
PUBMED		9525958				
REFERENCE		2 (bases 1 to 2920)				
AUTHORS		DeAngelis, P.L., Jing, W. and Achuthan, A.M.				
TITLE		Direct Submission				
JOURNAL		Submitted (26-NOV-1997) Biochem. & Molec. Biol., Univ. of Oklahoma Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City, OK 73104, USA				
REFERENCE		3 (bases 1 to 2920)				
AUTHORS		DeAngelis, P.L., Jing, W. and Achuthan, A.M.				
TITLE		Direct Submission				
JOURNAL		Submitted (04-MAR-2004) Biochem. & Molec. Biol., Univ. of Oklahoma Health Sciences Center, 940 Stanton L. Young Blvd., Oklahoma City, OK 73104, USA				
REMARK		Sequence update by submitter				
COMMENT		On Mar 4, 2004 this sequence version replaced gi:3043922.				
FEATURES		Location/Qualifiers				
source		1..2920				
		/organism="Pasteurella multocida"				
		/mol_type="genomic DNA"				
		/strain="P-1059: ATCC 15742"				
		/db_xref="ATCC:15742"				
		/db_xref="taxon:747"				
		/note="Carter Type A strain"				
		1..2919				
		gene				

```
/gene="PmHAS"
/notes="gene identified by transposon insertional
mutagenesis and verified by functional expression in
heterologous cells"
1. .2919
CDS
/gene="PmHAS"
/function="polymerizes hyaluronan (HA, hyaluronate,
hyaluronic acid) polysaccharide using UDP-GlcA and
UDP-GlcNAc precursors"
/notes="glycosyltransferase; HA synthase (synthetase);
membrane-bound enzyme"
/codon_start=1
/transl_table=11
/product="hyaluronan synthase"
/protein_id="AAC38318.2"
/db_xref="GI:44986832"
/translation="MNTLSQAIKAVNSDYOLALKPEKSAEIIYGRKIVFOLTKCKE
KLSAHPNSVNSHLVSNKEKVNVCDSPLDIATQLLSNVKLVLSDEKTLKMKWL
LTEKKSNAEVAVALVPKPPKOLVLAPDPVNDFTWYKKRKKRIGIKPEHOHVL
SIVTTFNPAILSITLACLNVKQTHYPFEIVVDDGSQEDLSPIIRIQENKLDIRV
RQKNGFQASARNGLRLAKYDFIGLLDCDMPNPLWVHSYVAELLEDLDTIIGPR
KYIDHIDPDKFNNASLSLSEPEVKTNNVSAKGGTSLDWRLBQFEKTEHLRLS
DSPPRFAAGNVAFAKKWLKSGFFDEEFNHMGDEVEFGVRLFRYGSFPKTIIDINA
YHQPFGKNETDREAGKNTLIDIMREKVPYIYRKLPIEDSHNRVPLVSIYIPAYN
CANTIQRCVDSALNQTVDVLEVCINDGSTDNTLEVLNKLYGNPNVRIMSKPNGGIA
SASNAVSPFAKYYIGQSDSDYLEDPAVELCKLEFKDKTLACVYTTNRNVNPDGLS
IANGYNWPEFREKLTAMIAHHEFMETIRAWHLTDGFNEKINAVDYDFMLKSEVG
KFKHLNKIYNRVLHGNTSIIKFLGIQKKNHFVVVNOSLNRRQGIYYNYDFDLDES
RKYIPNTAEQOEIDILKQIKONDKAKTAVSIFVENTLNGILVKLNNIIYVKNKI
FVVLVVDKHLTPDIKEILAFYHKQVNNLLNDISYVTSNRLIKTEAHLNKL
SOLNLCBIIIFDNDHSFVNDSTAYMKYDVGNSALTHDMEIKNAHPFKKLI
KTYFNDNLKSMNVKSGASQGMFTYALAHELLTIKIVITSQSIDSVPEYNTEDIMF
QFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKRGENI PVNKEIINSITL
"
```

## ORIGIN

Query Match	100.0%; Score 2920; DB 1; Length 2920;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 2920; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1	ATGAATACATTTATCAACAGCAATAAAGCATATACAGCAATGACTATCAATTAGCACTC	60
Db		
1	ATGAATACATTTATCAACAGCAATAAAGCATATACAGCAATGACTATCAATTAGCACTC	60
Qy 61	AAATTTATTTGAAAGTCGGCGGAAATCTATGAGCGGAAATTTGTTGAAATTTCAAATTACC	120
Db		
61	AAATTTATTTGAAAGTCGGCGGAAATCTATGAGCGGAAATTTGTTGAAATTTCAAATTACC	120
Qy 121	AAATGCAAGAAAAAATCTCTAGCACATCTTCTGTGTTAATTCAGCACATCTTCTGTAAAT	180
Db		
121	AAATGCAAGAAAAAATCTCTAGCACATCTTCTGTGTTAATTCAGCACATCTTCTGTAAAT	180
Qy 181	AAAGAAGAAAAAGTCAATGTTTGGCATAGTCGGTTAGATATTGCAACACAACTGTACTT	240
Db		
181	AAAGAAGAAAAAGTCAATGTTTGGCATAGTCGGTTAGATATTGCAACACAACTGTACTT	240
Qy 241	TCCAACGTAAAAAATAGTACTTCTTGACCTCGGAAAAAACAACGTTAAAAAATAAATGG	300
Db		
241	TCCAACGTAAAAAATAGTACTTCTTGACCTCGGAAAAAACAACGTTAAAAAATAAATGG	300
Qy 301	AAATGTGCTCAGTGAAGAAATCTGAAATTCGGAGGTAAGAGCGGTGCGCCTTGTACCA	360
Db		
301	AAATGTGCTCAGTGAAGAAATCTGAAATTCGGAGGTAAGAGCGGTGCGCCTTGTACCA	360
Qy 361	AAAGATTTTCCCAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAAATGATTTTACA	420
Db		
361	AAAGATTTTCCCAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAAATGATTTTACA	420
Qy 421	TGGTACAAAAAGCGAAGAAAGAATTGGCATAAAAACCTGAAACATCAACATGTTGGTCTT	480
Db		
421	TGGTACAAAAAGCGAAGAAAGAATTGGCATAAAAACCTGAAACATCAACATGTTGGTCTT	480
Qy 481	TCTATTATCGTTACAACTTCAATCGACAGCAATTTTATCGATTACATTAGCCTGTTTA	540
Db		

Db		481	TCATTATTCGTACAACTTCAATCGACAGCAATTTTATTCGATTACATTAGCCTGTTTA	540
Qy		541	GTAACCAAAAAACACATTAACCGTTTGAAGTTTATCGTGACAGATGATGTAGTCAGAA	600
Db		541	GTAACCAAAAAACACATTAACCGTTTGAAGTTTATCGTGACAGATGATGTAGTCAGAA	600
Qy		601	GATCTATCACCGATCATTCGCCAATATGAAAAATAAATTTGGATATTCGCTAGCTCAGACAA	660
Db		601	GATCTATCACCGATCATTCGCCAATATGAAAAATAAATTTGGATATTCGCTAGCTCAGACAA	660
Qy		661	AAAGATAACCGTTTCAAGCCAGTCGCGCTCGGAAATATGGATTTACGCTTAGCAAAATAT	720
Db		661	AAAGATAACCGTTTCAAGCCAGTCGCGCTCGGAAATATGGATTTACGCTTAGCAAAATAT	720
Qy		721	GACTTTATTCGGCTTACTTCGACTGTGATATGCGGCCAAATCCATTTATGGGTTCAATTC	780
Db		721	GACTTTATTCGGCTTACTTCGACTGTGATATGCGGCCAAATCCATTTATGGGTTCAATTC	780
Qy		781	GTTGCAGAGCTATTAGAAGATGATGATTTAAACAATTCATTCGTTCCAGAAAAATACATCGAT	840
Db		781	GTTGCAGAGCTATTAGAAGATGATGATTTAAACAATTCATTCGTTCCAGAAAAATACATCGAT	840
Qy		841	ACACAACATATTGACCCCAABAAGACTTCTTAAATAACCGAGTTTGTCTTGAATCATTACCA	900
Db		841	ACACAACATATTGACCCCAABAAGACTTCTTAAATAACCGAGTTTGTCTTGAATCATTACCA	900
Qy		901	GAAAGTAAAAACCAATATAGTGTTCGCCGCAAAAGGGAAGAAACAGTTCTCTGGATTGG	960
Db		901	GAAAGTAAAAACCAATATAGTGTTCGCCGCAAAAGGGAAGAAACAGTTCTCTGGATTGG	960
Qy		961	CGCTTAGAACAATTCGAAAAAACAAGAAATCTCGCTTATCCGATTCGCTTTCGCTTTT	1020
Db		961	CGCTTAGAACAATTCGAAAAAACAAGAAATCTCGCTTATCCGATTCGCTTTCGCTTTT	1020
Qy		1021	TTTTCGGCGGGTAAATGTTGCTTTCGCTAAAAAATGGCTAAATCAATCGGTTTCTTTGAT	1080
Db		1021	TTTTCGGCGGGTAAATGTTGCTTTCGCTAAAAAATGGCTAAATCAATCGGTTTCTTTGAT	1080
Qy		1081	GAGGAAATTTAATCACTCGGGTGGAGAAAGATGTGGAATTTGGATATCGCTTATTCGCTTAC	1140
Db		1081	GAGGAAATTTAATCACTCGGGTGGAGAAAGATGTGGAATTTGGATATCGCTTATTCGCTTAC	1140
Qy		1141	GGTAGTTTCTTTAAAACTATTGATGGCATTTATGCGCTTACCATCAAGAGCCACAGGTAAA	1200
Db		1141	GGTAGTTTCTTTAAAACTATTGATGGCATTTATGCGCTTACCATCAAGAGCCACAGGTAAA	1200
Qy		1201	GAAATGAAACCGATCGTGAAGCGGAAAAAATAATTACGCTCGATATTATGAGAGAAAAAG	1260
Db		1201	GAAATGAAACCGATCGTGAAGCGGAAAAAATAATTACGCTCGATATTATGAGAGAAAAAG	1260
Qy		1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTTCGCATATCAATAGAGTACCT	1320
Db		1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTTCGCATATCAATAGAGTACCT	1320
Qy		1321	TTAGTTTCAATTTATATFCCAGCTTATAA CTGTGCAAACTATATTTCACCGTTGCGTAGAT	1380
Db		1321	TTAGTTTCAATTTATATFCCAGCTTATAA CTGTGCAAACTATATTTCACCGTTGCGTAGAT	1380
Qy		1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA	1440
Db		1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA	1440
Qy		1441	GATAAATACCTTTAGAAAGTGATCAATAAGCTTTATGGTAAATATCTTAGGGTACGCATCATG	1500
Db		1441	GATAAATACCTTTAGAAAGTGATCAATAAGCTTTATGGTAAATATCTTAGGGTACGCATCATG	1500
Qy		1501	TCTAAA CAAATGCGGGAATAGCCTCAGCATCAAAATGCGAGCGGTTTCTTTTGTCTAAAGGT	1560
Db		1501	TCTAAA CCAATGCGGGAATAGCCTCAGCATCAAAATGCGAGCGGTTTCTTTTGTCTAAAGGT	1560
Qy		1561	TATTACATTCGGCAGTTTAGATTGATGATTTATCTTGAGCCTGATGAGTTGAATCTGTGT	1620
Db		1561	TATTACATTCGGCAGTTTAGATTGATGATTTATCTTGAGCCTGATGAGTTGAATCTGTGT	1620



1561 TATTACATTGGGCGAGTTAGATTAGATTGATTATCTTTGAGCGCTGATGCGAGTTGAACTGTGT 1620  
1621 TTTAAAGAAATTTTAAAGATAAAGCGCTAGCTGTGTTTATACACATAAATAGAAACGTC 1680  
1621 TTTAAAGAAATTTTAAAGATAAAGCGCTAGCTGTGTTTATACACATAAATAGAAACGTC 1680  
1681 AATCCGGATGGTAGCTTAATCGCTAATGGTTTACAATGGCCGAGAAATTTTCACGAGAAAAA 1740  
1681 AATCCGGATGGTAGCTTAATCGCTAATGGTTTACAATGGCCGAGAAATTTTCACGAGAAAAA 1740  
1741 CTCACAACGGCTATGATGCTCACACATTTAGAAATGTTTACGAAATTTAGAGCTTTGGCATTTA 1800  
1741 CTCACAACGGCTATGATGCTCACACATTTAGAAATGTTTACGAAATTTAGAGCTTTGGCATTTA 1800  
1801 ACTGATGGATTCGAATGAAAGAAATTCGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
1801 ACTGATGGATTCGAATGAAAGAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
1861 AGTGAAGTTGGAAAAATTTTAAACATCTTAAATAAATCTGCTATATAACCGGTGTTATACATGGT 1920  
1861 AGTGAAGTTGGAAAAATTTTAAACATCTTAAATAAATCTGCTATATAACCGGTGTTATACATGGT 1920  
1921 GATAACACATCAATTAAGAAACCTTGGCATTTCAAAAGAAACCAATTTTGTGTAGTCAAT 1980  
1921 GATAACACATCAATTAAGAAACCTTGGCATTTCAAAAGAAACCAATTTTGTGTAGTCAAT 1980  
1981 CAGTCATTAATAGACAGGCACTTATTAATTAATTAATTAATGACGAATTTGATGATTTAGAT 2040  
1981 CAGTCATTAATAGACAGGCACTTATTAATTAATTAATTAATGACGAATTTGATGATTTAGAT 2040  
2041 GAAAGTAGAAGGTATATTTTCAATAAACCCTGTAATCAAGAGAGAGATGATATCTTA 2100  
2041 GAAAGTAGAAGGTATATTTTCAATAAACCCTGTAATCAAGAGAGAGATGATATCTTA 2100  
2101 AAAGATATTTAAATCATCAGAAATAAAGATGCGAAATCGCAGTCAGTATTTTATCC 2160  
2101 AAAGATATTTAAATCATCAGAAATAAAGATGCGAAATCGCAGTCAGTATTTTATCC 2160  
2161 AATACATTAACCGCTTAGTGAAGAACTTAAACATATTTTGAATATTAATAAATAATA 2220  
2161 AATACATTAACCGCTTAGTGAAGAACTTAAACATATTTTGAATATTAATAAATAATA 2220  
2221 TTGCTTATTTCTACATGTTGATAAGATCATCTTACACAGATATCAAAAAAGAAATA 2280  
2221 TTGCTTATTTCTACATGTTGATAAGATCATCTTACACAGATATCAAAAAAGAAATA 2280  
2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2340  
2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2340  
2341 ACAGTAATAGATTAAATAAATCTGAGCGGCATTTAAGTAAATAATTAATAATTAAGTCAG 2400  
2341 ACAGTAATAGATTAAATAAATCTGAGCGGCATTTAAGTAAATAATTAATAATTAAGTCAG 2400  
2401 TTAATCTAAATTTGCTCAATACATCTTTTGTAAATCATGACAGCCTATTCGTTAAAAAT 2460  
2401 TTAATCTAAATTTGCTCAATACATCTTTTGTAAATCATGACAGCCTATTCGTTAAAAAT 2460  
2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTTAACACAT 2520  
2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTTAACACAT 2520  
2521 GATTGGATCGAGAAAAATCAATGCGCATTCACATTTTAAAGAGCTCAATTAAGACTTATTTT 2580  
2521 GATTGGATCGAGAAAAATCAATGCGCATTCACATTTTAAAGAGCTCAATTAAGACTTATTTT 2580  
2581 AATGACAAAGCTTAAAGATAAGATGTAAGAGGCGCATCAAGGTATGTTTATGACG 2640  
2581 AATGACAAAGCTTAAAGATAAGATGTAAGAGGCGCATCAAGGTATGTTTATGACG 2640  
2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAGAGTCAATCATCTTCCAGTCA 2700  
2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAGAGTCAATCATCTTCCAGTCA 2700

2701 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTTCCAATTTGCACTTTTAATC 2760  
2701 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTTCCAATTTGCACTTTTAATC 2760  
2761 TTAGAAAAGAAAACCGGCCATGTATTTAATAAACAATCGACCTGACTTATATATGCTTTGG 2820  
2761 TTAGAAAAGAAAACCGGCCATGTATTTAATAAACAATCGACCTGACTTATATATGCTTTGG 2820  
2821 GAAACGAAAATTTACAAATGGACAAAATGAACAATTTGAAAGTGCAAAAGAGGAGAAAATATA 2880  
2821 GAAACGAAAATTTACAAATGGACAAAATGAACAATTTGAAAGTGCAAAAGAGGAGAAAATATA 2880  
2881 CCTGTTAAACAAGTTCATTTAATAAGTATATACTCTATAAA 2920  
2881 CCTGTTAAACAAGTTCATTTAATAAGTATATACTCTATAAA 2920

RESULT 2  
AR616925  
LOCUS AR616925 2937 bp DNA linear PAT 14-FEB-2005  
DEFINITION Sequence 8 from patent US 6833264.  
ACCESSION AR616925  
VERSION AR616925.1 GI:59720260  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2937)  
AUTHORS Weigel,P.H., Kumari,K. and DeAngelis,P.  
TITLE Hyaluronan synthase gene and uses thereof  
JOURNAL Patent: US 6833264-A 8 21-DEC-2004;  
The Board of Regents of the University of Oklahoma; Norman, OK  
FEATURES  
source 1.2937  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 100.0%; Score 2919; DB 6; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATACATTATCAAGCAATAAAGCATATAAAGCAATGACTATCAATAGCACTC 60  
DB 19 ATGAATACATTATCAAGCAATAAAGCATATAAAGCAATGACTATCAATAGCACTC 78  
QY 61 AAATATTATTGAAAGTCGCGGAAATCTATGACGGAATAATTTGAAATTTCAAATACC 120  
DB 79 AAATATTATTGAAAGTCGCGGAAATCTATGACGGAATAATTTGAAATTTCAAATACC 138  
QY 121 AAATCGAAGAAAACCTCTCAGCACATCCTTCTGTTAAATTCAGCACATCTTTCTGTAAT 180  
DB 139 AAATCGAAGAAAACCTCTCAGCACATCCTTCTGTTAAATTCAGCACATCTTTCTGTAAT 198  
QY 181 AAGAGAAAAGTCAATGTTTTCGATAGTCGCTTAGATATTTGCAACACAACTGTTACTT 240  
DB 199 AAGAGAAAAGTCAATGTTTTCGATAGTCGCTTAGATATTTGCAACACAACTGTTACTT 258  
QY 241 TCCAAACGTAAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTAAAAAATAATCG 300  
DB 259 TCCAAACGTAAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTAAAAAATAATCG 318  
QY 301 AAATGCTCCTCAGAGAGAAATCTGAAATGCGAGGTAAAGAGCGTCCGCTTGTACCA 360  
DB 319 AAATGCTCCTCAGAGAGAAATCTGAAATGCGAGGTAAAGAGCGTCCGCTTGTACCA 378  
QY 361 AAGAGATTTTCCCAAGATCTGGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
DB 379 AAGAGATTTTCCCAAGATCTGGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACA 438  
QY 421 TGGTACAAAAGCGAAGAAAAGACTTGGGCATATAAACCTGAACATCAACATGTTGCTT 480

Db 439 TGGTACAAAAGCGAAGAAAGACTTTGGCATATAAACTCGAACATCAACATGTTGGTCTT 498  
Qy 481 TCTATTATCGTTTACAACTCAATCGACCGACCAATTTTATCGATTACATTTAGCCTGTTTA 540  
Db 499 TCTATTATCGTTTACAACTCAATCGACCGACCAATTTTATCGATTACATTTAGCCTGTTTA 558  
Qy 541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db 559 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
Qy 601 GATCTATCACCGATCAATTCGCAATATGAAAATAAAATTTGAATATTCGCTACGTCAGACAA 660  
Db 619 GATCTATCACCGATCAATTCGCAATATGAAAATAAAATTTGAATATTCGCTACGTCAGACAA 678  
Qy 661 AAAGATTAACGGTTTTCAAGCCAGTGGCCGCTCGGAATATGGGATTAACGTTTAGCAAAATAT 720  
Db 679 AAAGATAACGGTTTTCAAGCCAGTGGCCGCTCGGAATATGGGATTAACGTTTAGCAAAATAT 738  
Qy 721 GACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTTATGGTTTCATTCCTTAT 780  
Db 739 GACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTTATGGTTTCATTCCTTAT 798  
Qy 781 GTTCAGAGCTATTAGAGATGATGATTAACAATCATTTGCTCCAAAGAAAATACATCGAT 840  
Db 799 GTTCAGAGCTATTAGAGATGATGATTAACAATCATTTGCTCCAAAGAAAATACATCGAT 858  
Qy 841 ACACAACATATTGACCCAAAAGACTTCTTAATAAACCGAGTTTGTCTGAAATCATTTACCA 900  
Db 859 ACACAACATATTGACCCAAAAGACTTCTTAATAAACCGAGTTTGTCTGAAATCATTTACCA 918  
Qy 901 GAAGTGAACCAATATAGTTGTTGCCCAAAAGGGAGGAACAGTTTCTCTCGATTGG 960  
Db 919 GAAGTGAACCAATATAGTTGTTGCCCAAAAGGGAGGAACAGTTTCTCTCGATTGG 978  
Qy 961 CGCTTAGAAACAAATCGAAAAACAGAAAATCTCGCTTATCCGATTCGCCCTTTCGGTTTT 1020  
Db 979 CGCTTAGAAACAAATCGAAAAACAGAAAATCTCGCTTATCCGATTCGCCCTTTCGGTTTT 1038  
Qy 1021 TTTGGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTTAATAATAATCCGGTTTCTTTGAT 1080  
Db 1039 TTTGGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTTAATAATAATCCGGTTTCTTTGAT 1098  
Qy 1081 GAGGAATTTTATCACTGGGGTGGAGAGATCTGGAATTTGGATATCGCTTATTCGGTTTAC 1140  
Db 1099 GAGGAATTTTATCACTGGGGTGGAGAGATCTGGAATTTGGATATCGCTTATTCGGTTTAC 1158  
Qy 1141 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCCAGGTAAA 1200  
Db 1159 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCCAGGTAAA 1218  
Qy 1201 GAAATGAACCGATCGTGAAACGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG 1260  
Db 1219 GAAATGAACCGATCGTGAAACGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG 1278  
Qy 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGNAGATTCGCATATCAATAGAGTACCT 1320  
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGNAGATTCGCATATCAATAGAGTACCT 1338  
Qy 1321 TTAGTTTCAATTTTATATCCAGCTTATAACTGTGCAAACTATTATCAACGTTGCGTAGAT 1380  
Db 1339 TTAGTTTCAATTTTATATCCAGCTTATAACTGTGCAAACTATTATCAACGTTGCGTAGAT 1398  
Qy 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTPAACGATGGTTCAACA 1440  
Db 1399 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTPAACGATGGTTCAACA 1458  
Qy 1441 GATAATACCTTAGAGTGATCAATAAGCTTTATGCTAATAATCTTAGGGTAGCATCATG 1500  
Db 1459 GATAATACCTTAGAGTGATCAATAAGCTTTATGCTAATAATCTTAGGGTAGCATCATG 1518  
Qy 1501 TCTAAACCAAAATGGGGAAATAGCCTCAGCATCAAAATGCAGCGGTTCTTTTGTCTAAAGGT 1560  
Db 1519 TCTAAACCAAAATGGGGAAATAGCCTCAGCATCAAAATGCAGCGGTTCTTTTGTCTAAAGGT 1578

Qy 1561 TATTACATTTGGCGAGTTAGATTTCCAGATGATTATCTTTGAGCCTGATGCGAGTTGAACCTGTGT 1620  
Db 1579 TATTACATTTGGCGAGTTAGATTTCCAGATGATTATCTTTGAGCCTGATGCGAGTTGAACCTGTGT 1638  
Qy 1621 TTTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTAATAGAAAAACGTC 1680  
Db 1639 TTTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTAATAGAAAAACGTC 1698  
Qy 1681 AATCCGGATGGTAGCTTAATCGCTAATGGTTTACAAATTTGGCCAGAAATTTTTCAGGAAAAAA 1740  
Db 1699 AATCCGGATGGTAGCTTAATCGCTAATGGTTTACAAATTTGGCCAGAAATTTTTCAGGAAAAAA 1758  
Qy 1741 CTCAACACGGCTATGATGCTCACCACTTTTAGAATGTTTACGATTAGAGCTTGGCATTTTA 1800  
Db 1759 CTCAACACGGCTATGATGCTCACCACTTTTAGAATGTTTACGATTAGAGCTTGGCATTTTA 1818  
Qy 1801 ACTGATGGATTTCAATGAAAAAATTTGAAATGGCGTAGACTATGACATGTTTCTCTCAAACTC 1860  
Db 1819 ACTGATGGATTTCAATGAAAAAATTTGAAATGGCGTAGACTATGACATGTTTCTCTCAAACTC 1878  
Qy 1861 AGTGAAGTTGGAAAAATTTTAAACATCTTTAATAAAATCTGCTATTAACCGTGTTATTACATGGT 1920  
Db 1879 AGTGAAGTTGGAAAAATTTTAAACATCTTTAATAAAATCTGCTATTAACCGTGTTATTACATGGT 1938  
Qy 1921 GATAACACATCAATTAAGBAACCTTGGCATTTCBAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Db 1939 GATAACACATCAATTAAGBAACCTTGGCATTTCBAAGAAAAACCAATTTTGTGTAGTCAAT 1998  
Qy 1981 CAGTCATTAATAGAACGATCAAACTTTTATAAATTTATGACGAAATTTGATGATTTAGAT 2040  
Db 1999 CAGTCATTAATAGAACGATCAAACTTTTATAAATTTATGACGAAATTTGATGATTTAGAT 2058  
Qy 2041 GAAAGTAGAAAAATATTTTTCAATAAAACCGCTGAAATATCAAGAGAGATGATATCTTA 2100  
Db 2059 GAAAGTAGAAAAATATTTTTCAATAAAACCGCTGAAATATCAAGAGAGATGATATCTTA 2118  
Qy 2101 AAAGATATTAATAATCAATCCAGAAATTAAGATGCCAAATCCAGTCAGTATTTTTTATCCCC 2160  
Db 2119 AAAGATATTAATAATCAATCCAGAAATTAAGATGCCAAATCCAGTCAGTATTTTTTATCCCC 2178  
Qy 2161 AATACATTAACCGCTTAGTGAAAAAACTAAAACAATATTATTGAAATATAATAAAAAATATA 2220  
Db 2179 AATACATTAACCGCTTAGTGAAAAAACTAAAACAATATTATTGAAATATAATAAAAAATATA 2238  
Qy 2221 TTGCTTATGTTCTTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2239 TTGCTTATGTTCTTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCTTCTATCATTAACATCAAGTGAATATTTTTACTTAATATGATATCTCATATTAC 2340  
Db 2299 CTAGCCTTCTATCATTAACATCAAGTGAATATTTTTACTTAATATGATATCTCATATTAC 2358  
Qy 2341 ACAGATTAATAGATTAAATAAAAAATCGAGCGCATTTTAAGTAAATATAATAAAATTAAGTCAG 2400  
Db 2359 ACAGATTAATAGATTAAATAAAAAATCGAGCGCATTTTAAGTAAATATAATAAAATTAAGTCAG 2418  
Qy 2401 TTTAAATCTAAATTTGTGAATACATCAATTTTTGTGAATAATCATGACAGCCTATTTCGTTAAAAAT 2460  
Db 2419 TTTAAATCTAAATTTGTGAATACATCAATTTTTGTGAATAATCATGACAGCCTATTTCGTTAAAAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2520  
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 2521 GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTTAAAAAGCTCATTTAAACCTTATTTT 2580  
Db 2539 GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTTAAAGCTCATTTAAACCTTATTTT 2598  
Qy 2581 AATGACAAATGACTTTAAAAAGTATGAATGTGAAAGGGGATCAAGAGGTATGTTTATGACG 2640  
Db 2599 AATGACAAATGACTTTAAAAAGTATGAATGTGAAAGGGGATCAAGAGGTATGTTTATGACG 2658

QY 2641 TATGCGTAGCGCATGAGCTTCTGACGATTATTAAAGAGTCATCACATCTTGCCAGTCA 2700  
DB |||||||  
QY 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTATTAAAGAGTCATCACATCTTGCCAGTCA 2718  
DB |||||||  
QY 2701 ATTGATAGTGTGCCAGATATAAACACTGAGGATATTGGTCCCAATTTGCACTTTTAATC 2760  
DB |||||||  
QY 2719 ATTGATAGTGTGCCAGATATAAACACTGAGGATATTGGTCCCAATTTGCACTTTTAATC 2778  
DB |||||||  
QY 2761 TTAGAAAAGAAAACCGGCATGTATTAAATAAACAATGCAACCTGACCTTATATGCTTGG 2820  
DB |||||||  
QY 2779 TTAGAAAAGAAAACCGGCATGTATTAAATAAACAATGCAACCTGACCTTATATGCTTGG 2838  
DB |||||||  
QY 2821 GAAACAAAATTACAATGACCAAAATGAAAGTGAAGTGAAGAGGAGGAGAAATATA 2880  
DB |||||||  
QY 2839 GAAACAAAATTACAATGACCAAAATGAAAGTGAAGTGAAGAGGAGGAGAAATATA 2898  
DB |||||||  
QY 2881 CCTGTTAAACAAGTTCATTATTAAATAGTATACTCTATAA 2919  
DB |||||||  
QY 2899 CCTGTTAAACAAGTTCATTATTAAATAGTATACTCTATAA 2937  
DB |||||||

RESULT 3  
AF237926  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1. .2919  
/organism="Pasteurella multocida"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:747"  
1. .2919  
/genes="has"  
1. .2919  
/genes="has"  
/notes="pmhas"  
/codon\_start=1  
/transl\_table=11  
/product="hyaluronan synthase"  
/protein\_id="AF68412.1"  
/db\_xref="GI:7716513"  
/translation="MNTLSQAIKAYNSNDYQLAKLFEKSABYIGRKIVFQITKQOE  
KLSAPSVNSAHLVSNKSEKVNCDPLDIATQLLLSNVKLVLSDEKNTLNKWK  
LTKKSENAEVRVALVPKDFKDLVLPDPVNDFTWYKKRKLGLIKPEHQHVL  
SIIVTFNRPAILSLTCLVQKTHYPEVIVTDGSOEDLSPIIROYENKLDIRYV  
ROKNDGFQASAHNMGLRIKYDFIGLDCDMAAPNPLVHVSVAELLEDLITIGPR  
KYIDTQHDIPKDFLNNASLLESLEPVKTNNSVAAKGEVTSLOWRLEQFEKTEENLKL  
DSPFRFAAGNVAFAKKWIKSGFFDEEFNHMGWGEDVEFGYRLFRYSGFKTIDGIMA  
YHOEPKGENETDREAGKNTLIDIREKVPYIYKLLPLEDSHINRPVSVIYIPAYN  
CANVIOCVDSALNPTVDELVCINDGSTDNLTVINLKNPNRVRIMSKPNGGIA  
SASNAVSPAKGYIIGQLSDYLEPDAVELCLKELKDKTLACVYVTRNPNVPGSL  
IANGYNWPSREKLITAMIAHFRMFTIRAMHLTDGTFNEKINAVDYMFLKLSVG  
KFKHLNKIYCNRYVHGDNTSIKKLGIQKKNHVVNSLNROGITYNYNDEFDLDES  
RKYIFNKTAIEYQEBIDILDKIKIIONKDAKIAVSIYPNTLNLVKKLNIIEYNKI  
FVTLVHVDKNHLTPDKKEILAFYKHQVNIILNNDISVYTNRLIKTEAHLNINKL  
SQLNLNCEYIIFDHDLSLVKNDSDSYAMKKYDVGWNFSLTHDWIEKINAHPPFKLI

QY 1 ATGTAATACATTATCAACAGCAATAAAGCATATTAACAGCAATGACTATCAATATGCACTC 60  
DB |||||||  
QY 61 AAATATTGTAAGTTCGGCGGAAATCTATGGAACGGAATAATTTGTTGAATTTCAATATACC 120  
DB |||||||  
QY 121 AAATGCAAGAAAGAACTCTCAGCACATCTCTGTTAATTCAGCACATCTTTCTCTAAAT 180  
DB |||||||  
QY 181 AAAGAAGAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACAACCTGTACTT 240  
DB |||||||  
QY 241 TCCAAACGTAATAAATAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAATAAATGG 300  
DB |||||||  
QY 301 AAATGCTCCTCAGAGAGAAATCTGAAATCGGAGGTGAAGCGGTCGCTTGTACCA 360  
DB |||||||  
QY 361 AAAGATTTTCCAAAGATCTGTTTACGCGCTTTACCTGATCATGTTAAATGATTTTACA 420  
DB |||||||  
QY 421 TGSTACAAAAAGCGAAAAAGACTTGGCATATAAACTGAAACATCAACATGTTGGTCTT 480  
DB |||||||  
QY 481 TCTATTATCGTTGTAACATTCATCGACGCAATTTTATCGATTACATTTAGCCTGTTTAA 540  
DB |||||||  
QY 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATCGTACAGCAA 600  
DB |||||||  
QY 601 GATCTATCACCGATCAITTCGCCAATATGAAAAATAAATTTGGATATTCGCTACGTCAGCAA 660  
DB |||||||  
QY 661 AAAGATAACCGTTCCTCAGCAGTCCGCTCGAATATGGGATAGGCTTACGCAAAATAT 720  
DB |||||||  
QY 721 GACTTTATTTGGCTTACTGACCTGTGATATGGCGCCAAATCCATTTAGGGTTCATTCTTAT 780  
DB |||||||  
QY 781 GTTGCAAGAGCTATTAGAAGATGATATTTAAACAATCATTTGGTCCAGAAAAATATACATCGAT 840  
DB |||||||  
QY 841 ACACAAATATTGACCCAAAAAGACTTCTTAAATAACCGCAGTTTGGTTCGAATCATTTACCA 900  
DB |||||||  
QY 901 GAAGTGAACCAATTAATAGTGTGCGCGAAAAAGGGAAGGAAACAGTTTCTCTGGATTGG 960  
DB |||||||

ORIGIN

Query Match 99.9%; Score 2917.4; DB 1; Length 2919;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	961	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTATTCGATTCGCCTTTCCGTTTT	1021
Db	961	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCCTTTCCGTTTT	1020
Qy	1021	TTTTCGCGGGTAATGTTGCTTTTCGCTAAAAAAATGGCTAAATAAATCCGTTTTCTTTGAT	1080
Db	1021	TTTTCGCGCGGGTAATGTTGCTTTTCGCTAAAAAAATGGCTAAATAAATCCGTTTTCTTTGAT	1080
Qy	1081	GAGGAATTTAATCACTCGGGTGGAGAAGATGTGGAATTTTCGATATCGCTTATTTCCGTTAC	1140
Db	1081	GAGGAATTTAATCACTCGGGTGGAGAAGATGTGGAATTTTCGATATCGCTTATTTCCGTTAC	1140
Qy	1141	GGTAGTTTCTTTTAAAACTATTGATGGCAATTATGGCCTACCATCAAGAGCCACAGGTA	1200
Db	1141	GGTAGTTTCTTTTAAAACTATTGATGGCAATTATGGCCTACCATCAAGAGCCACAGGTA	1200
Qy	1201	GAAAAATGAAACCGGATCGTAGAGCGGGGAAAAAATATTAACGCTCGATATTAAGAGAAAAG	1260
Db	1201	GAAAAATGAAACCGGATCGTAGAGCGGGGAAAAAATATTAACGCTCGATATTAAGAGAAAAG	1260
Qy	1261	GTCCCTTATATCTATAGAAACCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT	1320
Db	1261	GTCCCTTATATCTATAGAAACCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT	1320
Qy	1321	TTAGTTTCAATTTATATCCGAGCTTATAAAGCTGTGCAAACTATATTCAAAGCTTCGCTAGAT	1380
Db	1321	TTAGTTTCAATTTATATCCGAGCTTATAAAGCTGTGCAAACTATATTCAAAGCTTCGCTAGAT	1380
Qy	1381	AGTGCACTGAATCAGATCTGTTGTTGATCTCGAGGTTTGATTTGTAAACGATGGTTCAACA	1440
Db	1381	AGTGCACTGAATCAGATCTGTTGTTGATCTCGAGGTTTGATTTGTAAACGATGGTTCAACA	1440
Qy	1441	GATTAATACCTTAGAAGTGATCAATAAGCTTATGTTAATAATCTCAGGTCACCATCATG	1500
Db	1441	GATTAATACCTTAGAAGTGATCAATAAGCTTATGTTAATAATCTCAGGTCACCATCATG	1500
Qy	1501	TCTAAACCAATGCGGAATAGCCCTCAGCATCAAAATGCAGCCGTTTTCTTTGCTAAAGGT	1560
Db	1501	TCTAAACCAATGCGGGNATAGCCCTCAGCATCAAAATGCAGCCGTTTTCTTTGCTAAAGGT	1560
Qy	1561	TATTACATTTGGCAGTTAGATTTAGATGAATATCTTGAGCCTGATGAGTTGAACTGTGT	1620
Db	1561	TATTACATTTGGCAGTTAGATTTAGATGAATATCTTGAGCCTGATGAGTTGAACTGTGT	1620
Qy	1621	TTTAAAGAAATTTTAAAGATATAACCGTAGCTTGCTTTATACCACTAATAGAAAGCTC	1680
Db	1621	TTTAAAGAAATTTTAAAGATATAACCGTAGCTTGCTTTATACCACTAATAGAAAGCTC	1680
Qy	1681	AATCCGATGGTAGCTTAATCCGCTAATGGTTTACAATTTGGCCAGAAATTTTTCAGAGAAAA	1740
Db	1681	AATCCGATGGTAGCTTAATCCGCTAATGGTTTACAATTTGGCCAGAAATTTTTCAGAGAAAA	1740
Qy	1741	CTCACACCGCTATGATTTGCTCAACATTTAGAAATGTTACAGATTAGAGCTTGCCATTTA	1800
Db	1741	CTCACACCGCTATGATTTGCTCAACATTTAGAAATGTTACAGATTAGAGCTTGCCATTTA	1800
Qy	1801	ACTGATGGATTCAATGAAAAAATTTGAAAAATGCCGTAGACTATGACATGTTCCCTCAAACTC	1860
Db	1801	ACTGATGGATTCAATGAAAAAATTTGAAAAATGCCGTAGACTATGACATGTTCCCTCAAACTC	1860
Qy	1861	AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAAATCTGCTATAACCGGTATTACATGGT	1920
Db	1861	AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAAATCTGCTATAACCGGTATTACATGGT	1920
Qy	1921	GATAACACATCAATTTAAGAAACTTTGGCATTCAAAAAGAAAAACCAATTTTGTGTAGTCAAT	1980
Db	1921	GATAACACATCAATTTAAGAAACTTTGGCATTCAAAAAGAAAAACCAATTTTGTGTAGTCAAT	1980
Qy	1981	CAGTCATTTAATAGACAGGCATTAACCTTATTAATTTATGACGAATTTGATGATTTAGAT	2040
Db	1981	CAGTCATTTAATAGACAGGCATTAACCTTATTAATTTATGACGAATTTGATGATTTAGAT	2040
Qy	2041	GAAGTAGAAAGTATATTTTCAATTAATAAACCCGCTGAAATATCAAGAAAGAGATTGATATCTTA	2100

[illegible]

RESULT 4  
BD087261

BD087261	BD087261	2937 bp	DNA	linear
LOCUS	Hyaluronan synthase gene and utilization thereof.			
DEFINITION	BD087261			
ACCESSION	BD087261			
VERSION	BD087261.1	GI:22632871		
KEYWORDS	JP 2001521741-A/13.			
SOURCE	unidentified			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 2937)			
AUTHORS	Weigel,P.H., Kumar,K. and Deangelis,P.			
TITLE	Hyaluronan synthase gene and utilization thereof			

JOURNAL Patent: JP 2001521741-A 13 13-NOV-2001;  
THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA  
OS Pasturella multocida  
COMMENT JP 2001521741-A/13  
PD 13-NOV-2001  
PF 30-OCT-1998 JP 2000519083  
PR 31-OCT-1997 US 60/064435,26-OCT-1998 US 09/178851 PI  
PAUL H WEIGEL, KSHAMA KUMARI, PAUL DEANGELIS  
PC C12N15/09,A61K31/728,A61P43/00,C12N1/21,C12N9/10,C12P19/04, PC  
C12Q1/68//  
PC (C12N15/09,C12R1:46),C12N15/00,(C12N15/00,C12R1:46) CC  
Hyaluronan synthase gene and utilization thereof FH Key  
Location/Qualifiers  
FT source 1..2899 /organism='Pasturella multocida'.  
FT Location/Qualifiers  
1..2937  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

FEATURES  
source

ORIGIN  
Query Match 99.9%; Score 2917.4; DB 6; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATACATTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
DB 19 ATGAATACATTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 78  
QY 61 AAATTATTGAAAGTCGCGGAAATCTATGACGGAATAATGTTGAAATTTCAAAATTACC 120  
DB 79 AAATTATTGAAAGTCGCGGAAATCTATGACGGAATAATGTTGAAATTTCAAAATTACC 138  
QY 121 AAATGCAAGAAAACTCTCAGCACATCCTCTGTTAAATTCAGCACATCTTTCTGTAAT 180  
DB 139 AAATGCCAAGAAAACTCTCAGCACATCCTCTGTTAAATTCAGCACATCTTTCTGTAAT 198  
QY 181 AAAGAAGAAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTTGCAACACACTGTTACTT 240  
DB 199 AAAGAAGAAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTTGCAACACACTGTTACTT 258  
QY 241 TCCACGTTAAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300  
DB 259 TCCACGTTAAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 318  
QY 301 AAATTGCTCACTGAGAGAAATCTGAAAAATGCGGAGGTAAAGACGCGTCCCTTGTACCA 360  
DB 319 AAATTGCTCACTGAGAGAAATCTGAAAAATGCGGAGGTAAAGACGCGTCCCTTGTACCA 378  
QY 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTACCTGATCATGTTAATGATTTTACA 420  
DB 379 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAATGATTTTACA 438  
QY 421 TGGTACAAAAGCGAAGAAAGACTTGGCATAAAAACCTGAAACATCAACATGTTGCTCTT 480  
DB 439 TGGTACAAAAGCGAAGAAAGACTTGGCATAAAAACCTGAAACATCAACATGTTGCTCTT 498  
QY 481 TCTATTATCGTTACACATTTCAATCGACAGCAATTTTATCGATTAATGATGCTGTTTAA 540  
DB 499 TCTATTATCGTTACACATTTCAATCGACAGCAATTTTATCGATTAATGATGCTGTTTAA 558  
QY 541 GTAAACCAAAAAACAATTACCGTTTGAAGTTATCGTGAACAGATGATGTTAGTACGAA 600  
DB 559 GTAAACCAAAAAACAATTACCGTTTGAAGTTATCGTGAACAGATGATGTTAGTACGAA 618  
QY 601 GATCTATCACCGATCAATCGCCCAATATGAATAAATTCGATATTCGCTACGTCACACAA 660  
DB 619 GATCTATCACCGATCAATCGCCCAATATGAATAAATTCGATATTCGCTACGTCACACAA 678  
QY 661 AAAGATAAAGCGTTTTCAGAGCCAGTGCCTGCGGAATATGCGGATTTAGCGTTAGCAAAATAT 720  
DB 679 AAAGATAAAGCGTTTTCAGAGCCAGTGCCTGCGGAATATGCGGATTTAGCGTTAGCAAAATAT 738

QY 721 GACTTTATTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTATGGGTTTCATTTCTTAT 780  
DB 739 GACTTTATTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTATGGGTTTCATTTCTTAT 798  
QY 781 GTTGCAGAGCTATTAGGAAGATGATTTTAAACAAATCATTGGTCCCAAGAAAATACATCGAT 840  
DB 799 GTTGCAGAGCTATTAGGAAGATGATTTTAAACAAATCATTGGTCCCAAGAAAATACATCGAT 858  
QY 841 ACACAAATATTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTGAATCAATACCA 900  
DB 859 ACACAAATATTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTGAATCAATACCA 918  
QY 901 GAAGTGAATAACCAATTAATAGTTTCCGCAAAAAGGGGAAGAAACAGTTTCTCTCGATTGG 960  
DB 919 GAAGTGAATAACCAATTAATAGTTTCCGCAAAAAGGGGAAGAAACAGTTTCTCTCGATTGG 978  
QY 961 CGCTTAGAACCAATTCGAAAAACAGAAAATCTCCGCTTATCCGATTCCGCTTTCCGTTTTT 1020  
DB 979 CGCTTAGAACCAATTCGAAAAACAGAAAATCTCCGCTTATCCGATTCCGCTTTCCGTTTTT 1038  
QY 1021 TTTCCGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTTAAATAAATCCGGTTTCTTTGAT 1080  
DB 1039 TTTCCGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTTAAATAAATCCGGTTTCTTTGAT 1098  
QY 1081 GAGGAATTTAATCACTGGGGTGGAGAAAGATGTGAAATTTGGATATCGCTTATTCGGTTTAC 1140  
DB 1099 GAGGAATTTAATCACTGGGGTGGAGAAAGATGTGAAATTTGGATATTCGGTTTATTCGGTTTAC 1158  
QY 1141 GGTAGTTTCTTTTAAAACTATTGATGGCATTTATGCGCTACCATCAAGGCCACCCAGGTAAA 1200  
DB 1159 GGTAGTTTCTTTTAAAACTATTGATGGCATTTATGCGCTACCATCAAGGCCACCCAGGTAAA 1218  
QY 1201 GAAATGAACCGATCGTGAAGCGGAAAAAATAATACGCTCGATATTATGAGAGAAAAAG 1260  
DB 1219 GAAATGAACCGATCGTGAAGCGGAAAAAATAATACGCTCGATATTATGAGAGAAAAAG 1278  
QY 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT 1320  
DB 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT 1338  
QY 1321 TTAGTTTCAATTTATATCCGAGCTTATAACCTGCGCAAACTATATCAACGTTGCGGTAGAT 1380  
DB 1339 TTAGTTTCAATTTATATCCGAGCTTATAACCTGCGCAAACTATATCAACGTTGCGGTAGAT 1398  
QY 1381 AGTCACACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTGTAACGATGGTTCAACA 1440  
DB 1399 AGTCACACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTGTAACGATGGTTCAACA 1458  
QY 1441 GATAATACCTTTAGAAAGTGAATCAATAAGCTTTATGGAATAAATCCTTAGGGTACGCATCATG 1500  
DB 1459 GATAATACCTTTAGAAAGTGAATCAATAAGCTTTATGGAATAAATCCTTAGGGTACGCATCATG 1518  
QY 1501 TCTAAACCAATATGGCGGAATAGCCTCAGCATCAATGCGCGGTTTCTTTTCTTAAAGGT 1560  
DB 1519 TCTAAACCAATATGGCGGAATAGCCTCAGCATCAATGCGCGGTTTCTTTTCTTAAAGGT 1578  
QY 1561 TATTACATTGGCGAGTATGATTTCAGATGATTATCTTGGCCCTGATGCGAGTTGAACTGTGT 1620  
DB 1579 TATTACATTGGCGAGTATGATTTCAGATGATTATCTTGGCCCTGATGCGAGTTGAACTGTGT 1638  
QY 1621 TTTAAAGAAATTTTAAAAAGATAAAAACGCTAGCTGTGTTTATACCACTAATAAGAAACGTC 1680  
DB 1639 TTTAAAGAAATTTTAAAAAGATAAAAACGCTAGCTGTGTTTATACCACTAATAAGAAACGTC 1698  
QY 1681 AATCCGGATGGTATGATTATTCGCTAATGGTTTAAATGGTCCAGAAATTTTTCAGAGAAAAA 1740  
DB 1699 AATCCGGATGGTATGATTATTCGCTAATGGTTTAAATGGTCCAGAAATTTTTCAGAGAAAAA 1758  
QY 1741 CTCACAAAGGCTATGATTGCTCACCACTTTTACAAATGTTTCCAGGATTTAGAGCTTTGGCATTTA 1800  
DB 1759 CTCACAAAGGCTATGATTGCTCACCACTTTTACAAATGTTTCCAGGATTTAGAGCTTTGGCATTTA 1818



Qy 1801 ACTGATGATTCATGAGAAATTTGAAATGCGGTAGCATGATGACATGTCCTCAACTC 1860  
Db 1819 ACTGATGATTCATGAGAAATTTGAAATGCGGTAGCATGATGACATGTCCTCAACTC 1878  
Qy 1861 AGTGAAGTTGGAAATTTTAAACATCTTAAATAATCTGCTATAACCGGTGATTACATGGT 1920  
Db 1879 AGTGAAGTTGGAAATTTTAAACATCTTAAATAATCTGCTATAACCGGTGATTACATGGT 1938  
Qy 1921 GATAACATCAATTAAGAAACTTGGCATTCAGAAAGAAACCAATTTTGTGTAGTCAAT 1980  
Db 1939 GATAACATCAATTAAGAAACTTGGCATTCAGAAAGAAACCAATTTTGTGTAGTCAAT 1998  
Qy 1981 CAGTCATTAAATAGACAGGATCACTTATTATTAATATGACGAATTTGATGATTTAGAT 2040  
Db 1999 CAGTCATTAAATAGACAGGATCACTTATTATTAATATGACGAATTTGATGATTTAGAT 2058  
Qy 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTGATATCTTA 2100  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATTGATATCTTA 2118  
Qy 2101 AAAGATATTAATAATCATCCAGAAATAAGATGCCAAATCGCAGTCAGTATTTTATCCC 2160  
Db 2119 AAAGATATTAATAATCATCCAGAAATAAGATGCCAAATCGCAGTCAGTATTTTATCCC 2178  
Qy 2161 AATACATTAACGGCTTAGTGAAAGAACTAAACATATATTATTAATTAATAAAATATA 2220  
Db 2179 AATACATTAACGGCTTAGTGAAAGAACTAAACATATATTATTAATTAATAAAATATA 2238  
Qy 2221 TTCGTTATTGTTTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2239 TTCGTTATTGTTTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2340  
Db 2299 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2358  
Qy 2341 ACGAGTAATAGATTAATAAAACTGAGCGGCATTTTAAAGTATATTAAATAATTAAAGTAC 2400  
Db 2359 ACGAGTAATAGATTAATAAAACTGAGCGGCATTTTAAAGTATATTAAATAATTAAAGTAC 2418  
Qy 2401 TTAATCTTAAATTTGTAATACATCATTTTGTATATCATGACAGCCTATTGTTTAAATAAT 2460  
Db 2419 TTAATCTTAAATTTGTAATACATCATTTTGTATATCATGACAGCCTATTGTTTAAATAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAATAATATGATGTGCGCATGAATTTCTCAGCATTTAACACAT 2520  
Db 2479 GACAGCTATGCTTATATGAAATAATATGATGTGCGCATGAATTTCTCAGCATTTAACACAT 2538  
Qy 2521 GATTGGATCGAGAAATCAATGCGCATCCACCATTTTAAAGAGCTCATTTAAACATTATTTT 2580  
Db 2539 GATTGGATCGAGAAATCAATGCGCATCCACCATTTTAAAGAGCTCATTTAAACATTATTTT 2598  
Qy 2581 AATGACAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCACAGGTATGTTTATGACG 2640  
Db 2599 AATGACAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCACAGGTATGTTTATGACG 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAAGTCATCACATCTTGCAGTCA 2700  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAAGTCATCACATCTTGCAGTCA 2718  
Qy 2701 ATTGATAGTGTGCCAGATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAAATC 2760  
Db 2719 ATTGATAGTGTGCCAGATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAAATC 2778  
Qy 2761 TTAGAAAAAGAAACCGCGCATGATTTTAAATAAACATCGACCTGACTTATATGCTTTGG 2820  
Db 2779 TTAGAAAAAGAAACCGCGCATGATTTTAAATAAACATCGACCTGACTTATATGCTTTGG 2838  
Qy 2821 GAACGAAATTAACAATGGAACAATGAACAATTTGAAAGTGCAGAAAGAGGAGAAATATA 2880  
Db 2839 GAACGAAATTAACAATGGAACAATGAACAATTTGAAAGTGCAGAAAGAGGAGAAATATA 2898  
Qy 2881 CCTGTTAACAGTTCATTATTAATAGTATTAACCTCTATAA 2919

Db 2899 CCTGTTAACAGTTCATTATTAATAGTATTAACCTCTATAA 2937  
RESULT 5  
BD205371  
LOCUS  
DEFINITION  
Nucleic acid encoding hyaluronan synthase and method of using the same.  
BD205371  
VERSION  
BD205371.1 GI:33015141  
KEYWORDS  
JP 2002510648-A/1.  
SOURCE  
Pasteurella multocida  
ORGANISM  
Pasteurella multocida  
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.  
REFERENCE  
1 (bases 1 to 2937)  
Deangelis,P.  
AUTHORS  
Nucleic acid encoding hyaluronan synthase and method of using the  
TITLE  
Patent: JP 2002510648-A 1 09-APR-2002.  
JOURNAL  
BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA  
COMMENT  
OS Pasteurella multocida  
PN JP 2002510648-A/1  
PD 09-APR-2002  
PF 01-APR-1999 JP 2000542035  
PR 02-APR-1998 US 60/080414,26-OCT-1998 US 09/178851 PI  
PAUL DEANGELIS  
PC A61K39/102,A61K39/00,A61K47/36,A61P31/04,C12N1/15,C12N1/19,PC  
C12N1/21,  
PC  
C12N5/10,C12N9/00,C12N15/09,C12P19/04,C12Q1/02,C12Q1/68,G01N33/PC  
48,  
PC G01N33/53,G01N33/566,C12N5/00,C12N15/00  
CC Nucleic acid encoding hyaluronan synthase and method of using  
the same.  
FH Key Location/Qualifiers  
FT source 1..2937 /organism='Pasteurella multocida'.  
FT source 1..2937 /organism='Pasteurella multocida'.  
FEATURES  
source  
1..2937  
/organism="Pasteurella multocida"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:747"  
ORIGIN  
Query Match 99.9%; Score 2917.4; DB 6; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGTAATACATTATCACAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
Db 19 ATGTAATACATTATCACAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 78  
Qy 61 AAATATTATGAAAAGTCGGCGGAAATCTATGGACGGAAAAATTTGTGAATTTCAAATTACC 120  
Db 79 AAATATTATGAAAAGTCGGCGGAAATCTATGGACGGAAAAATTTGTGAATTTCAAATTACC 138  
Qy 121 AAATGCAAGAAAAAATCTCTCAGCACATCTCTTCTGTTAAATTCAGCACATCTTCTGTAAT 180  
Db 139 AAATGCCAAGAAAAAATCTCTCAGCACATCTCTTCTGTTAAATTCAGCACATCTTCTGTAAT 198  
Qy 181 AAAGAAGAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACACTGTTACTT 240  
Db 199 AAAGAAGAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACACTGTTACTT 258  
Qy 241 TCCCAACGTAAAAAATTTAGTACTTTTCTGACTCGGAAAAAACACGTTAAAAAATAAATGG 300  
Db 259 TCCCAACGTAAAAAATTTAGTACTTTTCTGACTCGGAAAAAACACGTTAAAAAATAAATGG 318  
Qy 301 AAATTGCTCACTGAGAGAAAATCTGAAAAATGCGGAGGTAAAGCGGTCGCCCTTGTACCA 360  
Db 319 AAATTGCTCACTGAGAGAAAATCTGAAAAATGCGGAGGTAAAGCGGTCGCCCTTGTACCA 378

QY 361 AAAGATTTTCCAAAGATCTGGTTTACGCGCTTTACCTGATCATGTGTAATGATTTTACA 420  
DB |||||  
QY 379 AAAGATTTTCCAAAGATCTGGTTTACGCGCTTTACCTGATCATGTGTAATGATTTTACA 438  
DB |||||  
QY 421 TGGTACAAAAGCGGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACATGTTGGTCTT 480  
DB |||||  
QY 439 TGGTACAAAAGCGGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACATGTTGGTCTT 498  
DB |||||  
QY 481 TCTATTATCGTTACAAACATTCATCGACGACGCAATTTTATCGATTACATTAAGCCTGTTTA 540  
DB |||||  
QY 499 TCTATTATCGTTACAAACATTCATCGACGACGCAATTTTATCGATTACATTAAGCCTGTTTA 558  
DB |||||  
QY 541 GTAAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
DB |||||  
QY 559 GTAAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
DB |||||  
QY 601 GATCTATCACCGGATCAATTCGCAATATGAAAATAAAATTTGGATAATTCGGCTACGTCAGCAA 660  
DB |||||  
QY 619 GATCTATCACCGGATCAATTCGCAATATGAAAATAAAATTTGGATAATTCGGCTACGTCAGCAA 678  
DB |||||  
QY 661 AAAGATAACGGTTTCAAGCCAGTCGCCCTCGGAATATGGGATTAAGCTTAGCRAAATAT 720  
DB |||||  
QY 679 AAAGATAACGGTTTCAAGCCAGTCGCCCTCGGAATATGGGATTAAGCTTAGCRAAATAT 738  
DB |||||  
QY 721 GACTTTATTTGGCTTACTCGACTGTCATATGGCGCAAAATCCAAATATGGGTTCAATCTTAT 780  
DB |||||  
QY 739 GACTTTATTTGGCTTACTCGACTGTCATATGGCGCAAAATCCAAATATGGGTTCAATCTTAT 798  
DB |||||  
QY 781 GTTCGAGAGCTATTAGAAGATGATGATTTTAAACAATCATTTGGTCCAAAGAAAATACATCGAT 840  
DB |||||  
QY 799 GTTCGAGAGCTATTAGAAGATGATGATTTTAAACAATCATTTGGTCCAAAGAAAATACATCGAT 858  
DB |||||  
QY 841 ACAACAATATTGACCCAAAAGACTTCTTAAATAACGCGAGTTTCGTTGAAATCATTTACCA 900  
DB |||||  
QY 859 ACAACAATATTGACCCAAAAGACTTCTTAAATAACGCGAGTTTCGTTGAAATCATTTACCA 918  
DB |||||  
QY 901 GAAGTGAAACCAATAATAGTGTCCGCAAAAGGGAAGAAAGAGTTCTCTCGATTGG 960  
DB |||||  
QY 919 GAAGTGAAACCAATAATAGTGTCCGCAAAAGGGAAGAAAGAGTTCTCTCGATTGG 978  
DB |||||  
QY 961 CGCTTAGAACCAATTGCAAAAAACAGAAAATCTCCGCTTATCCGATTCGCTTTCGTTTT 1020  
DB |||||  
QY 979 CGCTTAGAACCAATTGCAAAAAACAGAAAATCTCCGCTTATCCGATTCGCTTTCGTTTT 1038  
DB |||||  
QY 1021 TTTCGGGGGGTAATGTTGCTTTCGCTTAAAAAATGGCTTAAATTAATTCGGTTCTTTGAT 1080  
DB |||||  
QY 1039 TTTCGGGGGGTAATGTTGCTTTCGCTTAAAAAATGGCTTAAATTAATTCGGTTCTTTGAT 1098  
DB |||||  
QY 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATTCGTTAC 1140  
DB |||||  
QY 1099 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATTCGTTAC 1158  
DB |||||  
QY 1141 GGTAGTCTTCTTAAACTATGATGGCATTTATGGCTTATCCGCTACCATCAAGAGCCACAGGTAAA 1200  
DB |||||  
QY 1159 GGTAGTCTTCTTAAACTATGATGGCATTTATGGCTTATCCATCAAGAGCCACAGGTAAA 1218  
DB |||||  
QY 1201 GAAATGAAACCGATCGTGAAGCGGGAAGAAAATATTAATTCGCTCGATATTAATGAGAGAAAG 1260  
DB |||||  
QY 1219 GAAATGAAACCGATCGTGAAGCGGGAAGAAAATATTAATTCGCTCGATATTAATGAGAGAAAG 1278  
DB |||||  
QY 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
DB |||||  
QY 1279 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1338  
DB |||||  
QY 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTTCAACGTTGCGTAGAT 1380  
DB |||||  
QY 1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTTCAACGTTGCGTAGAT 1398  
DB |||||  
QY 1381 AGTGCACTGAATCAGACTGTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1440  
DB |||||  
QY 1399 AGTGCACTGAATCAGACTGTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1458  
DB |||||  
QY 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATACCTTAGGCTACGATCATG 1500

DB |||||  
QY 1459 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATATCTAGGTCGATCATG 1518  
DB |||||  
QY 1501 TCTAAACCAATGCGGAATAGCCTCAGCATCAAAATGACGCGGTTCTTTTGTCTAAAGGT 1560  
DB |||||  
QY 1519 TCTAAACCAATGCGGAATAGCCTCAGCATCAAAATGACGCGGTTCTTTTGTCTAAAGGT 1578  
DB |||||  
QY 1561 TATTACATTTGGCAGTTAGATTCCAGATGATTTATCTTGAGCCTGATGAGTTGAACTGTGT 1620  
DB |||||  
QY 1579 TATTACATTTGGCAGTTAGATTCCAGATGATTTATCTTGAGCCTGATGAGTTGAACTGTGT 1638  
DB |||||  
QY 1621 TTTAAAGAAATTTTAAAGAGATAAAACGCTAGCTTTGTGTTATACCACTAATAGAAAACGTC 1680  
DB |||||  
QY 1639 TTTAAAGAAATTTTAAAGAGATAAAACGCTAGCTTTGTGTTATACCACTAATAGAAAACGTC 1698  
DB |||||  
QY 1681 AATCCGATGTTAGCTTAATCGCTAAATGGTTTACAAATTTGGCCAGAAATTTTTCACGAGAAAA 1740  
DB |||||  
QY 1699 AATCCGATGTTAGCTTAATCGCTAAATGGTTTACAAATTTGGCCAGAAATTTTTCACGAGAAAA 1758  
DB |||||  
QY 1741 CTCAAAACGGCTATGATTTGCTCACCATTTTAAAGATTTTACGATTTAGAGCTTTGGCATTTA 1800  
DB |||||  
QY 1759 CTCAAAACGGCTATGATTTGCTCACCATTTTAAAGATTTTACGATTTAGAGCTTTGGCATTTA 1818  
DB |||||  
QY 1801 ACTGATGATTTCAATGAAAAAATTTGAAAAATGCGCTAGACTATGACATGTTCTCTCAAACTC 1860  
DB |||||  
QY 1819 ACTGATGATTTCAATGAAAAAATTTGAAAAATGCGCTAGACTATGACATGTTCTCTCAAACTC 1878  
DB |||||  
QY 1861 AGTCAAGTTGGAAAAATTTAAACATCTTAAATAAAATCTGCTATAACCGTGATTTACATCGT 1920  
DB |||||  
QY 1879 AGTCAAGTTGGAAAAATTTAAACATCTTAAATAAAATCTGCTATAACCGTGATTTACATCGT 1938  
DB |||||  
QY 1921 GATAACACATCAATTTAAGAAACTTTGGCAATTTCAAAAGAAAAAACCAATTTTGTGTAGTCAAT 1980  
DB |||||  
QY 1939 GATAACACATCAATTTAAGAAACTTTGGCAATTTCAAAAGAAAAAACCAATTTTGTGTAGTCAAT 1998  
DB |||||  
QY 1981 CAGTCATTTAAATAGACAAGGCAATTAATTTATTAATATGACGAATTTTGATGATTTAGT 2040  
DB |||||  
QY 1999 CAGTCATTTAAATAGACAAGGCAATTAATTTATTAATATGACGAATTTTGATGATTTAGT 2058  
DB |||||  
QY 2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAAGAGATTTGATATCTTA 2100  
DB |||||  
QY 2059 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAAGAGATTTGATATCTTA 2118  
DB |||||  
QY 2101 AAAGATATTTAAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2160  
DB |||||  
QY 2119 AAAGATATTTAAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2178  
DB |||||  
QY 2161 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAATATTTATGAAATATAAATAAATATA 2220  
DB |||||  
QY 2179 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAATATTTATGAAATATAAATAAATATA 2238  
DB |||||  
QY 2221 TTCGTTATTTGTTTACATGTTGATAAGAAATCATCTTTACACCAAGATATCAAAAAAGAAATA 2280  
DB |||||  
QY 2239 TTCGTTATTTGTTTACATGTTGATAAGAAATCATCTTTACACCAAGATATCAAAAAAGAAATA 2298  
DB |||||  
QY 2281 CTAGGCTTCTATCAAAAAACATCAAGTGAATATTTTACTAAAAATAATGATATCTCATATTAC 2340  
DB |||||  
QY 2299 CTAGGCTTCTATCAAAAAACATCAAGTGAATATTTTACTAAAAATAATGATATCTCATATTAC 2358  
DB |||||  
QY 2341 ACGAGTAATAGATTAAATAAAAACTGAGCGGCAATTTTAAGTAAATTAATAAATAAGTCAG 2400  
DB |||||  
QY 2359 ACGAGTAATAGATTAAATAAAAACTGAGCGGCAATTTTAAGTAAATTAATAAATAAGTCAG 2418  
DB |||||  
QY 2401 TTAATCTAAATTTGGAATACATCAATTTTGTGAATATCATGACAGCCTATTCGTTAAAAAT 2460  
DB |||||  
QY 2419 TTAATCTAAATTTGGAATACATCAATTTTGTGAATATCATGACAGCCTATTCGTTAAAAAT 2478  
DB |||||  
QY 2461 GACACCTATGCTTATATGAAAAATAATGATGTGCGCATGAATTTCTCAGCATTTAACACAT 2520  
DB |||||  
QY 2479 GACACCTATGCTTATATGAAAAATAATGATGTGCGCATGAATTTCTCAGCATTTAACACAT 2538  
DB |||||  
QY 2521 GATTGGATCGAGAAAAATCAATCGCATCCACATTTTAAAAAGCTCATTTAAAACTTATTTT 2580  
DB |||||



Db	2539	GATTGGATCGAGAAAATCAATCGCATCCACCATTATAAAGACTCATTAACCTTATTTT	2598
Qy	2581	AATGCAATGACTTAAAGAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGACG	2640
Db	2599	AATGCAATGACTTAAAGAGTATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGACG	2658
Qy	2641	TATCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAAGTCATCACATCTTGCCAGTCA	2700
Db	2659	TATCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAAGTCATCACATCTTGCCAGTCA	2718
Qy	2701	ATTGATAGTGTGCAGAAATATAACATGAGGATATTTGGTTCCCAATTTGCACTTTTAATC	2760
Db	2719	ATTGATAGTGTGCAGAAATATAACATGAGGATATTTGGTTCCCAATTTGCACTTTTAATC	2778
Qy	2761	TTAGAAAAGAAAACCGGCCATGTATTTAATTAACATCGACCCCTGACTTATATGCTTTGG	2820
Db	2779	TTAGAAAAGAAAACCGGCCATGTATTTAATTAACATCGACCCCTGACTTATATGCTTTGG	2838
Qy	2821	GAAAGAAAATACATGAGCAAAATGAACAAATTTGAAAGTGCAAAAGAGGAGGAAATATA	2880
Db	2839	GAAAGAAAATACATGAGCAAAATGAACAAATTTGAAAGTGCAAAAGAGGAGGAAATATA	2898
Qy	2881	CCTGTTAACAAAGTTCATTATTAATAGTATACTCTATAA	2919
Db	2899	CCTGTTAACAAAGTTCATTATTAATAGTATACTCTATAA	2937

RESULT 6  
LOCUS AF067175  
DEFINITION Pasteurella multocida capsule biosynthesis gene cluster, complete sequence.  
ACCESSION AF067175  
VERSION AF067175.2  
KEYWORDS GI:7710189  
SOURCE Pasteurella multocida  
ORGANISM Pasteurella multocida  
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.  
REFERENCE 1 (bases 1 to 16727)  
Chung, J. Y., Zhang, Y. and Adler, B.  
TITLE The capsule biosynthetic locus of Pasteurella multocida A:1  
JOURNAL FEMS Microbiol. Lett. 166 (2), 289-296 (1998)  
PUBMED 9770287  
REFERENCE 2 (bases 1 to 16727)  
Chung, J. Y., Zhang, Y. and Adler, B.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAY-1998) Microbiology, Monash University, Wellington Road, Clayton, VIC 3168, Australia  
REFERENCE 3 (bases 1 to 16727)  
Chung, J. Y., Zhang, Y. and Adler, B.  
TITLE Direct Submission  
JOURNAL Submitted (05-MAY-2000) Microbiology, Monash University, Wellington Road, Clayton, VIC 3168, Australia  
REMARK Sequence update by submitter  
COMMENT On May 5, 2000 this sequence version replaced gi:3435183.  
FEATURES  
source  
1..16727  
/organism="Pasteurella multocida"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:747"  
complement (1157..2383)  
/gene="phxB"  
complement (1157..2383)  
/gene="phxB"  
/note="LipB, KpsS homolog"  
/codon\_start=1  
/transl\_table=11  
/product="PhyB"  
/protein\_id="AAC67247.1"  
/db\_xref="GI:3435184"  
/translation="MDVLKHNLDLLESSTVLLQLQGPFGPFTLSAWLXTFHKQVF  
KINFGSGDEAFYFNSIPQTFAYQGLDQDQYLRFPCQHSIDALICFGDTRAHRIA

gene  
CDS

complement (2393..4483)  
/gene="phyA"  
/notes="KpsS, LipA homolog"  
/codon\_start=1  
/transl\_table=11  
/product="PhyA"  
/protein\_id="AAC67248.1"  
/db\_xref="GI:3435185"  
/translation="MSTLYDIYRLNMYQEFILFSGKMLKIPYLSGFFTQBLKMFSPV  
TWKERTCILEMGYKASSKKARHFAQHDLPYATIEDGFLRSIGLVGDPYFPLSLVVD  
DIGIYDINQPSLENLILSQDVLLOEKVDQVEYATIELICTHNSLKYTHAIDPLQVOT  
KRIVLVQDTGDMAYTGNARQSDFLHMLERAIENPTAEILWLKTHPDMVCGKKG  
YLTEYQQFPRKVLSDFNLSILSKHVLYKYCVTSHTGFALLLKGTVTVTFGAWPFG  
WGTDHRHAYIRQLKQSKRRKRSLLQLFYAAYFYQCRYINPTNGSGTLFVDIYL  
QAAKVTNQLAGDIYCVGMRFWKRVVQFFQPRCLHFLVNLHKLRCHEKRAQAKI  
VMGHSHEVWEYAKOQQLPLLRMEDGFLRSVGLGSLNLTPIISLVDLDDIYVDAQR  
SRLEDILQHSFTLLKDLQRAETLKKTLEQHIQKYNVGHTHCLCTHTRONKLLVVGQV  
ENDASIQYSGPHIRTNALLCTVRKNPQAYIYKHPDVPVAGNKVTDRLDDYQVA  
DFVVEKNILDCINQVDEVHTMTSLAGFEALREKVKHCYGLFPYNSWGLTVDHLSLN  
RRSKLSLLELIAAGVLIIYYPQYIDPKTKTMDVQRAVDILIEQRRKIKNNKJHTNYFM  
NIFMKLNYSVLNR"

gene  
CDS

4832..6700  
/gene="hyae"  
4832..6700  
/gene="hyae"  
/note="KfiB homolog"  
/codon\_start=1  
/transl\_table=11  
/product="Hyae"  
/protein\_id="AAC67249.1"  
/db\_xref="GI:3435186"  
/translation="MKKVIIGHKQSNYQVEKVFQCYGNPNPLPSKREKMSPIEIGH  
VLNKLVPSPFHTPKNVSLSNKSCKKGSANAKNKHAKTNTIQTSSIDWLSLD  
LMLANTEQNFQWSDPNAIQILDYWANLDNPIHFVYDKPENLFOVHSLSEALKJLDK  
HTVQEFEEQWYTNKILTYFNKYKDRSVLLNTQOLQNTKTSLSLEYKHSAPDALV  
KLNPSLNKEMELIIVNQDLSHQSECPISNFVISOIKNSPTVTVYVELEQSHADLP  
YISEQLVNDADFALLAWKMDIOQDANOYQHEKELELSTIKERQLEVTEKQLTSEQ  
IKIDEAYHITTKTISDKKALKTHQDEIEALKIFNENISQVEDMQKQFETNKRKE  
LEQBLKASIDSKALLETENSQKTVQSELENENKVLIAQLQIQEELKLYIDNQVLK  
AKPRLVGAADRIKNOLTYRIGYKIORGRSLFGLIFLPFILFTYLGFKEMKKYBNW  
TLPIHEYEDAHEANRIKSHLSYKLVGLVFLQEIINNPFKWLTLPYKLIKEGKRFKQG"  
6717..9635  
/gene="hyad"  
6717..9635  
/gene="hyad"  
/note="Hyad"  
/codon\_start=1  
/transl\_table=11  
/product="glycosyl transferase"  
/protein\_id="AAC67250.2"  
/db\_xref="GI:7710190"

gene  
CDS

6717..9635  
/gene="hyad"  
6717..9635  
/gene="hyad"  
/note="Hyad"  
/codon\_start=1  
/transl\_table=11  
/product="glycosyl transferase"  
/protein\_id="AAC67250.2"  
/db\_xref="GI:7710190"  
/translation="MNTLSQAIKAYNSNDYELAKLPEKSAEIVGRKIVFOIKCKE  
KLSAHSVNSAHLSSVNBKEKNVCDSPLDIATQLLSNVKKVLSDSEKNTKNKKL  
LTERKSENARVALVPKDFPKDLVLAPDHVNDFTYKRRKRGIRKEHQHVGL  
SIIVTFENRPAIILSIILACLVNQKTHYPFEVITDDGSDLSPIIHQYENKLDIRYV  
ROKDNQFQAARNMGLAKYDFIGLLDCDAMPNPLWVHSYVALELDDDLTIIGPR  
KYIDTOHIQDQFLNNASLLESLPEVKTNNNSVAAKGGTQVSLDWLRQFKEKTNLRS  
DSPPRFAAGNVAFAKKWLNKSGFFDEEFNMGWGEDVEFGVRLFRYSGFFKTIQIMA  
YHQEPCKENETREAGKNITLIDIREKVPYIYRKLPIEDSHIRVPLYSIYIPAYN  
CANYIQRCVDSALNQTVVDLEVCICNDGSDTNTLEVLNKLPIGNPNVRIRMSKPNGGIA  
SAGNAVSPFAGYIIGQDSDDDLEPDAVELCLKFLDKTKLACVYITNNRPNPGLS  
IANGYWPFSREKLTAMIAHFRFMFTIRAWHLTDGFNEKINADVDFNKLSEVGL  
KFHLNKICYNRVLHGDNSTIKKLGIOQKHFFVWNQSLNRQGTYYTNYDFDLDDES  
RKYIFNKTAEVQBEIDILKDIKIQNKDAKIAVSIFYPNTLNGLVKLNLIIEYNKNI

```

FVILVHVDKQHLTPDIKKEILAFYHKQVNLNNDISYYTSNRLIKTEAHLNSINKL
SQLNCEYLIFFDNHDSLIFVKNDSYAYAMKKYDVGWNFSAITHDWIEIKNAHPPPKGI
KTYFNDELKSMVNGKASQSGMFMTYALAHELLTIIKEVITSCQISDGPVETWDIWF
QFALLILEKKTGHVPNKSTSTIYMPWERKLQWTEQIESAKRGENIPVNFIEINSITL
"
9699. .10871
/gene="hyac"
CDS
9699. .10871
/gene="hyac"
/feature="hyac"
/codon_start=1
/transl_table=1
/product="UDP-glucose dehydrogenase"
/protein_id="AAC67251.2"
/db_xref="GI:7710191"
/translation="MKKTIAGAGVGLSNVLAQHNVILLDDIQNKVDLINNKKK
PITKEIEDFQNSLQKSMATDKREVALKNADFVIIATPTDYNTEGTGYFNTSTVEAVI
EQTLISINPQATIIKSTIPGVFTENMREKFNPNLIFSPFVREGKALIDNLYPSRII
VGSTSYQAKVFADMLTQCARKKDVTFLFTHNTEABAVKLFANTYLAMRVAFNBLDTY
ASLHLNKDIIINGISTQPRIGTHYNNPSFGYGCYLPKDKQLLANVADVPONLIEA
IVKSNTEKRFITHDVLNKPKTGVIYRLIMKSGSDNPRASAILDIMPHLKENGVEIV
IYEPTLNQAEFEDYFVNLQSEFINRSVDILANRSEPDNLQCSHKIYTRDIFGGDA"
10864. .12297
/note="glycosyl transferase"
/codon_start=1
/transl_table=1
/product="Hyab/Hyaa fusion protein"
/protein_id="AAC67252.2"
/db_xref="GI:7710192"
/translation="MLNLFKIIKKYVHIQSLLHKKBAYALLYAKYINLLSINOQAVVC
OLKLYDLIDPDKWSHVSFFQGLIARGHADHNDMERRLITCTDFSKNQKLIISQLL
AVSPOIATLPCPKYRYALYLSLVANLKFVRLKEELNKLPSCVLKNTPHYCLIQNF
VEKNSKLEINNOFLPYKLGLEITTIKTEDPNTNNTVSHSMVNDNTYLNAPLITI
LVTYNSOKSIXNTLNSLPQSGYFNEIIEIIVDDHSQDNMTSILQAKTYQYKNIKILS
KENVTYVAKNIGLKYASGEFITCQSDSDHWAHQSLQALQVAPLQHKLIYVPSKWR
LDPIGNFYARTIYPLMRNPSALSALFRKVECEKLTALWDVWRIGADSEFNALKLIFGH
KGYTYVKNPLTFGAHRENSLMTAQSTGYVNGVSLPREAYWKAWNIIWHISQLQRGHAPL
LSSSPKREFFOYDQHPIMDVISYAIIN"
12316. .13497
/gene="hexD"
CDS
12316. .13497
/gene="hexD"
/note="CpxD, BexD homolog"
/codon_start=1
/transl_table=1
/product="HexD"
/protein_id="AAC67254.1"
/db_xref="GI:3435191"
/translation="MKPIKTLISFITTILLAGCHSMPTSGPAQNHHIILKKPQNESL
PSVDVLEMDNKVAHTLFKOKSQSFTQFKQNSYADIINVGDITLDVLIWEAAPILF
GSVLQTSQGGANLTLTPEQIVARNGKITIPELGPILVKGKTPQEIORDIAHALSSLA
NKPVIVRLNKNNSKNVITLROGNSVRMPLTSQSERVLDALNAVGATENLQDISVOL
TRGEVYMLSLSEKLAATHPEENTLLRSDVNTLLNKLPSFTGLGALGTNKKQKPSANGL
TLAEGTGEIMGGLDNRADPKGVFRYIIPFNKLSLAETQKWKARGYDNDMEIPTYSV
NLLNPVALFWLQRFPIQDKDLVYVSNAPMAEFQKFLKLVSITSPTVGTGLHNINVK
L"
13507. .14643
/gene="hexC"
CDS
13507. .14643
/gene="hexC"
/note="BexC, CpxC homolog"
/translation="MIETKIQKQPKWSBKPKISTLFKYMVILPTCCSLFYFSLWASDIYISQSFVVRT
PNKQALSGVGLLQSGSPARAQDDTYTVQEFMRSRSTLELLEKSIPIRQFYEDKGD
FGRFNPLNIFSBQEFAYQYFSKKLSVNFDSVGIATLNIKRAFDPEAQINQELLKQG
EYILNLRERARDTVMFAELAVSEAKKVTETSSALSSEYRKNGVFDLQSGSEVOLS
LYTLQNELIITQTOLDQVRSISPNNPQVOTLLARANSIRKEMQVQVQVQVQVQVQV
TOTAEYQRLVNLNTLAQQQLGTATISLQNARSEADROQLYLEIISYPNEPDLALEPYR
LYNILATLFSILLYGITLILLASIREHKN"
/codon_start=1
/transl_table=1
/product="HexC"
/protein_id="AAC67255.1"
/db_xref="GI:3435192"
/translation="MIETKIQKQPKWSBKPKISTLFKYMVILPTCCSLFYFSLWASDIYISQSFVRLA
SDIYISQSFVVRTPNKQALSGVGLLQSGSPARAQDDTYTVQEFMRSRSTLELLEK
SIPRQFYEDKGDIFGRFNPLNIFSBQEFAYQYFSKKLSVNFDSVGIATLNIKRAFD
PQVFDLQSGSEVOLSLYTLQNELIITQTOLDQVRSISPNNPQVOTLLARANSIRK
EMQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV
QVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV
SYNEPDLALEPYRLYNILATLFSILLYGITLILLASIREHKN"
14643. .15440
/gene="hexB"
CDS
14643. .15440
/gene="hexB"
Query Match 99.8%; Score 2913.6; DB 1; Length 16727;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2916; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGAATACATTATCA CAAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC 60
Db 6717 ATGAATACATTATCA CAAGCAATAAAGCATATTAACAGCAATGACTATGAATTAGCACTC 6776
Qy 61 AAATTTATTTGAAAAGTCGGCGGAAATCTATGGACGGAAAAATTTGTTGAATTTCAAATTACC 120
Db 6777 AAATTTATTTGAGAAGTCGGCGGAAATCTATGGACGGAAAAATTTGTTGAATTTCAAATTACC 6836
Qy 121 AAATGCAAGAAAAAAGCTCTCAGCACATCTCTCTGTAATTCAGCACATCTTTCTGTAAT 180
Db 6837 AAATGCAAGAAAAAAGCTCTCAGCACATCTCTCTGTAATTCAGCACATCTTTCTGTAAT 6896
Qy 181 AAAGAAGAAAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACAACAACCTGTTACTT 240
Db 6897 AAAGAAGAAAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACAACAACCTGTTACTT 6956
Qy 241 TCCAACGTAAAAAAATAGTACTTTCTGACTCGGAAAAAACAAGTAAAAAAATAAATGG 300
Db 6957 TCCAACGTAAAAAAATAGTACTTTCTGACTCGGAAAAAACAAGTAAAAAAATAAATGG 7016
Qy 301 AAATTGCTCACTGAGAGAAATCTGAAATCGGAGGTGAAGCGGTCGCCCTCTGACCA 360
Db 7017 AAATTGCTCACTGAGAGAAATCTGAAATCGGAGGTGAAGCGGTCGCCCTCTGACCA 7076
Qy 361 AAAGATTTCCTCAAGATCTGTTTACGCGCTTTACCTGATCATGTTTAATGATTATACA 420
Db 7077 AAAGATTTCCTCAAGATCTGTTTACGCGCTTTACCTGATCATGTTTAATGATTATACA 7136
Qy 421 TGGTACAAAAAGCGAAAAAGAAAGACTTGGCATAAAACTGAAACATCAATGTTGGTCTT 480
Db 7137 TGGTACAAAAAGCGAAAAAGAAAGACTTGGCATAAAACTGAAACATCAATGTTGGTCTT 7196
Qy 481 TCTATTATCGTTACAGATTCAATCGACACGCAATTTTATCGATTACATTAGCCTGTTTA 540
Db 7197 TCTATTATCGTTACAGATTCAATCGACACGCAATTTTATCGATTACATTAGCCTGTTTA 7256
Qy 541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600
Db 7257 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 7316
Qy 601 GATCTATCACCGATCATTCGCAATATGAAATAAAATTTGATTCGCTACGTACGACAA 660
Db 7317 GATCTATCACCGATCATTCGCAATATGAAATAAAATTTGATTCGCTACGTACGACAA 7376
Qy 661 AAAGATAACGGTTTCAAGCCGAGTCGCCCTCGGAATATGGGATTAGCTTACGCAAAATAT 720
Db 7377 AAAGATAACGGTTTCAAGCCGAGTCGCCCTCGGAATATGGGATTAGCTTACGCAAAATAT 7436
Qy 721 GACTTTATTTGGCTTACTGACTGTCATATGGCGCAAAATCCCAATATGGGTTCACTTCTTAT 780
Db 7437 GACTTTATTTGGCTTACTGACTGTCATATGGCGCAAAATCCCAATATGGGTTCACTTCTTAT 7496
Qy 781 GTTGACAGACTATTAGAAGATGATGATTTAACAATCATTTGGTCCCAAGAAAAATACATCGAT 840
Db 7497 GTTGACAGACTATTAGAAGATGATGATTTAACAATCATTTGGTCCCAAGAAAAATACATCGAT 7556
Qy 841 ACACAAATATTTGACCCCAAAAGACTTCTTAAATAACGGGAGTTTGGTTGAATCATTTACCA 900
Db 841 ACACAAATATTTGACCCCAAAAGACTTCTTAAATAACGGGAGTTTGGTTGAATCATTTACCA 900
```

```

/translation="MIETKIQKQPKWSBKPKISTLFKYMVILPTCCSLFYFSLWA
SDIYISQSFVVRTPNKQALSGVGLLQSGSPARAQDDTYTVQEFMRSRSTLELLEK
SIPRQFYEDKGDIFGRFNPLNIFSBQEFAYQYFSKKLSVNFDSVGIATLNIKRAFD
PQVFDLQSGSEVOLSLYTLQNELIITQTOLDQVRSISPNNPQVOTLLARANSIRKEMQ
QVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV
SYNEPDLALEPYRLYNILATLFSILLYGITLILLASIREHKN"
14643. .15440
/gene="hexB"
CDS
14643. .15440
/gene="hexB"
```

Db 7557 ACACACATATTGACCCAAAAGACTTCTTAATAACGGGAGTTTGCTTGAATCAATTACCA 7616  
Qy 901 GAAGTGAACCAATAATAGTGTTCGCCGCAAAAGGGGAAGGAACAGTTTCTCTGGATTGG 960  
Db 7617 GAAGTGAACCAATAATAGTGTTCGCCGCAAAAGGGGAAGGAACAGTTTCTCTGGATTGG 7676  
Qy 961 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGGCTTCCGTTTT 1020  
Db 7677 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGGCTTCCGTTTT 7736  
Qy 1021 TTTCCGGCGGGTAATGTTGCTTTTCGCTAAATAATGGCTTAATAATCCGGTTTCTTTGAT 1080  
Db 7737 TTTCCGGCGGGTAATGTTGCTTTTCGCTAAATAATGGCTTAATAATCCGGTTTCTTTGAT 7796  
Qy 1081 GAGGAATTTAATCACTCGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1140  
Db 7797 GAGGAATTTCAATCACTCGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 7856  
Qy 1141 GGTAGTTTCTTTAAAACTATTGATGGCAATTATGGCTTACCATCAAGAGCCACCAAGTTAAA 1200  
Db 7857 GGTAGTTTCTTTAAAACTATTGATGGCAATTATGGCTTACCATCAAGAGCCACCAAGTTAAA 7916  
Qy 1201 GAAATGAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATCGAGAGAAAG 1260  
Db 7917 GAAATGAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATCGAGAGAAAG 7976  
Qy 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAATTCGCATATCAATAGAGTACCT 1320  
Db 7977 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAATTCGCATATCAATAGAGTACCT 8036  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGTCAAACTATATTCAAGTTGGGTAGAT 1380  
Db 8037 TTAGTTTCAATTTATATCCAGCTTATAACTGTGTCAAACTATATTCAAGTTGGGTAGAT 8096  
Qy 1381 AGTCACGTGAATCAGACTGTGTTGATCTCGAGGTTTGTAATTGTGAACGATGGTTCAACA 1440  
Db 8097 AGTCACGTGAATCAGACTGTGTTGATCTCGAGGTTTGTAATTGTGAACGATGGTTCAACA 8156  
Qy 1441 GATAATACCTTTAGAGTGATCAATAAGCTTTATGGTAAATAATCTCTAGGGTACGCATCATG 1500  
Db 8157 GATAATACCTTTAGAGTGATCAATAAGCTTTATGGTAAATAATCTCTAGGGTACGCATCATG 8216  
Qy 1501 TCTAAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCGCTTCTTTTGGCTAAAGGT 1560  
Db 8217 TCTAAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCGCTTCTTTTGGCTAAAGGT 8276  
Qy 1561 TATTACATTGGCGAGTTAGATTCAAGATTTATCTTGAGCCTGATGCAGTTGAACTGTGT 1620  
Db 8277 TATTACATTGGCGAGTTAGATTCAAGATTTATCTTGAGCCTGATGCAGTTGAACTGTGT 8336  
Qy 1621 TTAAGAAGATTTTAAAAAGATAAAACGCTAGCTTGTGTTTATACCACCTAATAGAAACGTC 1680  
Db 8337 TTAAGAAGATTTTAAAAAGATAAAACGCTAGCTTGTGTTTATACCACCTAATAGAAACGTC 8396  
Qy 1681 AATCCGGATGGTAGCTTAATCGTTAATCGTTACAAATTCGCCAGAAATTTTTCACGAGAAAA 1740  
Db 8397 AATCCGGATGGTAGCTTAATCGTTAATCGTTAATCGTTAATTCGCCAGAAATTTTTCACGAGAAAA 8456  
Qy 1741 CTCACACGGCTATGATTGCTCACCATTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
Db 8457 CTCACACGGCTATGATTGCTCACCATTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 8516  
Qy 1801 ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 8517 ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 8576  
Qy 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAATCTGCTATAACCGGTGTTATACATGGT 1920  
Db 8577 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAATCTGCTATAACCGGTGTTATACATGGT 8636  
Qy 1921 GATACACATCAATTTAAGAACTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1980  
Db 8637 GATACACATCAATTTAAGAACTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 8696

Qy 1981 CAGTCATTAATAGACAAAGCATAACTTATTATAATTATGACGAATTTGATGATTTAGAT 2040  
Db 8697 CAGTCATTAATAGACAAAGCATAACTTATTATAATTATGACGAATTTGATGATTTAGAT 8756  
Qy 2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100  
Db 8757 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 8816  
Qy 2101 AAAGATATTAAAAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTTTATPCC 2160  
Db 8817 AAAGATATTAAAAATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTTTATPCC 8876  
Qy 2161 AATAATTAACCGCTTAGTGAATAAATCAATAATTTATTGAAATATAATAAATAATA 2220  
Db 8877 AATAATTAACCGCTTAGTGAATAAATCAATAATTTATTGAATATAATAAATAATA 8936  
Qy 2221 TTCGTTATTGCTTACATGTTGATAAGAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 8937 TTCGTTATTGCTTACATGTTGATAAGAATCATCTTACACAGATATCAAAAAAGAAATA 8996  
Qy 2281 CTAGCCTTCTATCATAAACATCAAGTGAATTTTACTATAAATATGATATCTCATATTAC 2340  
Db 8997 CTAGCCTTCTATCATAAACATCAAGTGAATTTTACTATAAATATGATATCTCATATTAC 9056  
Qy 2341 ACAGATTAATAGATTAATAAAACCTGAGGCGCATTTAAGTAAATATAATAATTAAAGTCAG 2400  
Db 9057 ACAGATTAATAGATTAATAAAACCTGAGGCGCATTTAAGTAAATATAATAATTAAAGTCAG 9116  
Qy 2401 TTTAAATCTAAATTTGTAATACATCATTTTGTGATAATCATCAGACGCTTATTCGTTAAAAAT 2460  
Db 9117 TTTAAATCTAAATTTGTAATACATCATTTTGTGATAATCATCAGACGCTTATTCGTTAAAAAT 9176  
Qy 2461 GACAGCTATCTTATATGAAAAAATATGATGTCCGCATGAATTTCTCAGCATTAACACAT 2520  
Db 9177 GACAGCTATCTTATATGAAAAAATATGATGTCCGCATGAATTTCTCAGCATTAACACAT 9236  
Qy 2521 GATTGGATCGAGAAATCAATGGCATCCACCAATTTTAAAGGCTCATTAAACCTTATTTT 2580  
Db 9237 GATTGGATCGAGAAATCAATGGCATCCACCAATTTTAAAGGCTCATTAAACCTTATTTT 9296  
Qy 2581 AATGACAATGACTTAAAGAGTATGAATGTGAAGGGGCATCAAGAGTATGTTTATGACG 2640  
Db 9297 AATGACAATGACTTAAAGAGTATGAATGTGAAGGGGCATCAAGAGTATGTTTATGACG 9356  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAAGTCATCACATCTGCGCAGTCA 2700  
Db 9357 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAAGTCATCACATCTGCGCAGTCA 9416  
Qy 2701 ATTGATAGTGGCAGAAATAAACA CTGAGGATATTTGGTTCCAAATTTGCACATTTTAATC 2760  
Db 9417 ATTGATAGTGGCAGAAATAAACA CTGAGGATATTTGGTTCCAAATTTGCACATTTTAATC 9476  
Qy 2761 TTGAAAAGAAAAACCGCCCATGTTTAAATAAAACATCGACCTGACTTATATGCCCTTGG 2820  
Db 9477 TTGAAAAGAAAAACCGCCCATGTTTAAATAAAACATCGACCTGACTTATATGCCCTTGG 9536  
Qy 2821 GAAACGAAAAATTAACAATGGACAAATGAACAAATTTGAAAGTGCMAAAGAGGAGAAAAATA 2880  
Db 9537 GAAACGAAAAATTAACAATGGACAAATGAACAAATTTGAAAGTGCMAAAGAGGAGAAAAATA 9596  
Qy 2881 CCTGTTAAACAGTTCATTATTATAGTATAACTCTATAAA 2920  
Db 9597 CCTGTTAAACAGTTCATTATTATAGTATAACTCTATAAA 9636

RESULT 7  
BD228712  
LOCUS  
DEFINITION Polymer grafting by polysaccharide syntheses.  
ACCESSION BD228712  
VERSION BD228712.1 GI:33038482  
KEYWORDS JP 2002529064-A/2.

linear  
PAT 17-JUL-2003

SOURCE  
ORGANISM  
Pasteurella multocida  
Bacteria: Proteobacteria; Gammaproteobacteria; Pasteurellales;  
Pasteurellaceae; Pasteurella.  
REFERENCE  
1 (bases 1 to 2979)  
AUTHORS  
Deangelis, P.L.  
TITLE  
Polymer grafting by polysaccharide syntheses  
JOURNAL  
Patent: JP 2002529064-A 2 10-SEP-2002;  
THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA  
COMMENT  
OS Pasteurella multocida  
PN JP 2002529064-A/2  
PD 10-SEP-2002  
PF 10-NOV-1999 JP 2000580666  
PR 11-NOV-1998 US 60/107929, 01-APR-1999 US 09/283402 PI  
PC C12N15/09, A61K47/36, C12N1/21, C12P19/26, C12N9/26, C12N15/00 CC  
PAUL L. DEANGELIS  
Polymer grafting by polysaccharide syntheses  
FH Key Location/Qualifiers  
FT source 1..2979  
FT 1..2979 /organism='Pasteurella multocida'.  
FEATURES  
source  
1..2979 Location/Qualifiers  
/organism='Pasteurella multocida'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:747'  
ORIGIN  
Query Match 77.8%; Score 2271.2; DB 6; Length 2979;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;  
QY 1 ATGAATACATATCAACGAATAAAGCATATAACAGCAATGACTATCAATAGCACTC 60  
DB 61 ATGAATACATATCAACGAATAAAGCATATAACAGCAATGACTATCAATAGCACTC 120  
QY 61 AAATATTTTGAAGTTCGCGGAAATCTATGGACGGAAATTTGTTCAATTTCAATACC 120  
DB 121 AAATATTTGAGAGTCTCTGAAACCTACGGCGGAAATCGTTGAAATTCGAATATC 180  
QY 121 AAATGCAAGAAATCTCTCAGCAGATCCCTCTGTTAATTCAGCAGATCTTCTGTAAT 180  
DB 181 AAATGTAAGAAATCTCTCGACCAATTC-----TTATGTAAGT 219  
QY 181 AAGAGAAAGAACTCAATCTTTCGATAGTCCGTAGATATTCGAACACAACTGTTACTT 240  
DB 220 GAAGATAAAGAAAGCAAGTGTTCGGATAGCTCATTTAGATATCGAACACAGCTCTACTT 279  
QY 241 TCAACGTAAGAAATTTAGTACTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300  
DB 280 TCCACGTAAGAAATTTACTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 339  
QY 301 AAATTCCTCAGTGAAGAAATCTGAAATGCGGAGGTAAAGACGCTCGCCCTTGTACCA 360  
DB 340 AAATCTATCACTGGGAAAAATCGGAGAACCGAGAAATCAGAAAGGTGGAACCTAGTACC 399  
QY 361 AAAGATTTTCCAAAGATCTGTTTTCGATAGTCCCTTACCTGATCATCTTAATGATTTTACA 420  
DB 400 AAAGATTTTCCAAAGATCTGTTTTCGATAGTCCCTTACCTGATCATCTTAATGATTTTACA 459  
QY 421 TGTGTACAAAAGCGAAAGAAAGACTTGGCATAAAAACCTGAAACATCAACATGTTGTCCTT 480  
DB 460 TGTGTACAAAAGCGAAAGAAAGACTTGGCATAAAAACCTGTAATTAAGATATCGGTCTT 519  
QY 481 TCTATTATCGTTACAACTCAATTCGACCAAGCAATTTTATCGATTACATTTAGCCTGTTTA 540  
DB 520 TCTATTATTTCTTACATTTAATTCGTAGCCGATTTTATAGATATAACGTTAGCCTGTTT 579  
QY 541 GTAACCAAAAAACATTTACCCGTTTGAAGTTATCGTGACAGATCATGTAGTCAGGAA 600  
DB 580 GTCAATCAGAAAAACAACTACCCATTTGAAGTCGTTGTCAGATGATGTAGTAGGAA 639  
QY 601 GATCTATCCGATCATTCGCCAATATGAAAAATAATTTGGATATTCGCTACGTCAGACAA 660

DB 640 AACTTACTTACCATTGTGCAAAATATACGAACAAAACTTGACATATAAGTATGTAAACAA 699  
QY 661 AAAGATAACCGTCTTCAAGCCAGTCGCGCTCGGAATATGGGATTCGCTTACGAAAAATAT 720  
DB 700 AAAGATTTGGATATCAATTTGTGTCAGTCAGAACTTAGGTTTACGTCACGCAAAAGTAT 759  
QY 721 GACTTTATGGCTTACTCGACTGTGATATGGCGCAATCCATTTATGGGTTTCATCTTAT 780  
DB 760 GATTTTGTCTCGATTTAGACTGCGATATGGCACCACAAATATATGGGTTTCATCTTAT 819  
QY 781 GTTCGAGAGCTATTAGAGATGATTTTAAACAATCATTTGTCCTCAAGAAAAATACATCGAT 840  
DB 820 CTTACAGAACTATTAGAGACAAATGATATTGTTTAAATGGACCTAGAAATATGTGGAT 879  
QY 841 ACACAAACATATTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTGGAATCATACCA 900  
DB 880 ACTCATATATTACCGCAGAACTTCTTAAACGATCCATATTAAATAGAAATCACTACCT 939  
QY 901 GAAGTGAACCAATATAGTTGTTGCCCAAAAGGGGAGGAAACAGTTTCTCTGGATTGG 960  
DB 940 GAAACCGCTACAAATAACAATCTTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999  
QY 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCGCTTATCGGATTCGCTTTCGCTTTT 1020  
DB 1000 AGATTAGAACATTTCAAAAAACCGATTAATCTAGCTATGTGATTTCTCCGTTTCGTTAT 1059  
QY 1021 TTTGCGCGGCTAATTTGCTTTTCGCTAAAAAATGGCTAAATAAATCAATCGGTTTCTTGTAT 1080  
DB 1060 TTTGTTGCGGTAAATTTGTCATTTTCTAAAGATGGCTAAATAAAGTAGGTGGTTTCGAT 1119  
QY 1081 GAGGAATTTAATCTACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGTTTAC 1140  
DB 1120 GAAGAAATTTAATCAATTTGGGGGGGAGAGATGTAGAAATTTGGTTACAGAAATTTTCCCAA 1179  
QY 1141 GGTAGTTTCTTTAAACCTATTGATGGCATTTATGGCTACCATCAAGAGCACACAGTAAA 1200  
DB 1180 GGCTGTTTTTCAGAGTAATTTGACCGCGGATTTACCGTTTAAATTTGTGAAGAAAG 1239  
QY 1201 GAAATGAAACCGATCGTGAAGCGGGAAAAAATATTACGCTCGATATTATAGAGAAAG 1260  
DB 1240 GAAATGAAACAGAACGCGAGCTGGTAAAGTATTACCGTTTAAATTTGTGAAGAAAG 1299  
QY 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGAGTACT 1320  
DB 1300 GTACTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTTCATAGAAATAC 1359  
QY 1321 TTAGTTTCAATTTATATCCAGCTTATTAACCTGTCAAAACATATTATCAAGCTTCGCTAGAT 1380  
DB 1360 TTAGTTTCTTATTTATATCCCGCTTATTAACCTGTCAAAATTTATTTCAAGATGTAGAT 1419  
QY 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAACGATGGTTCAACA 1440  
DB 1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTGTAACGATGGTTCAACA 1479  
QY 1441 GATAATACCTTGAAGATGATCAATTAAGCTTTATGTTAATTAATCTAGGATAGCATCATG 1500  
DB 1480 GATAATACCTTGAAGATGATCAATTAAGCTTTATGTTAATTAATCTAGGATAGCATCATG 1539  
QY 1501 TCTAAACCAATGGCGGAATAGCCTCAGCATCAATGAGCGGTTTCTTTTCTAAAGGT 1560  
DB 1540 TCTAAACCAATGGCGGAATAGCCTCAGCATCAATGAGCGGTTTCTTTTCTAAAGGT 1599  
QY 1561 TATTACATTTGGCAGTTAGATTTCAGATGATTTATCTTGAGCCTGATGACGTTGAACCTGT 1620  
DB 1600 TATTACATTTGGCAGTTAGATTTCAGATGATTTATCTTGAGCCTGATGACGTTGAACCTGT 1659  
QY 1621 TTAAGAAATTTTAAAGATAAAAACGCTAGCTGTGTGTTTATACCACTAATAGAAACGTC 1680  
DB 1660 TTAAGAAATTTTAAAGATAAAAACGCTAGCTGTGTGTTTATACCACTAATAGAAACGTC 1719  
QY 1681 AATCCGGATGGTAGCTTAATCCCTTAATGTTTCAATTTGCCAGAAATTTTTCAGGAGAAAA 1740  
DB 1720 AATCCGGATGGTAGCTTAATCCCTTAATGTTTCAATTTGCCAGAAATTTTTCAGGAGAAAA 1779

1741 CTCACACGGCTATGATTGCTCACCACCTTTAGATGTTTCAGATTAGAGCTTGCGATTTA 1800  
Db CTCAACACGGCTATGATTGCTCACCACCTTTAGATGTTTACGATTAGAGCTTGCGATTTA 1839  
Qy 1801 ACTGATGATTTCAATGAAAAAATTGAAAAATGCCGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1840 ACGATGATTTACGAAAAATATTGAAAAACGGCGTGGATATGACATGTTCTCTTAAACTC 1899  
Qy 1861 AGTGAAGTTGAAAAATTTTAAACATCTTTAATAAAAATCTGCTATAAACCGGTGATTAACATGGT 1920  
Db 1900 AGTGAAGTTGAAAAATTTTAAACATCTTTAATAAAAATCTGCTATAAACCGGTATTACATGGT 1959  
Qy 1921 GATAACACATCAATTAAGAAAATCTGGCATTCAAAAAGAAAACCAATTTTGGTGTAGTCAAT 1980  
Db 1960 GATAACACATCCATTAAGAAAATCTGGCATTCAAAAAGAAAACCAATTTTGGTGTAGTCAAT 2019  
Qy 1981 CAGTCATTAATAGACAGGATTAATTTATTAATTAATAGCAATTTTGTATGATTTAGAT 2040  
Db 2020 CAGTCATTAATAGACAGGATCAATTTATTAATTAATTAATAGCAATTTTGTATGATTTAGAT 2079  
Qy 2041 GAAAGTAGAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
Db 2080 GAAAGTAGAAGTATATCTTCAATAAAAACCGCTGAATATCAAGAGAGAAATCGATATGTTA 2139  
Qy 2101 AAAGATATTAATATCATCAGAAATTAAGATGCAAAATCGCAGTCAGTATTTTATATCCC 2160  
Db 2140 AAAGATATTAATATCATCAGAAATTAAGATGCAAAATCGCAGTCAGTATTTTATATCCC 2199  
Qy 2161 AATCATTAAACGGCTTAGTGAATAAACTAAACCAATATTATTGAATATAATAAAAAATATA 2220  
Db 2200 AATCATTAAACGGCTTAGTGAATAAACTAAACCAATATTATTGAATATAATAAAAAATATA 2259  
Qy 2221 TTCGTTATTTGTTCTACATGTTGATAAGAAATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
Db 2260 TTCGTTATTTGTTCTACATGTTGATAAGAAATCATCTTACACCAGATATCAAAAAAGAAATA 2319  
Qy 2281 CTAGCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTTAC 2340  
Db 2320 TTGGCTTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTTAC 2379  
Qy 2341 ACGAGTAATAGATTAATAAAACCTGAGCGCATTTTAAGTAATATTAAATAAATTAAGTCAG 2400  
Db 2380 ACGAGTAATAGATTAATAAAACCTGAGCGCATTTTAAGTAATATTAAATAAATTAAGTCAG 2439  
Qy 2401 TTAATCTAAATTTGTAATAATCATCATCTTTTGTATATCATGACAGCTATTCGTTAAAAAT 2460  
Db 2440 TTAATCTAAATTTGTAATAATCATCATCTTTTGTATATCATGACAGCTATTCGTTAAAAAT 2499  
Qy 2461 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2520  
Db 2500 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2559  
Qy 2521 GATTGGATCGAGAAAATCAATCGCATCCACCATTTTAAAAAGCTCATTTAAAACTTATTTT 2580  
Db 2560 GATTGGATCGAGAAAATCAATCGCATCCACCATTTTAAAAAGCTGATTTAAAACTTATTTT 2619  
Qy 2581 AATGACAAATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGACG 2640  
Db 2620 AATGACAAATGACTTTAAAGATGATGAATGTGAAAGGGGCATCAAGGTATGTTTATGAG 2679  
Qy 2641 TATGGCTAGGCGATAGAGCTTCTGACGATTAATAAGAAATGATCAATCTTGCCAGTCA 2700  
Db 2680 TATGGCTAGGCGATAGAGCTTCTGACGATTAATAAGAAATGATCAATCTTGCCAGTCA 2739  
Qy 2701 ATTGATGTCGAGAAATATAAACACTGAGGATATTGTTTCCCAATTTTGCACCTTTTAATC 2760  
Db 2740 ATTGATGTCGAGAAATATAAACACTGAGGATATTGTTTCCCAATTTTGCACCTTTTAATC 2799  
Qy 2761 TTAGAAAAAGAAACCGGCCATGTATTTTAAATAAACATCGACCTGACCTTATATGCTTTGG 2820  
Db 2800 TTAGAAAAAGAAACCGGCCATGTATTTTAAATAAACATCGACCTGACCTTATATGCTTTGG 2859

2821 GAACGAAAATTACATGACAAATGAACAAATTTGAAAGTGCAAAAAGAGGAGAAAAATATA 2880  
Db 2860 GAACGAAAATTACATGACAAATGAACAAATTTGAAAGTGCAAAAAGGCGGAAATATC 2919  
Qy 2881 CCTGTTAAACAGTTCATTTAATTAATAGTATTAACCTCTATAA 2920  
Db 2920 CCGTTAAACAGTTCATTTAATTAATAGTATTAACGCTATAA 2959  
RESULT 8  
AR225814  
LOCUS AR225814 2979 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 4 from patent US 6444447.  
ACCESSION AR225814  
VERSION AR225814.1 GI:27263929  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2979)  
AUTHORS DeAngelis,P.L.  
TITLE Polymer grafting by polysaccharide syntheses  
JOURNAL Patent: US 644447-A 4 03-SEP-2002;  
The Board of Regents of the University of Oklahoma; Norman, OK  
FEATURES  
source 1..2979  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 77.8%; Score 2271.2; DB 6; Length 2979;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;  
Qy 1 ATGAATACATTATCACAAGCAATAAAGCATATAACAGCAATGACATATCAATTAGCACTC 60  
Db 61 ATGAATACATTATCACAAGCAATAAAGCATATAACAGCAATGACATATGAATTAGCACTC 120  
Qy 61 AAATTATTTGAAAAGTCGGGGAAATCTATGGACGGAATTTGTTGAATTTCAATTTACC 120  
Db 121 AAATTATTTGAGAAGTCGCTGAAACCTACGGCGGAAAAATCGTTGAATTTCCAAATTTATC 180  
Qy 121 AAATGCAAGAAAAAATCTCAGACACATCTCTGTTTAATTCAGCACATCTTTCTGTAAAT 180  
Db 181 AAATGTAAGAAAAAATCTCAGACATCTCTGACCAATTC-----TTATGTAAGT 219  
Qy 181 AAAGAAGAAAAAGTCAATTTTGGATAGTCGATAGTATGCAACACACACTGTTACTT 240  
Db 220 GAAGATAAAAAAACAAGTCGTTTGCATAGCTCATTAGATATCGCAACACAGCTCTTACTT 279  
Qy 241 TCCAACTGTAATAAATTTAGTACTTTCTGACTCGGAAAAAACACGTTAAAAAATAAATGG 300  
Db 280 TCCAACTGTAATAAATTTAATCTCTATCCGAATCAGAAAAAACAGTTTAAAAAATAAATGG 339  
Qy 301 AAATTTGCTCACTGAGAAGAAATCTGAAATTCGGAGGTAGAGCGGTCGCGCTTTGTACCA 360  
Db 340 AAATCTATCACTGGAAAAAATTCGAGAACGCAAAATCAGAAAGGTGGAACCTAGTACCC 399  
Qy 361 AAAGATTTTCCCAAGATCTGGTTTATAGCCGCTTTACCTGATCATGTTAATGATTTTACA 420  
Db 400 AAAGATTTTCCTAAGATCTGTTTCTTGTCTTCCATTTGCCAGATCATGTTAATGATTTTACA 459  
Qy 421 TGGTACAAAAAGCAAGAAAAAGACTTTGGCATATAAAACCTGAACTCAACATGTTGGTCTT 480  
Db 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATAAAGCCCTGTAATTAAGAATATATCGGCTT 519  
Qy 481 TCTATTATCTGTTACAAACATTCACACCGACCAATTTTATCGATTACATTAGCCTGTTTA 540  
Db 520 TCTATTATTTCTCATTTAATCTGAGCGGTATTTTAGATATAAAGTGTAGCTGTTTGG 579  
Qy 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTGAAGATGTTAGTGCAGGAA 600  
Db 580 GTCAATCAGAAAAACAAACTACCCATTTGAAAGTCGTTGTCAGATGATGTTAGTAAAGAA 639



QY 601 GATCTATCACCGATCATTCGCAATATGAAATAAATTTGGATATTCGCTACGTACAGCAA 660  
DB 640 AACTTACTTACCATTTGTCGAATAATACGAACAAACTTGCATTAAGATATGTAAGACAA 699  
QY 661 AAAAGATAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATATAGCTTTAGCAAAATAT 720  
DB 700 AAAGATTATGGATATCAATTTGTGTCAGTTCAGAAACTTTAGGTTTACGTACACGCAAGTAT 759  
QY 721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAATCCATTTATGGTTTCATCTTAT 780  
DB 760 GATTTTGTCTCGAATCTAGACTGCCATATGGCACCACCAATTAATGGTTCATCTTAT 819  
QY 781 GTTGCAGAGCTATTAGAAGATGATCATTTAACTATTTGGTCCAGAAATAACATCGAT 840  
DB 820 CTTACAGAACTATTAGAAGCAATGATTTGTTTTAATTTGGACCTAGAAATATGTTGGAT 879  
QY 841 ACACAACATATTTGACCCAAAGACTTCTTAATAACGCGAGTTTGCCTTGAATCATACCA 900  
DB 880 ACTCATAATATTTACCGCAGAACAAATTCCTTTACGATCCATATTTAATAGAACTACCT 939  
QY 901 GAAGTGAACCAATTAATAGTGTTCGCGCAAAAGGGAGGAACAGTTTCTCTGGATTTGG 960  
DB 940 GAAACCGCTACAAATAACAAATCCCTTCGATTAATCAAAAGGAAATATATCGTTGGATTTGG 999  
QY 961 CGCTTAGAACATTTGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTTCGTTTT 1020  
DB 1000 AGATTAGAACATTTCAAAAAACCGATTAATCTACGTCTATGTGATTTCCGTTTCGTTAT 1059  
QY 1021 TTTGGCGGGTAATTTGCTTTTCGCTAAAAAATGCTAAATTAATTAATCGGTTTTCTTTGAT 1080  
DB 1060 TTTGTTGCGGGTAATTTGCTTTTCGCTAAAAAATGCTAAATTAATTAATCGGTTTTCTTTGAT 1119  
QY 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTTCCGTTAC 1140  
DB 1120 GAAGAATTTAATCAITGGGGGGCGAAGATGTAGAATTTGGTTACAGATTTATTTGCCAAA 1179  
QY 1141 GGTAGTTTCTTTAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200  
DB 1180 GGCTGTTTTTTCAGAGTAATTTGACGGCGGAATGGCCATCCATCAAGAACACCTGGTAAA 1239  
QY 1201 GAAATGAAACCGATCGTGAAGCGGGAAAAAATATTTACGCTCGATATTTATGAGAGAAAG 1260  
DB 1240 GAAATGAAACAGAACCGAAGCTGTGTAAGTATTTACGCTTTAAATTTGTAAGAAAG 1299  
QY 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGATATCAATAGAGTACCT 1320  
DB 1300 GTACCTTTACATCTATAGAAAGCTTTTACCAATAGAAAGATTCACATATTTCAAGAAATACCT 1359  
QY 1321 TTAGTTTCAATTTATATCCAGCTTATTAATCTGTCGCAATATATTTCAAGCTTTGCGTAGAT 1380  
DB 1360 TTAGTTTCTTATTTATATCCCGCTTATTAATCTGTCGCAATATATTTCAAGAGATGTGTAGAT 1419  
QY 1381 AGTGCACTGAATCAGACTGTGTGTATCTCGAGTTTGTATTTGTAAACGATGGTTCAACA 1440  
DB 1420 AGTCTCTTAACTAACTGTGTGATCTCGAGTTTGTATTTGTAAACGATGGTTCAACA 1479  
QY 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTAAATATCCTTAGGGTACGCATCATG 1500  
DB 1480 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTAAATATCCTTAGGGTACGCATCATG 1539  
QY 1501 TCTAAACCAATTCGGCGGAATAGCTCAGCATCAATGTCAGCGCTTTCTTTGCTAAAGGT 1560  
DB 1540 TCTAAACCAATTCGGCGGAATAGCTCAGCATCAATGTCAGCGCTTTCTTTGCTAAAGGT 1599  
QY 1561 TATTACATTTGGGCGAGTTAGATTCAGATGATTATCTTGAGCGCTGATGAGTTGAACCTGTGT 1620  
DB 1600 TATTACATTTGGGCGAGTTAGATTCAGATGATTATCTTGAGCGCTGATGAGTTGAACCTGTGT 1659  
QY 1621 TTAAGAGAAATTTTAAAGATAAAGCGCTAGCTTGTGTTTATACCACTAATAGAAACGCTC 1680  
DB 1660 TTAAGAGAAATTTTAAAGATAAAGCGCTAGCTTGTGTTTATACCACTAATAGAAACGCTC 1719

QY 1681 AATCCGATGGTAGCTTAATCGCTAATGCTTAATTTGGCCAGAAATTTTCACGAGAAAAA 1740  
DB 1720 AATCCGATGGTAGCTTAATCGCTAATGCTTAATTTGGCCAGAAATTTTCACGAGAAAAA 1779  
QY 1741 CTCACACGGCTATGATTTGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1800  
DB 1780 CTCACACGGCTATGATTTGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1839  
QY 1801 ACTGATGGATTCATTAAGAAAAATTTGAAATGCGCTAGACTATGATGATGCTTCTCAACTC 1860  
DB 1840 ACGGATGGATTTAACGAAAAATTTGAAAAACCCCGTGGATTTATGACATGCTTCTTAAACTC 1899  
QY 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAATCTGCTATAACCGTGTATTTACATGCT 1920  
DB 1900 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAATCTGCTATAACCGGCTATTTACATGCT 1959  
QY 1921 GATAACACATCAATTTAGAAAACTTTGGCAATTCAAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
DB 1960 GATAACACATCCATTTAGAAAACTTTGGCAATTCAAAAAGAAAAACCAATTTTGTGTAGTCAAT 2019  
QY 1981 CAGTCATTTAAATAGACAAAGGCATAACTTTATTTAATTAATGACGAATTTGTAGATTTAGAT 2040  
DB 2020 CAGTCATTTAAATAGACAAAGGCATCAATTTATTTAATTAATGACMAATTTGTAGATTTAGAT 2079  
QY 2041 GAAAGTAGAAAGTATATTTTCAATAAAACCCGCTGATATCAAGAAGAGATTTGATATCTTA 2100  
DB 2080 GAAAGTAGAAAGTATATCTTCAATAAAACCCGCTGATATCAAGAAGAAATTTGATATGTTA 2139  
QY 2101 AAAGATTTAAATCAATCCAGATTAAGATTCGCAAAATCGCAGTCAGTATTTTATATCCC 2160  
DB 2140 AAAGATCTTAACTCAATTTCAAAATTAAGATTCGCAAAATCGCAGTCAGTATTTTCTATCCC 2199  
QY 2161 AATACATTTAAACGGCTTAGTGAAAAAACTAAACATATTTATTTGAATATAATAAAAATATA 2220  
DB 2200 AATACATTTAAACGGCTTAGTGAAAAAACTAAACATATAATTTGAATATAATAAAAATATA 2259  
QY 2221 TTTGTTATTTGTTCTACATGTTGATGAAGATCACTTTTACACCAAGATATCAAAAAAGAAATA 2280  
DB 2260 TTTGTTATTTTCTACATGTTGATGAAGATCACTTTTACACCAAGATATCAAAAAAGAAATA 2319  
QY 2281 CTAGCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTTAC 2340  
DB 2320 TTTGCTTTCTATCATTAAGCACCAAGTGAATATTTTACTAAATATGACATCTCATATTTAC 2379  
QY 2341 ACGAGTAATAGATTAATAAAAACTGAGGCGCATTTTAAAGTAATTTAATAAATTTAAGTCAG 2400  
DB 2380 ACGAGTAATAGATTAATAAAAACTGAGGCGCATTTTAAAGTAATTTAATAAATTTAAGTCAG 2439  
QY 2401 TTTAAATCTAAATTTGTAATACATCATTTTTTTGATTAATCATGACAGCTTATTCGTTAAAAAT 2460  
DB 2440 TTTAAATCTAAATTTGTAATACATCATTTTTTTGATTAATCATGACAGCTTATTCGTTAAAAAT 2499  
QY 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGCGCATGAAATTTCTCAGCATTTAACACAT 2520  
DB 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGCGCATGAAATTTCTCAGCATTTAACACAT 2559  
QY 2521 GATTGATCGAGAAAAATCAATCGCATCCACCATTTTAAAAAGCTCATTTAAAACTTATTTT 2580  
DB 2560 GATTGATCGAGAAAAATCAATCGCATCCACCATTTTAAAAAGCTCATTTAAAACTTATTTT 2619  
QY 2581 AATGACAAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGATGTTTATGACG 2640  
DB 2620 AATGACAAATGACTTAAAGAGTATGAATGTGAAAGGGGCATCAAGGATGTTTATGACG 2679  
QY 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAGAGTATCATCATCTTGCAGTCA 2700  
DB 2680 TATGCGCTAGCGCATGAGCTTCTGACGATTAATTAAGAGAGTATCATCATCTTGCAGTCA 2739  
QY 2701 ATTGATAGTGTCCAGAAATATAAAGTGTGAGGATATTTGGTTCCAAATTTGACCTTTTAAATC 2760  
DB 2740 ATTGATAGTGTCCAGAAATATAAAGTGTGAGGATATTTGGTTCCAAATTTGACCTTTTAAATC 2799  
QY 2761 TTAGAAAAAGAAAAACCGGCCATGTTTATTAATAAACAATCGACCCCTGATTTATATGCTTGG 2820





Db 880 ACTCATATATTCGCGAGAACAAATTCCTTAACGATCCATATTTAAATAGAAATCACTACCT 939  
Qy 901 GAAGTGAAGAACCAATATAGTGTGGCCGCAAAAAGGGGAAGAACGATTTCTCTGGATGG 960  
Db 940 GAAACCGCTACAAATTAACAAATCCTTCGATTAACATCAAAAGGAAAATATATCGTTGGATGG 999  
Qy 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCGCTTATCCGATTTCCGCTTTCCGTTT 1020  
Db 1000 AGATTAGAACCAATTTCAAAAAAACCGATTAATCTACGTCTATGTGATTTCCGTTTCGTTAT 1059  
Qy 1021 TTTCGGCGGGTAATGTGCTTTTCGCTAAAAATGCGCTAAATAAATCCGGTTTCTTTGAT 1080  
Db 1060 TTTAGTTCGGGTAAATGTGCAATTTCTTAAGAAATGGCTAAATAAAGTAGGTGGTTTCGAT 1119  
Qy 1081 GAGGAATTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1140  
Db 1120 GAAGAAATTAATCAATTCGGGGGGCGAAGATGTAGAATTTGGTTACAGATTAATTTGCCAAA 1179  
Qy 1141 GGTAGTTTCTTTAAACTATTGATGGCAATTTATGGCTTACCATCAAGAGCCACCGGTAAA 1200  
Db 1180 GGCTGTTTTTCAGAGTAATTTGACGGCGGAATGGCATACCATCAAGAACCCACTGGTAAA 1239  
Qy 1201 GAAATAGAAACCGATCGTGAAGCGGGAATAATATTACGCTCGATTAATATGAGAGAAAAG 1260  
Db 1240 GAAATAGAAACAGACCGCGAGCTGTAAGAGTATTACGCTTAAATTTGTGAAGAAAAG 1299  
Qy 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAAGATTCGCATATCAATAGATACCT 1320  
Db 1300 GTACCTTATATCTATAGAAAGCTTTTACCAATAGAAAGATTCACATTAATTCATAGAAATCCT 1359  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATTAACGTGTGCAAACTATTAACAGTTGCGCTAGAT 1380  
Db 1360 TTAGTTTCTATTTATATCCCGCTTATAACGTGTGCAAACTATTAACAGATGTGTAGAT 1419  
Qy 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1440  
Db 1420 AGTGCTCTTAATCAAACTGTTGTGCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1479  
Qy 1441 GATAATACCTTTAGAAAGTGAATCAATTAAGCTTTTATGTTATTAATATTAATCCCTAGGGTACGATCATG 1500  
Db 1480 GATAATACCTTTAGAAAGTGAATCAATTAAGCTTTTATGTTATTAATATTAATCCCTAGGGTACGATCATG 1539  
Qy 1501 TCTAAACCAATGGCGGAATAGCCTCAGCATCAATGCGAGCGTTCTTTTGTCTAAAGGT 1560  
Db 1540 TCTAAACCAATGGCGGAATAGCCTCAGCATCAATGCGAGCGTTCTTTTGTCTAAAGGT 1599  
Qy 1561 TATTACATTTGGCGAGTTAGATTGATGATTAATCTTGAGCCTGATGCGAGTTGAACTGTGT 1620  
Db 1600 TATTACATTTGGCGAGTTAGATTGATGATTAATCTTGAGCCTGATGCGAGTTGAACTGTGT 1659  
Qy 1621 TTTAAAGAAATTTTAAAGATAAAACGGTAGCTGTGTTTATATCCATTAATAGAAACGTC 1680  
Db 1660 TTTAAAGAAATTTTAAAGATAAAACGGTAGCTGTGTTTATATCCATTAATAGAAACGTC 1719  
Qy 1681 AATCCGGATGGTAGCTTAATCGCTAATGCTTAATGCGGAGAAATTTTACAGAGAAA 1740  
Db 1720 AATCCGGATGGTAGCTTAATCGCTAATGCTTAATGCGGAGAAATTTTACAGAGAAA 1779  
Qy 1741 CTCACAAACGGCTATGATTCCTCACCACTTTTAGAATGTTTACGATTTAGAGCTTTGGCATTTA 1800  
Db 1780 CTCACAAACGGCTATGATTCCTCACCACTTTTAGAATGTTTACGATTTAGAGCTTTGGCATTTA 1839  
Qy 1801 ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1840 ACGGATGGATTTAAACGAAAATATTGAAAACGCGGTGGAATTAATGACATGTTCTTAAACTC 1899  
Qy 1861 AGTGAAGTTGGAAAATTTTAAACATCTTAATAAAATCTGCTATAAACCGTGTATTAATGCT 1920  
Db 1900 AGTGAAGTTGGAAAATTTTAAACATCTTAATAAAATCTGCTATAAACCGGCTATTTACATGCT 1959  
Qy 1921 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAACCATTTGTTGTAGTCAAT 1980

Db 1960 GATAACACATCCATTTAAGAAACTCGGCAATTCAAAAGAAAACCAATTTTGTGTAGTCAAT 2019  
Qy 1981 CAGTCATTTAAATAGACAAGGCATAACTTTATATATTTATATGACGAATTTTGATGATTTAGAT 2040  
Db 2020 CAGTCATTTAAATAGACAAGGCATCAATTTATATATTTATATGACAAAATTTGATGATTTAGAT 2079  
Qy 2041 GAAAGTAGAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAGAGAGATTTGATATCTTA 2100  
Db 2080 GAAAGTAGAAGTATATCTTCAATAAAAACCGCTGAATATCAAGAGAGAAATGGATATTTTA 2139  
Qy 2101 AAAGATTTAAAAATCAATCCAGAAATTAAGATGCCAAAATTCGCAGTCAGTATTTTATCCCC 2160  
Db 2140 AAAGATCTTAAACTCAATTTCAAAATTAAGATGCCAAAATTCGCAGTCAGTATTTTCTATCCC 2199  
Qy 2161 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAATATTTTGAATATAAATAAAATATA 2220  
Db 2200 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAATATTTTGAATATAAATAAAATATA 2259  
Qy 2221 TTGCTTATTTGTCTACATGTTTGAATGAATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
Db 2260 TTGCTTATTTGTCTACATGTTTGAATGAATCATCTTACACCAGATATCAAAAAAGAAATA 2319  
Qy 2281 CTAGCTTCTATCATTAACATCAAGTGAATATTTTACTAAATATATGATATCTCATATTAC 2340  
Db 2320 TTGGCTTTCTATCATTAAGCACCAAGTGAATATTTTACTAAATATATGACATCTCATATTAC 2379  
Qy 2341 ACGAGTATAGATTAATAAAAACTGAGGCGCATTTTAAGTAATATTAATAAATAAGTCAG 2400  
Db 2380 ACGAGTATAGATTAATAAAAACTGAGGCGCATTTTAAGTAATATTAATAAATAAGTCAG 2439  
Qy 2401 TTTAAATCTAAATTTGTGAATACATCATTTTGTGAATCATGACAGCTATTCGTTAAAAAT 2460  
Db 2440 TTTAAATCTAAATTTGTGAATACATCATTTTGTGAATCATGACAGCTATTCGTTAAAAAT 2499  
Qy 2461 GACAGTATGCTTATATGAAAAATATGATGTCGCGATGAATTTCTCAGCATTTAACACAT 2520  
Db 2500 GACAGTATGCTTATATGAAAAATATGATGTCGCGATGAATTTCTCAGCATTTAACACAT 2559  
Qy 2521 GATTGGATCGAGAAATCAATCGCGATCCACATTTTAAAAAGCTCATTTAAAACTTATTTT 2580  
Db 2560 GATTGGATCGAGAAATCAATCGCGATCCACATTTTAAAAAGCTCATTTAAAACTTATTTT 2619  
Qy 2581 AATGACAAATGACTTTAAAAAGTATGAATGTGAAAAGGGGCATCAAGGATGTTTATGAGC 2640  
Db 2620 AATGACAAATGACTTTAAAAAGTATGAATGTGAAAAGGGGCATCAAGGATGTTTATGAGC 2679  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATAAGAGTCAATCAGATCTTGCGAGTCA 2700  
Db 2680 TATGCGCTAGCGCATGAGCTTCTGACGATTTATAAGAGTCAATCAGATCTTGCGAGTCA 2739  
Qy 2701 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGTTTCCAAATTTGCACTTTTAAATC 2760  
Db 2740 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGTTTCCAAATTTGCACTTTTAAATC 2799  
Qy 2761 TTAGAAAAAGAAAACCGGCGCATGTTTAAATAAAACATCGACCTGATTTATGCTTATGCTTGG 2820  
Db 2800 TTAGAAAAAGAAAACCGGCGCATGTTTAAATAAAACATCGACCTGATTTATGCTTATGCTTGG 2859  
Qy 2821 GAACGAAAATTAATGAGCAAAATGAACAAATTTGAAGTGCAAAAGAGGAGAGAAATATA 2880  
Db 2860 GAACGAAAATTAATGAGCAAAATGAACAAATTTGAAGTGCAAAAGAGGAGAGAAATATA 2919  
Qy 2881 CCTGTTTAAACAGTTCATTTAATAGTATAACCTATATAA 2920  
Db 2920 CCCGTTTAAACAGTTCATTTAATAGTATAACGCTATATAA 2959

RESULT 10  
BD228711  
LOCUS  
DEFINITION  
ACCESSION  
VERSION

BD228711 2112 bp DNA linear PAT 17-JUL-2003  
Polymer grafting by polysaccharide synthases.  
BD228711  
BD228711.1 GI:33038481

KEYWORDS JP 2002529064-A/1.  
SOURCE Pasteurella multocida  
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
Pasteurellaceae; Pasteurella.  
REFERENCE 1 (bases 1 to 2112)  
AUTHORS Deangelis, P.L.  
TITLE Polymer grafting by polysaccharide syntheses  
JOURNAL Patent: JP 2002529064-A 1 10-SEP-2002;  
THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA  
COMMENT OS Pasteurella multocida  
PN JP 2002529064-A/1  
PD 10-SEP-2002  
PF 10-NOV-1999 JP 2000590666  
PR 11-NOV-1998 US 60/107929, 01-APR-1999 US 09/283402 PI  
PAUL L DEANGELIS  
PC C12N15/09, A61K47/36, C12N1/21, C12P19/26//C12N9/26, C12N15/00 CC  
Polymer grafting by polysaccharide syntheses  
FH Key Location/Qualifiers  
FT source i. .2112  
FT Location/Qualifiers /organism='Pasteurella multocida'.  
source 1. .2112  
/organism='Pasteurella multocida'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:747'  
ORIGIN  
Query Match 72.2%; Score 2108.8; DB 6; Length 2112;  
Best Local Similarity 99.9%; Pred. No. 1.8e-296;  
Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGAATACATTATCACAGCAATAAAGCATATATACAGCAATGACTATCAATTAGCACTC 60  
Db 1 ATGAATACATTATCACAGCAATAAAGCATATATACAGCAATGACTATCAATTAGCACTC 60  
Qy 61 AAATTATTTGAAAAGTCGGCGGAATCTATCGACGGAATAATGTTGAATTTCAATATACC 120  
Db 61 AAATTATTTGAAAAGTCGGCGGAATCTATCGACGGAATAATGTTGAATTTCAATATACC 120  
Qy 121 AAATGCAAGAAAACCTCTGACGACATCCTTCTGTTAATTCAGACATCTTCTGTTAAAT 180  
Db 121 AAATGCCAGAAAACCTCTGACGACATCCTTCTGTTAATTCAGACATCTTCTGTTAAAT 180  
Qy 181 AAAGAAGAAAAGTCAATGTTTGGATAGTCGTTAGATATTTGCAACAACACTGTTACTT 240  
Db 181 AAAGAAGAAAAGTCAATGTTTGGATAGTCGTTAGATATTTGCAACAACACTGTTACTT 240  
Qy 241 TCCAACGTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATAAATGG 300  
Db 241 TCCAACGTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATAAATGG 300  
Qy 301 AAATTTGCTCAGTGAAGAAAATCTGAAAATCGGAGGTAAGAGCGGTCGCCCTTGTACCA 360  
Db 301 AAATTTGCTCAGTGAAGAAAATCTGAAAATCGGAGGTAAGAGCGGTCGCCCTTGTACCA 360  
Qy 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTTAAATGATTTTACA 420  
Db 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTTAAATGATTTTACA 420  
Qy 421 TGGTACAAAAAGCGAAGAAAAGACTTGGCATATAAACCTGAAACATCAACATGTTGGTCTT 480  
Db 421 TGGTACAAAAAGCGAAGAAAAGACTTGGCATATAAACCTGAAACATCAACATGTTGGTCTT 480  
Qy 481 TCTATTATCGTTACAACTTCAATCGACGCAATTTTATCGATTACATTAGCCCTGTTTGA 540  
Db 481 TCTATTATCGTTACAACTTCAATCGACGCAATTTTATCGATTACATTAGCCCTGTTTGA 540  
Qy 541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db 541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Qy 601 GATCTATCACCAGTCAATTCGCGCAATATGAAAATAAATTTGGATATTCGGTACGTACAGCAA 660

Db 601 GATCTATCACCAGTCAATTCGCGCAATATGAAAATAAATTTGGATATTCGGTACGTACAGCAA 660  
Qy 661 AAAGATAACGGTTTTTCAAGCCAGTGGCGTTCGGAATATGGAATTAACGCTTAGCAAAATAT 720  
Db 661 AAAGATAACGGTTTTTCAAGCCAGTGGCGTTCGGAATATGGAATTAACGCTTAGCAAAATAT 720  
Qy 721 GACTTTATTTGGCTTACTCGACTGTGATATGCGCCAAATCCATTATGGGTTCAATCTTAT 780  
Db 721 GACTTTATTTGGCTTACTCGACTGTGATATGCGCCAAATCCATTATGGGTTCAATCTTAT 780  
Qy 781 GTTGCAGAGCTATTAGAAAGATGATTTAAACAATCATTCGTCCAAGAAAATACATCGAT 840  
Db 781 GTTGCAGAGCTATTAGAAAGATGATTTAAACAATCATTCGTCCAAGAAAATACATCGAT 840  
Qy 841 ACAACAATATGACCCCAAGAACTTCTTAAATAACGCGAGTTGCTTGAATCATTTACCA 900  
Db 841 ACAACAATATGACCCCAAGAACTTCTTAAATAACGCGAGTTGCTTGAATCATTTACCA 900  
Qy 901 GAAGTGAACCAATTAATAGTGTTCGCGCAAAAGGGGAAGGAACAGTTTCTCTGGATTGG 960  
Db 901 GAAGTGAACCAATTAATAGTGTTCGCGCAAAAGGGGAAGGAACAGTTTCTCTGGATTGG 960  
Qy 961 CGCTTAGAACCAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCTTTCCGTTTT 1020  
Db 961 CGCTTAGAACCAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCTTTCCGTTTT 1020  
Qy 1021 TTTGCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGCGTAAATAAATCCGGTTCTTTGAT 1080  
Db 1021 TTTGCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGCGTAAATAAATCCGGTTCTTTGAT 1080  
Qy 1081 GAGGAATTTAATCACTGGGTTGAGAGATGTGGAATTTTGGATATCGCTTATTTCCGTTAC 1140  
Db 1081 GAGGAATTTAATCACTGGGTTGAGAGATGTGGAATTTTGGATATCGCTTATTTCCGTTAC 1140  
Qy 1141 GGTAGTTTCTTTAAACTATTGATGCGATTAATGCGCTTACCATCAAGAGCCACCAGGTAAA 1200  
Db 1141 GGTAGTTTCTTTAAACTATTGATGCGATTAATGCGCTTACCATCAAGAGCCACCAGGTAAA 1200  
Qy 1201 GAAAATGAAAACCGATCGTGAAGCGGGAAAAAATAATTACGCTCGATATATAGAGAGAAAAG 1260  
Db 1201 GAAAATGAAAACCGATCGTGAAGCGGGAAAAAATAATTACGCTCGATATATAGAGAGAAAAG 1260  
Qy 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
Db 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
Db 1321 TTAGTTTCAATTTATATCCAGCTTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
Qy 1381 AGTCACTGAATCAGACTGTGTTGATCTCGAGTTTGTATTTGTATAACGATGGTTCAACA 1440  
Db 1381 AGTCACTGAATCAGACTGTGTTGATCTCGAGTTTGTATTTGTATAACGATGGTTCAACA 1440  
Qy 1441 GATTAATCCTTAGAAGTATCAATAAGCTTTATGTTAATTAATTCCTAGGTTACGATCATG 1500  
Db 1441 GATAATACCTTAGAAGTATCAATAAGCTTTATGTTAATTAATTCCTAGGTTACGATCATG 1500  
Qy 1501 TCTAAACCAATGCGGAATAGCCTCAGCATCAAAATGAGCGGTTTCTTTTGTCTAAAGGT 1560  
Db 1501 TCTAAACCAATGCGGAATAGCCTCAGCATCAAAATGAGCGGTTTCTTTTGTCTAAAGGT 1560  
Qy 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTTCTTGAGCCGTGATGCAATTGAACTGTGT 1620  
Db 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTTCTTGAGCCGTGATGCAATTGAACTGTGT 1620  
Qy 1621 TTTAAAGAAATTTTAAAGATAAAACCGTAGCTTGTGTTTATACACTAATAGAAACGTC 1680  
Db 1621 TTTAAAGAAATTTTAAAGATAAAACCGTAGCTTGTGTTTATACACTAATAGAAACGTC 1680  
Qy 1681 AATCCGATGTTAGCTTAATCGCTAAATGTTTACAAATTTGGCCAGAAATTTTTCAGAGAAAAA 1740

Db	1681	AATCGGATGTAGCTTAATCGTAAATGGTTACAAATGGCCAGAAATTTTCACGAGAAAA	1740	Db	241	TCCAACGTAAAAAATTAGTACTTTTCTGACTCGGAAAAAACAACGTAAAAAATAAATGG	300
Qy	1741	CTCACAACGGCTATGATTTGCTCACCACCTTTTGAATGTTTACGATTTAGAGCTTTGGCATTTA	1800	Qy	301	AAATTTGCTCACTGAGAGAAAATCTGAAAATCGCGAGGTAGAGCGGTTCGCTTGTACCA	360
Db	1741	CTCACAACGGCTATGATTTGCTCACCACCTTTTGAATGTTTACGATTTAGAGCTTTGGCATTTA	1800	Db	301	AAATTTGCTCACTGAGAGAAAATCTGAAAATCGCGAGGTAGAGCGGTTCGCTTGTACCA	360
Qy	1801	ACTGATGATTTCAATGAAAAAATTTGAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC	1860	Qy	361	AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAAATGATTTTACA	420
Db	1801	ACTGATGATTTCAATGAAAAAATTTGAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC	1860	Db	361	AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAAATGATTTTACA	420
Qy	1861	AGTGAAGTTGGAAAATTTTAAACATCTTAATAAATCTGCTATAACCGGTGATTTACATGGT	1920	Qy	421	TGGTACAAAAAGCCAAAGAAAAGACTTGGCATAAAACTGGAACATCAACATGTTGGTCTT	480
Db	1861	AGTGAAGTTGGAAAATTTTAAACATCTTAATAAATCTGCTATAACCGGTGATTTACATGGT	1920	Db	421	TGGTACAAAAAGCCAAAGAAAAGACTTGGCATAAAACTGGAACATCAACATGTTGGTCTT	480
Qy	1921	GATAACACATCAATTTAAGAACTTGGCATTTCAAGAAAACCACTTTTGTGTAGTCAAT	1980	Qy	481	TCTATTATCGTTTACAAATCTCAATCGACCAACAATTTTATCGATTACATTTAGCCCTGTTTA	540
Db	1921	GATAACACATCAATTTAAGAACTTGGCATTTCAAGAAAACCACTTTTGTGTAGTCAAT	1980	Db	481	TCTATTATCGTTTACAAATCTCAATCGACCAACAATTTTATCGATTACATTTAGCCCTGTTTA	540
Qy	1981	CAGTCATTAATAGACAAGGCATACTTATTATAATTTATGACGAATTTTGCATGATTTAGAT	2040	Qy	541	GTAAACCAAAAAACAATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGAA	600
Db	1981	CAGTCATTAATAGACAAGGCATACTTATTATAATTTATGACGAATTTTGCATGATTTAGAT	2040	Db	541	GTAAACCAAAAAACAATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGAA	600
Qy	2041	GAAAGTAGAAGATATATTTTCAATAAAAAACCGCTGAATATCAAGAAAGATTTGATATCTTA	2100	Qy	601	GATCTATCACCGATCATTTGCGCAATATGAAAATTAATTTGGATATTCGCTACGTACAGAAA	660
Db	2041	GAAAGTAGAAGATATATTTTCAATAAAAAACCGCTGAATATCAAGAAAGATTTGATATCTTA	2100	Db	601	GATCTATCACCGATCATTTGCGCAATATGAAAATTAATTTGGATATTCGCTACGTACAGAAA	660
Qy	2101	AAAGATATTTAA 2112		Qy	661	AAAGATTAACGGTTTCAAGCCAGTTCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT	720
Db	2101	AAAGATATTTAA 2112		Db	661	AAAGATTAACGGTTTCAAGCCAGTTCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT	720
RESULT 11							
AR225813							
LOCUS							
Sequence 2 from patent US 644447.							
AR225813							
VERSION							
AR225813.1 GI:27263928							
KEYWORDS							
Unknown.							
SOURCE							
Unknown.							
ORGANISM							
Unclassified.							
REFERENCE							
1 (bases 1 to 2112)							
DeAngelis, P.L.							
AUTHORS							
Polymer Grafting by polysaccharide syntheses							
TITLE							
Patent: US 644447-A 2 03-SEP-2002;							
JOURNAL							
The Board of Regents of the University of Oklahoma; Norman, OK							
FEATURES							
Location/Qualifiers							
1..2112							
/organism="unknown"							
/mol_type="genomic DNA"							
ORIGIN							
Query Match 72.2%; Score 2108.8; DB 6; Length 2112;							
Best Local Similarity 99.9%; Pred. No. 1.8e-296;							
Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;							
Qy	1	ATGAATACATTTACAAAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC	60	Qy	1081	GAGGAATTTAATCACTGGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGGTTAC	1140
Db	1	ATGAATACATTTACAAAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC	60	Db	1081	GAGGAATTTAATCACTGGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGGTTAC	1140
Qy	61	AAATTTTGAAGTTCGGGGAATCTATGGAGCAAAATTTGTTGAAATTTCAAAATTACC	120	Qy	1141	GGTAGTTCTTTTAAACTATTGATGGCATTTATGGCTTACCATTCAAGAGCCACCAGTAAA	1200
Db	61	AAATTTTGAAGTTCGGGGAATCTATGGAGCAAAATTTGTTGAAATTTCAAAATTACC	120	Db	1141	GGTAGTTCTTTTAAACTATTGATGGCATTTATGGCTTACCATTCAAGAGCCACCAGTAAA	1200
Qy	121	AAATGCAAGAAAACCTCTCAGCACATCTTCTGTTAATTCAGCACATCTTCTCTGTAAT	180	Qy	1201	GAAATGAACCGATCGTGAACGGGGAATAATATTACGCTCGATATTATGAGAGAAAAG	1260
Db	121	AAATGCAAGAAAACCTCTCAGCACATCTTCTGTTAATTCAGCACATCTTCTCTGTAAT	180	Db	1201	GAAATGAACCGATCGTGAACGGGGAATAATATTACGCTCGATATTATGAGAGAAAAG	1260
Qy	181	AAAGAAAGAAAAGTCAATGTTTGGGATAGTCCGTTTAGATATTGCAACACAACTGTTACTT	240	Qy	1261	GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT	1320
Db	181	AAAGAAAGAAAAGTCAATGTTTGGGATAGTCCGTTTAGATATTGCAACACAACTGTTACTT	240	Db	1261	GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT	1320
Qy	241	TCCAACGTAAAAAATTAGTACTTTTCTGACTCGGAAAAAACAACGTTAAAAAATAATGG	300	Qy	1321	TTAGTTTCAATTTATATCCAGCTTATAAATCTGTGCAAACTATATTCCAACTGTCGCTAGAT	1380

Db 1321 TTAGTTTCAATTTATATATCCAGCTTATAACCTGTCGCAAACTATATTCAACGTTGCGTAGAT 1380  
Qy 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGTTTGTATTTGTTAAACGATGGTTCAACA 1440  
Db 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGTTTGTATTTGTTAAACGATGGTTCAACA 1440  
Qy 1441 GATNATACCTTAGAAGTGATCAATAAGCTTTATGTTATATCTAGGTCACGATCATG 1500  
Db 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTATATCTAGGTCACGATCATG 1500  
Qy 1501 TCTAAACCAATGCGCGAATAGCCTCAGACATCAAAATGCGCGCTTTCTTTTGTCTAAAGGT 1560  
Db 1501 TCTAAACCAATGCGCGAATAGCCTCAGACATCAAAATGCGCGCTTTCTTTTGTCTAAAGGT 1560  
Qy 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCGCTGATGCGATTGAACTGTGT 1620  
Db 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTGAGCGCTGATGCGATTGAACTGTGT 1620  
Qy 1621 TTAAGAATTTTTAAAGATATAAAGCGTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
Db 1621 TTAAGAATTTTTAAAGATATAAAGCGTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
Qy 1681 AATCCGATGCTAGCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTACGAGAAAAA 1740  
Db 1681 AATCCGATGCTAGCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTACGAGAAAAA 1740  
Qy 1741 CTCAACACGGCTATGATTGCTCACCACCTTTAGAAATGTTACGATTAGAGCTTGGCATTTA 1800  
Db 1741 CTCAACACGGCTATGATTGCTCACCACCTTTAGAAATGTTACGATTAGAGCTTGGCATTTA 1800  
Qy 1801 ACTGATGATTCATGAAATTAAGAAATGAAATGCGCTAGACATGACATGTTCTCAAACTC 1860  
Db 1801 ACTGATGATTCATGAAATTAAGAAATGAAATGCGCTAGACATGACATGTTCTCAAACTC 1860  
Qy 1861 AGTCAAGTTGGAATTTAAACATCTTAATAAATCTGCTATAACCGTGATTTACATGGT 1920  
Db 1861 AGTCAAGTTGGAATTTAAACATCTTAATAAATCTGCTATAACCGTGATTTACATGGT 1920  
Qy 1921 GATAACACATCAATTAAGAAACCTTGGCATTCGCAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Db 1921 GATAACACATCAATTAAGAAACCTTGGCATTCGCAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Qy 1981 CAGTCATTAATAGACAGGCAATCACTTATTAATATGATGCGAATTTGATGATTTAGAT 2040  
Db 1981 CAGTCATTAATAGACAGGCAATCACTTATTAATATGATGCGAATTTGATGATTTAGAT 2040  
Qy 2041 GAAAGTAGAAGTATATTTTCAATAAACCCTGAAATCAAGAAGAGAGATTGATATCTTA 2100  
Db 2041 GAAAGTAGAAGTATATTTTCAATAAACCCTGAAATCAAGAAGAGATTGATATCTTA 2100  
Qy 2101 AAAGATATTAAA 2112  
Db 2101 AAAGATATTAAA 2112

RESULT 12  
AE006116  
LOCUS  
DEFINITION Pasteurella multocida subsp. multocida str. Pm70 section 83 of 204 of the complete genome.  
ACCESSION AE006116 AE004439  
VERSION AE006116.1 GI:12721075  
KEYWORDS  
SOURCE  
ORGANISM Pasteurella multocida subsp. multocida str. Pm70  
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.  
REFERENCE 1 (bases 1 to 11885)  
AUTHORS May,B.J., Zhang,Q., Li,L.L., Paustian,M.L., Whittam,T.S. and Kapur,V.  
TITLE Complete genomic sequence of Pasteurella multocida, Pm70  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)  
PUBMED 11248100

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

FEATURES  
source

2 (bases 1 to 11885)  
Zhang,Q. and Kapur,V.  
Direct Submission  
Submitted (24-OCT-2000) Department of Veterinary Pathobiology,  
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN  
55108, USA  
Location/Qualifiers  
1. 11885  
/organism="Pasteurella multocida subsp. multocida str.  
Pm70"  
/mol\_type="genomic DNA"  
/strain="Pm70"  
/sub\_species="multocida"  
/db\_xref="taxon:272843"  
205. .2073  
/genes="hyaE"  
/notes="synonym: PM0774"  
205. .2073  
/genes="hyaE"  
/codon\_start=1  
/transl\_table=11  
/product="HyaE"  
/protein\_id="AAK02858.1"  
/db\_xref="GI:12721076"  
translations="MKKVIILGHKQSNQVDEKVFQCYGNPPLPSKREKMSPIEIGH  
VLMKVLPSLEHTPKVSLNSLNKSKIKGNSAKNSHKHAKTNTIQTTSIMDNLSID  
LMLANEQPMGSDNPNAIQIDYWANLDNHFVFDYDKPENLQTHSLEELAKLDK  
HTVQEPFEMQTYNEKILTYFNKYKORSVLLNTQOLQNTKTSLSLSEIKHSIAPDALV  
KLNELPSLNKEMBIIEVNQDLHQEBCPLSNFVSQIINKSPVTQVYELQSHADLP  
VISEQKLVNDADFALLAKWMIQKVVDVNOYQHEKELELSTIKERQLVEVTRVQLTQ  
KLSETOKEIIOIKDENRKVKSEKALKTASVQSTSKLSEKEISICSEKFOEANKRQOE  
IKDEAHLTKTSLDSKEALKTQBEIEALKIIPNENISVQEDMOEKFQFANKRQOE  
LEQELKASIDKALLETENSQKTOVSESENENKVLALQQLQOELEKLYIDNQVLK  
AKRLYCAADRIKNQLTIRGLYKIQRHGRSLGLIPLFFILFFYLGFKKEMKYEWN  
TLPPIHIEYDEANRINKSHLSYKLGVLFLQEIINPFPKWLTPYKLIKEGKRFQKQ"  
2090. .4987  
/genes="PM0775"  
2090. .4987  
/genes="PM0775"  
/codon\_start=1  
/transl\_table=11  
/product="unknown"  
/protein\_id="AAK02859.1"  
/db\_xref="GI:12721077"  
translations="MNTLSQAIKAYNSNDVELAKLFEKSAETYGRIKIVFQIICKKE  
KLSNYSVSEDKNSVCDSSLDIATQLLSNVKKLTLSSEKNSLKNKWSITGKSE  
NASIRKVELVPKDFPKDLVLAPLDHVDFTYKNRKKSLGIPKPNKNIIGLSIIPFP  
NRRIILDI TLACLVNOKTNPYFVWVADGSKENLLTI VQYEQKLDIKTVRQKDYQ  
OLCAVRNLGTAKYDPVSI LDCDMA PQOLWVHSLYTELLEDNDIVLIGPRKYVDTHN  
ITAEQFLNDPYLIESLPETATNNPSTSKGNISLDRLEHFKKTDNLRCDSPRYE  
SCGNVAFSEKWLKNKWFDEEFNHGGEDEVFGRLPAKGCFFRVIDGGHAYHQEPFG  
KENETDREAGKSITLKI VKEKPYIYRKLPIEDSHIHRISYIIPAYNCANYIQR  
CVDSALNQTVVLEVCICNDGSDNTLEVNKLYGNNPRVIRIMSKPNGGISASNAAV  
SPAGYVIGQLSDDDYLPDPAVELCKLKEFLDKTACVYTTNRNVNPDGSLIANGYNW  
PEPSREKLTAMIAHPRMFTIRAWHLTDGFNEKIENAVDYDMFLKLSVEGKFKHLAK  
ICTNRVLHGNTSINKLDTOKKHVSVVNSQNRQVSNYNVDNDRSKYIENK  
TADYQEBIDILDKIKIVQRDAKVAISFYFNRDLGVLKLNLIIEYKNVLLIHLHI  
DKHLSLSDIKKEILEFHNKQINILLNDVSYTTNNRLIKTKAHLSSNNKLRQLNLI  
EYIIFNDHSLFINKDSYNIHKYIDGNFSSLTNDWINKNPKFKNLTKIKYFNND  
DLKTIINNKGASQGMFKYITLAHDIAITIMEKVI TLQSTDVSPEYNTEDIWFOALLIL  
EKKTGHVFNKTSITLTYMPWERKLTQWNEQIESAKRGENIPVNKFIINSITL"  
5051. .6223  
/genes="PM0776"  
5051. .6223  
/genes="PM0776"  
/codon\_start=1  
/transl\_table=11  
/product="unknown"  
/protein\_id="AAK02860.1"  
/db\_xref="GI:12721078"  
translations="MKKITTAGAGYVGLSNVLAQHHNVILLDIDQNKVDLINNKKKS  
PITDKIEDEFLQNKSLTMMATTDKEVALKNADFVIATPTDYNTEGTGYFNTSTVEAVI  
EQTLISINPQATIIIKSTIPVGTENMRKFTPNLI PSPEFREGKALYNLPSRII

gene	CDS	VGSTSYQAKVFADMLTCARKKQDVTVLFTHTNTEAIVAKVLFANTYLANRVAFNFELDTY ASLHLNTKDIINGISLTDPRIGTHYNNPSFGYGVGCLPKDPTKQLLANVAVPONLIEA IVKSNETRKRFITHDLNKKPKTKVIGLIMKSGDNFRASAILDIMPHLKNGEIV IYEPTLNQAFEDYFVINQLSEFINRSDVILANRSEPDNLQCSHKIYTRDIFGDA" 6216..7649 /gene="PM0777" 6216..7649 /gene="PM0777" /codon_start=1 /transl_table=11 /product="unknown" /protein_id="AAK02861.1" /db_xref="GI:12721079"		gene	CDS	/gene="hexA" /note="synonym: PM0781" 10789..11448 /gene="hexa" /codon_start=1 /transl_table=11 /product="Hexa" /protein_id="AAK02865.1" /db_xref="GI:12721083" /translation="MIYVENVCCKYLNRGTWHTVLDVVSFSLRGQVKVGLGKNGAGK STLIRLSGVEPTSGKITRKMSISWPLGFSGAFQSLTGMNLRFTIARIYNADIDYV KRFTEEFSELGKLYEPVRYTSSGMRKARLAPALSLSIEFDCVLDLIELIIVAGDARFADK KCYELFEKRRKDRSLILVSHSPNAIREYCDNAMVULHNGIMHHFNSIDITAYQPHNALQT K" complement(11484..11813) /gene="PM0782" complement(11484..11813) /gene="PM0782" /transl_table=1 /codon_start=1 /product="unknown" /protein_id="AAK02866.1" /db_xref="GI:12721084" /translation="METLDRKKQISENPILIMKGSPPKPSGFSARAVEALMHCKV PFGYVDILQHPDIRAELPAYANWPTFFPOLWVDGELVGGCDIILEMFQOGSELQTLADV AAKYPQ8"	
		Query Match 70.8%; Score 2066.4; DB 1; Length 11885; Best Local Similarity 82.1%; Pred. No. 1.3e-290; Matches 2398; Conservative 0; Mismatches 501; Indels 21; Gaps 1;					
		QY	1			ATGAATACATTATCAAGCAATAAAGCATATATAAGCATATATAAGCATACACTATCAATTAGCACTC 60	
		DB	2090			ATGAATACATTATCAAGCAATAAAGCATATATAAGCATACACTATGAATTAGCACTC 2149	
		QY	61			AAATTATTGAAAGTCGGCGGAAATCTATGAGCGGAAATCTTGTAATTTCAAATTACC 120	
		DB	2150			AAATTATTGAAAGTCGCTGAACCTACGGCGGAAATCTGTGNAATTCGAATTTATC 2209	
		QY	121			AAATGCAAGAAAAAAGCTCTCAGCACATCCTTCTGTTAATTCAGCACATCTTCTGTAAAT 180	
		DB	2210			AAATGTAAGAAAAAAGCTCTCGACCAATTC-----TTATGTAAGT 2248	
		QY	181			AAAGAAGAAAAAGTCAATGTTTCGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 240	
		DB	2249			GAAGAATAAAAAAAGTGTTCGGATAGTCAATTAGATATCGCAACACAGCTCTTACTT 2308	
QY	241	TCCAAGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAAGTTAAAAAATAAATGG 300					
DB	2309	TCCAAGTAAAAAATTTAACTCTTCATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 2368					
QY	301	AAATTCCTCACTGAGAAAGAAATCTGAAAAATCGCGAGGTGAAGACGGTCGCGCTTTGTACCA 360					
DB	2369	AAATCTATCATCGGAAAAAATTCGGAGACGCAAGAAATCAGAAAGGTGGAACTAGTAGCCC 2428					
QY	361	AAAGATTTTCCCAAGATCTGTTTTAGCGCCTTTACTGATCATGTATATGATTTTACA 420					
DB	2429	AAAGATTTTCCCAAGATCTGTTGTTCTGTCTCCATGTCAGATCATGTATATGATTTTACA 2488					
QY	421	TGTTACAAAAAGCGAAGAAAAAGACTTTGGCATAAAACTTCAACATCAACATGTTGGTCTT 480					
DB	2489	TGTTACAAAAATCGAAAAAAGAAAGCTTAGGTATAAAGCCTGTAAATAAGATATCGGTCTT 2548					
QY	481	TCTATTATCGTTACAAACATTCAATCGACCAAGCAATTTTATCGATTACATTAGCCTGTTTA 540					
DB	2549	TCTATTATTATTCCTACATTTAATCGTAGCCGTATTTTAGATATAACGTTAGCCTGTTTG 2608					
QY	541	GTAACCAAAAAACACATTACCCGTTTGAAGTTATCTGTGACAGATGATGTTAGTCAGGAA 600					
DB	2609	GTCAATCAGAAAAACAACCTACCCATTTGAAAGTCGTTCTGTCAGATGATGTTAGTAGGAA 2668					
QY	601	GATCTATACCCGATCATCTCCCAATATGAAAAATGAAAAATGGAATATTCGCTACGTCAGACAA 660					

Db	2669	AACTTACTTACCAATTTGTGCAAAATAACGAAACAAAACTTGACATAAAGTATGTGAACAA	2720
Qy	661	AAAGATAACGGTTTTCAAGCCAGTGGCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT	720
Db	2729	AAAGATTATGGATCAATTTGTGTGCAGTCAGAAACTTAGGTTTACGTACAGCAAAAGTAT	2788
Qy	721	GACTTTATTTGGCTTACTCGACTGTGTATATGGCGCCAAATCCATTATGGGTTCATTTCTTAT	780
Db	2789	GAITTTGTCTCGATTTCTAGACTCGGATATGCGACCCACAACAAATATGGGTTCATTTCTTAT	2848
Qy	781	GTTCGAGAGCTATTAGAAGATGATGATTAACAATCATTTGGTCCAGAAAAATACATCGAT	840
Db	2849	CTTACAGAACTATTAGAAGACAATGATATTGTTTTAATTTGGCACTAGAAAAATATGTGGAT	2908
Qy	841	ACACAACATATTGACCCCAAAAGACTTCTTAAATAACCGGAGTTTGTCTGAATCATTTACCA	900
Db	2909	ACTCATTAATATTACCGCAGAAACAATTCCTTAAACGATCCATATTTAATAGAAATCACCTACCT	2968
Qy	901	GAAGTGAACACCAATATATAGTTGTTCGCCGCAAAAGGGGAAGAAACAGTTTCTCTGGAATGG	960
Db	2969	GAACCGCTACAAATAACATCTTTCGATTACATCAAAAGGAATAATATCGTTGGATTGG	3028
Qy	961	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTTGGCTTTCCTGTTTT	1020
Db	3029	AGATTAGAACATTTCAAAAAAACCGATAATCTACGCTCATGTGATTCACCGTTTCTGTTAT	3088
Qy	1021	TTTTGCGCGGGTAATGTTGCTTTTCGCTTAAAAAATGGCTAAATAAATCCGGTTTCTTTGAT	1080
Db	3089	TTTTAGTTGCGGTAAATGTTGCAATTTTCTTAAAGAAATGGCTTAAATAAGTAGTGGTTCCGAT	3148
Qy	1081	GAGGAATTTAATCACTGGGTGGAGAAGATGTGGAAATTTGGATATCGCTTATTCGGTTAC	1140
Db	3149	GAAGAAATTTAATCATTTGGGGGGGGAAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA	3208
Qy	1141	GGTAGTTTCTTTAAAACTATTGATGGCAATTTATGGCCTTACCATCAAGAGCCACAGGTAAA	1200
Db	3209	GGCTGTTTTTTTCAGAGTAAATTTGACGGCGGAATGGCATACCATCAAGAACACACCTGGTAAA	3268
Qy	1201	GAANAATGAACCCGATCGTGAAGCGGGAAAAAATAATTACGCTCGATATTATGAGAGAAAG	1260
Db	3269	GAANAATGAACAGACCCGGAAGCTGTGTAAAGATTTACGCTTAAAAATTTGTAAGAAAAAG	3328
Qy	1261	GTCCCTTTATATCTATAGAAAACTTTTTACCAATAGAAGATTTGCGATATCAATAGAGTACCT	1320
Db	3329	GTACCTTTCAATCTATAGAAAGCTTTTACCAATAGAGATTTCAATTTCATAGAAATACCT	3388
Qy	1321	TTAGTTTCAATTTATATCCAGCTTATPAACGTGTGCAAACTATATTCAACGTTCCGTAGAT	1380
Db	3389	TTAGTTTCTTATTTATATCCCGCTTATAAATGTGTGCAAAATTTATTTCAAGATGTGTAGAT	3448
Qy	1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGATTTGTATACGATGGTTCAACA	1440
Db	3449	AGTGCTCTTAATCAAACTGTGTGTCGATCTCGAGGTTTGATTTGTATACGATGGTTCAACA	3508
Qy	1441	GATAAATACCTTTAGAAGTGATCAATAAGCTTTTATGGTAAATAATCTAGGGTACCATCATG	1500
Db	3509	GATAATACCTTTAGAAGTGATCAATAAGCTTTTATGGTAAATAATCTAGGGTACCATCATG	3568
Qy	1501	TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCCGTTTCTTTGCTAAAGGT	1560
Db	3569	TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCCGTTTCTTTGCTAAAGGT	3628
Qy	1561	TATTACATTTGGCAGTTAGATTACAGATGATTAATCTTGAGCGCTGATGAGTTGAATGTGT	1620
Db	3629	TATTACATTTGGCAGTTAGATTACAGATGATTAATCTTGAGCGCTGATGAGTTGAATGTGT	3688
Qy	1621	TTAAAGAAATTTTTAAAGATAAAACCGCTAGCTGTGTTTATACCACTAATAGAAAGCTC	1680
Db	3689	TTAAAGAAATTTTTAAAGATAAAACCGCTAGCTGTGTTTATACCACTAATAGAAAGCTC	3748
Qy	1681	AATCCGGATGGTAGCTTTAAATCGCTTAATGTTTACAAATTTGGCCAGAAATTTTTCACGAAAAA	1740

3749	Db	AATCCGGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTTCACGAGRAAAA	3800
1741	Qy	CTCAACCGCTATGATGTCTCACCACTTTAGAAATGTTACAGATTAGAGCTTGGCATTTTA	1800
3809	Db	CTCAACCGCTATGATGTCTCACCACTTTAGAAATGTTACAGATTAGAGCTTGGCATTTTA	3868
1801	Qy	ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTTCCTCNAACCTC	1860
3869	Db	ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTTCCTCNAACCTC	3928
1861	Qy	AGTGAAGTTGGAAAAATTTTAAACATCTTAATAAAATCTGCTATAAACCGTGTATTACATGGT	1920
3929	Db	AGTGAAGTTGGAAAAATTTTAAAGCATCTTAATAAAATTTGTTATAAACCGCGTATTACATGGT	3988
1921	Qy	GATAACACATCAATTAAAGAAACCTTGGCATTTCAAAAGAAAAACCATTTTTGTGTAGTCAAT	1980
3989	Db	GATAATACATCAATTAAAAATCTAGACACTCAAAAGAAAAATCATTTTGTGTGCTTTAAT	4048
1981	Qy	CAGTCATTAATAGACAAGGCATAACTTATTATAATTATGACAGAAATTTGATGATTAGAT	2040
4049	Db	CAATCATTAATAAGGCAGAGAGTAAGTAATTATAACTATGATGAATTCGATAACTTAGAT	4108
2041	Qy	GAAGGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA	2100
4109	Db	GAAGGTAGAATAATACATTTTCAATAAAACGAGAGATTTACAGAAGAAATTGATATCTTA	4168
2101	Qy	AAAGATATTAAAAATCATCCAGAAATAAGATGCCAAAAATCGCAGTCAGTATTTTTTATCCC	2160
4169	Db	AAAGATATCDAANATGATACAGCGTAAAGATGCAAAAGTTGCAATAGTATATTTATCCA	4228
2161	Qy	AATACATTAACCGCTTAGTGAAGAAAACTAAACAATATTATTTGAAATATAATAAAAAATATA	2220
4229	Db	AATAGATTAGATGGGTAGTTTAAATAAAATTTAAACAATATTATTCGAATATACAAAAAATGTA	4288
2221	Qy	TTGCTTATTTGTTCTACATGTTTGATAGAAATCATCTTTACACAGATATCAAAAAAGAAATA	2280
4289	Db	CTCATTTATTTGTTTTACACATTTGACAAAAATCATCTTCACATTCAGACATCAAAAAAGAAATA	4348
2281	Qy	CTAGCTTCTCATATAAAACATCAAGTGAATATTTTACTAAATTAATGATATCTCATATATAC	2340
4349	Db	CTAGAAATTTCTAAACAGAAATCAATATCTTTGTTAAATTAATGATGTTTCTTATTAT	4408
2341	Qy	ACGAGTAATAAGATTAAATAAAAACTGAGGGCGATTTAAGTAAATATAATAAATTAAGTCAG	2400
4409	Db	ACAAAACAACAGGCTCATAAAACTAAAGCTCATTTAAGCAATATGAAACAAGTTAAGACAA	4468
2401	Qy	TTAAATCTAAATTTGTGATAACATCATTTTGTGATAANTCAGACGCTTATTCGTTAAAAAT	2460
4469	Db	CTAAATCTTAAATTTAGAAATATAATTTTTTGAACAACCATGACAGCTTATTTATTAANAAT	4528
2461	Qy	GACAGCTATGCTTATATGAAAAAATATGATGTGGCATGAATTTCTCAGCATTTAAACACAT	2520
4529	Db	GATAGTTATAACCATATAAAAAATATGATATCGGCATGAACCTTCTCTCATTTAACAAAT	4588
2521	Qy	GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTAAAAAGCTCATTTAAAACTTATTTT	2580
4589	Db	GATTTGGATAAATAAAATTTAATGTCACACTCACCATTTAAAAATCTGATAAAAAAATATTTT	4648
2581	Qy	AATGACAAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCACAAAGTATGTTTATGACG	2640
4649	Db	AATGATAATGATTTTAAAAACAATAAATAATGAAGGGCGCGTCACAAGGAATGTTTCATAAAA	4708
2641	Qy	TATGGCTAGCGATGAGCTTCTGACGATTTATAAGAAGTCATCACATCTTGGCAGTCA	2700
4709	Db	TACACTTTTGCAACATGATATTTGCTACGATTTATGAAAGAGTCATTAATATATGCAATCT	4768
2701	Qy	ATTGATAGTGTGCCAGAAATAAACACTTGAGGATATTTTGGTTCCAAATTTGCATTTTAAATC	2760
4769	Db	ACAGATAGTGTCTCGAATAATATACTGAAGATATTTTGGTTCCAAATTTGCATTTTAAATC	4828
2761	Qy	TTGAAAAAGAAAAACCGGCCATGTATTTTAATATAAACATCGACCCCTGACTATATGCGCTTGG	2820
4829	Db	TTGAAAAAGAAAAACCGGCCATGTATTTTAATATAAACATCGACCCCTGACTTATATGCCCTTGG	4888





Db 1202 GAAGAAATTTAATCATTTGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTATTGGCCAAA 1261  
Qy 1141 GGTAGTTTCTTTAAAACCTATTGATGGCATTATAGCCCTTACCATCAAGAGCCACCAAGGTAAA 1200  
Db 1262 GGCTGTTTTTTTTCAGAGTAATTTAGCGGGAATGCGATACCATCAAGAAACCAACCTGGTAAA 1321  
Qy 1201 GAAAATGAACCCGATCGTAGCGGGGAAAATAATTACGCTCGATATATTATGAGGAAAAG 1260  
Db 1322 GAAAATGAACAGACCCGAGCTGGTAAAAGTATTACGCTTAAATTTGTGAAAGAAAAG 1381  
Qy 1261 GTCCCTTATCTATAGAAAACCTTTTACCAATAGAAGATTGCGCATATCAATAGAGTACCT 1320  
Db 1382 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGATTACATATTCATAGATACCT 1441  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTTAATCTGTCGCAACTATATTTCAACGTTGCGGTAGAT 1380  
Db 1442 TTAGTTTCTATTTATATCCCGCTTTATACTGTGCAAAATATATTCAAAAGATGTGTAGAT 1501  
Qy 1381 AGTGCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAGCATGGTTCAACA 1440  
Db 1502 AGTGCCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTGTTAAGCATGGTTCAACA 1561  
Qy 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATATCTAGGTAACGCATCATG 1500  
Db 1562 GATATATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATATCTAGGTAACGCATCATG 1621  
Qy 1501 TCTAAACCAAATGCGGGAATAGCTCAGCATCAAAATGCAAGCCGTTTCTTTTGTAAAAGGT 1560  
Db 1622 TCTAAACCAAATGCGGGAATAGCTCAGCATCAAAATGCAAGCCGTTTCTTTTGTAAAAGGT 1681  
Qy 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTTATCTTGAGCCGTGATGCACTGTGT 1620  
Db 1682 TATTACATTTGGCGAGTTAGATTTCAGATGATTTATCTTGAGCCGTGATGCACTGTGT 1741  
Qy 1621 TTTAAAGAAATTTTAAAGATATAAAGCGTACTGTTGTGTTTATACCACTAATAGAAAAGTC 1680  
Db 1742 TTTAAAGAAATTTTAAAGATATAAAGCGTACTGTTGTGTTTATACCACTAATAGAAAAGTC 1801  
Qy 1681 AATCCGGATGGTAGCTTAATCGCTTAATGGTTTACAAATTTGGCCAGAAATTTTTCACGAGAAAA 1740  
Db 1802 AATCCGGATGGTAGCTTAATCGCTTAATGGTTTACAAATTTGGCCAGAAATTTTTCACGAGAAAA 1861  
Qy 1741 CTCAACAGCGTATGATGCTCACCATTTCAGATGATTTTCAGATTTAGCTTGGCATTTA 1800  
Db 1862 CTCAACAGCGTATGATGCTCACCATTTCAGATGATTTTCAGATTTAGCTTGGCATTTA 1921  
Qy 1801 ACTGATGATTCATGAATAAATTTGAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1922 ACTGATGATTCATGAATAAATTTGAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1981  
Qy 1861 AGTGAAGTTGGAAAATTTAAACATCTTTAATAAATCTGCTATAACCCGTTGATTTACATGGT 1920  
Db 1982 AGTGAAGTTGGAAAATTTAAGCATCTTAATAAATTTGTTTATAACCCGTTGATTTACATGGT 2041  
Qy 1921 GATTAACATCAATTAAGAAACTTTGGCATTCAAAAGAAAACCAATTTTGTGTTAGTCAAT 1980  
Db 2042 GATAATACATCAATTAAGAAACTTTAGACACTCAAAAGGAAAATTCATTTGTTGTCGTTAAT 2101  
Qy 1981 CAGTCATTAAATAGACAGGCATACTTTATTATTAATATGACGAATTTGATGATTTAGAT 2040  
Db 2102 CAATCATTAATAGCAGAGATGATTAATTTATTAATGATGATTTGATTTGATTAATTTAGAT 2161  
Qy 2041 GAAAGTAGAAAGTATATTTCATATAAACCCTGAATATCAAGAGAGATTTGATATCTTA 2100  
Db 2162 GAAAGTAGAAAGTATATTTCATATAAACCAGCATGATTAAGAGAAATTTGATATCTTA 2221  
Qy 2101 AAGATATTAATATCATCCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2160  
Db 2222 AAAGATATCAAAATAGTACCGTAAAGATGCAAAAGTTGCAATAAGTATATTTTATCCA 2281  
Qy 2161 AATACATTTAAACGGCTTAGTGAATAAATACTAAACCAATATTTTGAATATAAATAAATAATA 2220  
Db 2282 AATAGATTAGATGGTTAGTTTAAATAAATTAACCAATATTTTCGAATATNACAAAATGTA 2341

Qy 2221 TTGCTTATTGTTTACATGTTGATAAGAAATCATCTTTACACCAGATATCAAAAAAGAAATA 2280  
Db 2342 CTCAATTATTGTTTTTACATTTGACAAAATCATCTCCTCAGCATCAAAAAGGAAATA 2401  
Qy 2281 CTAGCCCTTCTATCATAAACATCAAGTGAATATTTTACTATAATTAATGATATCTCATATTAC 2340  
Db 2402 CTAGAATTTCTAATAACAAGATCAATATCTTGTTAATAATGATGTTCTTTATTAT 2461  
Qy 2341 ACAGGTAATAGATTAATAAAAACTGAGGCGCATTTTAAGTAATAATTAATAAATTAAGTCAG 2400  
Db 2462 ACAACAACAGCGCTCATAAAACTAAAGCTCATTTAAGCAATATGAACAAGTTTAAGACAA 2521  
Qy 2401 TTAATCTAAATTTGTGAATACATCATTTTGTAAATCATGACAGCCCTATTCGTTAAAAAT 2460  
Db 2522 CTAAATCTTAAATTTGAATATATTTTGTGAACCATGACAGCCCTATTTTATTTAAAAAT 2581  
Qy 2461 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2520  
Db 2582 GATAGTTTATACCATATAAAAAATATGATATCGGCATGAATTTCTCTCATTAACAAAT 2641  
Qy 2521 GATTGGATCGAGAAAATCAATGCGCATCCACCATTTTAAAAAGCTCATTAATAACTTTATTT 2580  
Db 2642 GATTGGATTAATTAATTAATGACACTCACCATTTTAAAAATCTGATAAAAAAATAATTTT 2701  
Qy 2581 AATGACATGACTTAAAAAGTATGAATGTAAGGGGCGCATCACAAGGTATGTTTATGACG 2640  
Db 2702 AATGATAATGATTTTAAAAACAATAAATAATGAAGGGCGGTCACAAGGAATGTTCATAAAA 2761  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAAAGAGTCAATCATCTTGCCAGTCA 2700  
Db 2762 TACATTTAGCACATGATTTGCTAGATATGAAAGAGTCAATTAATTTATGCCATCT 2821  
Qy 2701 ATTGATAGTGTGCGAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAATC 2760  
Db 2822 ACAGATAGTGTCTCTGAATATAACTGAAGATATTTGGTTCCAAATTTGTAATTTAATC 2881  
Qy 2761 TTAGAAAAGAAAACCGCCATGTTTATTAATAAACAATCGACCTGACTTATATGCTTTGG 2820  
Db 2882 TTAGAAAAGAAAACCGCCATGTTTATTAATAAACAATCGACCTGACTTATATGCTTTGG 2941  
Qy 2821 GAACGAAAATTTACAATGGACAAAATGAACAAATTTGAAAGTGCAAAAGAGAGAGAAAATATA 2880  
Db 2942 GAACGAAAATTTACAATGGACAAAATGAACAAATTTGAAAGTGCAAAAGAGAGAGAAAATATA 3001  
Qy 2881 CTTGTTAAACAAGTTCAATTTAATAATGATTAATCACTCTATAA 2920  
Db 3002 CTTGTTAAACAAGTTCAATTTAATAATGATTAATACTCTATAA 3041

RESULT 14  
AF302467

LOCUS 8838 bp DNA linear BCT 12-MAR-2001  
DEFINITION Pasteurella multocida p4218 region 2 capsule biosynthesis gene cluster, partial sequence.

ACCESSION AF302467  
VERSION AF302467.1 GI:13274373

## KEYWORDS

## SOURCE

## ORGANISM

Pasteurella multocida  
Pasteurella multocida  
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
Pasteurellaceae; Pasteurella.

## REFERENCE

## AUTHORS

## TITLE

1 (bases 1 to 8838)  
Townsend,K.M., Boyce,J.D., Chung,J.Y., Frost,A.J. and Adler,B.  
Genetic organization of Pasteurella multocida cap Loci and  
development of a multiplex capsular PCR typing system

## JOURNAL

## PUBMED

## AUTHORS

## TITLE

## JOURNAL

2 (bases 1 to 8838)  
Townsend,K.M., Boyce,J.D., Chung,J.Y., Frost,A.J. and Adler,B.  
Direct Submission  
Submitted (03-SEP-2000) Veterinary Pathology and Anatomy, The  
University of Queensland, School of Veterinary Science, Brisbane,



Db 2863 AAATCTATCACTGGGAAAAAATCGGAGAACGCGAABATCAGAAAGTGGAACCTAGTACCC 2922  
Qy  
361 AAAGATTTTCCAAAGATCTGGTTTTAGCGCTTTACCTGATCATGTTAATGATTTTACA 420  
Db  
2923 AAAGATTTTCTAAAGATCTTGTTCTTGCTCCATTCGACATCATGTTAATGATTTTACA 2982  
Qy  
421 TGGTACAAAAGCGAAGAAAGACTTGGCATAAAACTGCAACATCAACATGTTGGTCTT 480  
Db  
2983 TGGTACAAAATCGAAAAAAGCTTAGGTATAAGCCTGTAAATAAGAAATATCGGTCTT 3042  
Qy  
481 TCTATTATCGTTACAAACATTCATCGACCGACGAAATTTATCGATTACATTAGCCTGTTTA 540  
Db  
3043 TCTATTATCTCTCATTTAATCGTAGCGGTATTTAGATATAACGTCAGCCTGTTG 3102  
Qy  
541 GTAAACCAAAAAACACATTTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGAA 600  
Db  
3103 GTCAATCAGAAAAACAAACTACCCATTTGAAGTCGTGTTGAGATGATGGTAGTAAGAA 3162  
Qy  
601 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGATATTCGTCAGTCAGACAA 660  
Db  
3163 AACTTACTTACCATTTGTGCAAAAATAGAAACAAAACCTTGACATAAAGTATGTAAGCAA 3222  
Qy  
661 AAAGATAACGGTTTCAAGCCAGTGCCTCGGAATATGGATTAACGCTTAGCAAAATAT 720  
Db  
3223 AAAGTTATGGATATCAATTTGTGTGAGTCAGAACTTAGGTTTACGTACAGCAAGTAT 3282  
Qy  
721 GACTTTATGGCTTACTCGACTGTGATATGCGGCCAAATCCATTTATGGGTTTCATCTTAT 780  
Db  
3283 GATTTGTGCTGATCTTAGACTGCGATATGACCAACAAATTTATGGGTTTCATCTTAT 3342  
Qy  
781 GTTCAGAGCTATTAGAAGATGATTTAACAATCATTTGTCAGAAATATACATCGAT 840  
Db  
3343 CTTACGAACATTTAGAAGACAATGATTTGTTTAAATTTGACCTAGAAAAATATGTGGAT 3402  
Qy  
841 ACACAAATATTTGACCCAAAAGACTCTTAAATAACGCGAGTTTGTGTAATCATTAACCA 900  
Db  
3403 ACTCATATATTACCGGAGAACATTCCTTAAACGATCCATATTTAATAGATCACTACCT 3462  
Qy  
901 GAAGTGAACCAATAATAGTGTGCGCCAAAAGGGGAAAGAAAGTTCTCTCGATGG 960  
Db  
3463 GAAACCGCTACAAATAACAACTCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 3522  
Qy  
961 CGCTTAGAACAAATCGAABAAACAGAAATCTCGCTTATCCGATTCGCCCTTCGGTTTT 1020  
Db  
3523 AGATTAGAACAATTTCAAAAAAACCGATAATCTACGCTGATGTGATTCACCGTTTCGTTAT 3582  
Qy  
1021 TTTGCGGCGGTAATGTGTTCTCGCTAAAAAATGGCTTAAATAATCCGTTTCTTTGAT 1080  
Db  
3583 TTTAGTTGCGGTAAATGTGCAATTTCTAAGAAATGGCTTAATTAAGTAGGTTGTTGAT 3642  
Qy  
1081 GAGAAATTAATCACTCGGGTGGAGAGATGTGAAATTTGGATATCGCTTAATTCGGTTAC 1140  
Db  
3643 GAAGAAATTAATCATTTGGGGGGCGAGATGTAGAAATTTGGTTACAGATTAATTTGCCAAA 3702  
Qy  
1141 GGTAGTTCTTTAAACCTAATTTAGTGGCATTTATGCGCTACCATCAAGGCCACCAAGTAAA 1200  
Db  
3703 GGCTGTTTTTTTTCAGAGTAAATTTGACGGCGGAATGGCATACCATCAAGAACCACTGGTAAA 3762  
Qy  
1201 GAAATGAACCGATTCGTGAAGCGGAAAAAATATTACGCTCGATATTATCAGAGAGAAAG 1260  
Db  
3763 GAAATGAAACAGACCGCGAAGCTGGTAAAGTATTACGCTTAAATTTGTGAAAGAAAG 3822  
Qy  
1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
Db  
3823 GTACCTTACATCTATAGAAGCTTTTACCAATAGAAGATTCACATATTTCATAGAATACCT 3882  
Qy  
1321 TTAGTTTCAATTTATATCCAGCTTATAAATGTCGCAACTATATTCAAGTTTCGCTAGAT 1380  
Db  
3883 TTAGTTTCTAATTTATATCCCGCTTATAAATGTCGCAAAATTAATTTCAAGATGTGTAGAT 3942  
Qy  
1381 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTGAACGATGGTTCAACA 1440  
Db  
3943 AGTGTCTTAATCAAACTGTTGTGATCTCGAGGTTGTATTTGTNACGATGGTTCAACA 4002

Qy 1441 GATAATACCTTAGAAGTGATCAATAGCTTTATGGTAAATAATCCTAGGGTACGCATCATG 1500  
Db 4003 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCATCATG 4062  
Qy 1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCGAGCGGTTTCTTTTGTGTAAGGT 1560  
Db 4063 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCGAGCGGTTTCTTTTGTGTAAGGT 4122  
Qy 1561 TATTACATTTGGGCGGTTAGATTTCAGATGATTATCTTTGAGCCTGATGCGAGTTGAACCTGTGT 1620  
Db 4123 TATTACATTTGGGCGGTTAGATTTCAGATGATTATCTTTGAGCCTGATGCGAGTTGAACCTGTGT 4182  
Qy 1621 TTAAGAAGATTTTAAAGATAAAACGCTAGCTTTGTTTATACCACTAATACAAACGTC 1680  
Db 4183 TTAAGAAGATTTTAAAGATAAAACGCTAGCTTTGTTTATACCACTAATACAAACGTC 4242  
Qy 1681 AATCCGGATGGTAGCTTAATCGCTAATGTTTACAATTTGGCCAGAATTTTTCACGAGAAAAA 1740  
Db 4243 AATCCGGATGGTAGCTTAATCGCTAATGTTTACAATTTGGCCAGAATTTTTCACGAGAAAAA 4302  
Qy 1741 CTCAAAACGGCTATGATGCTCAACCTTTTAGAATGTTTCAGGATTTAGAGCTTGGCATTTA 1800  
Db 4303 CTCAAAACGGCTATGATGCTCAACCTTTTAGAATGTTTCAGGATTTAGAGCTTGGCATTTA 4362  
Qy 1801 ACTGATGGATTCAATGAAAAAATTTGAATGCGGTAGACTATCAGCATGTTTCTCAAACTC 1860  
Db 4363 ACTGATGGATTCAATGAAAAAATTTGAATGCGGTAGACTATCAGCATGTTTCTCAAACTC 4422  
Qy 1861 AGTGAAGTTGGAATAATTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTACATGGT 1920  
Db 4423 AGTGAAGTTGGAATAATTTAGCATCTTAATAAAATTTGTTATTAACCGGTATTACATGGT 4482  
Qy 1921 GATAACACATCAATTAAGAAACCTTGGCATTTCAAAAGAAAAACCATTTTGTGTTGATCAAT 1980  
Db 4483 GATAATACATCAATTAATAAATCTAGACACTCAAAAGAAAAAATCATTTCTGTTGCTGTTAAT 4542  
Qy 1981 CAGTCATTAATAGACAGGCATACTTATTATAATTTATGACCAATTTTGATGATTTTATAGAT 2040  
Db 4543 CAATCATTAATAGGACAGAGTAGTAATTTAATCATGATGTAATTCGATTAACCTTAGAT 4602  
Qy 2041 GAAAGTAGAAATGATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100  
Db 4603 GAAAGTAGAAATAACATTTTCAATAAACAGACAGATTATCAAGAAGAAATTTGATATCTTA 4662  
Qy 2101 AAAGATATTAAATCAATCCAGAAATAAGATGCCAAAAATCCGAGTCAGTATTTTTTATCCC 2160  
Db 4663 AAAGATATCAAAATAGTACAGCGTAAAGATGCAAAAGTTGCAATAAGTATATTTTATCCA 4722  
Qy 2161 AATACATTAACCGCTTAGTGAABAAACCTAAACAATATTATGAAATATAATAAAAAATA 2220  
Db 4723 AATAGATTAGATGGGTTAGTTTAAATAATTAACAATATTATCGAATATAACAANAATGTA 4782  
Qy 2221 TTGTTATTGCTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 4783 CTATTTATTGTTTACACATTTGCAAAAATCATCTCACTCAGACATCAAAAAGAAATA 4842  
Qy 2281 CTAGCCTTCTATCATAAACCAAGTGAATATTTTACTAAATTAATGATATCTCATATTAC 2340  
Db 4843 CTAGAAATTTCAACAAGAATCAATCAATATCTTGTTAATAATGATGTTTCTTATTAT 4902  
Qy 2341 ACGAGTAATAGATTAAATAAACTGAGCGCATTTTAAGTAATTAATAAATTAAGTCAG 2400  
Db 4903 ACAAACCAAGGCTCAAAAAAATTAAGCTCATTTAAGCAATATGAACAAGTTAAGACAA 4962  
Qy 2401 TTAATCTAAATTTGTGAATACATCATTTTGTATAATCATGACAGCCTTATTCGTTAAAAAT 2460  
Db 4963 CTAAATCTTAATTTAGAAATATATTATTTTGAACCAACCATGACAGCCTATTATTAAAAAT 5022  
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTGGCGATGAATTTTCTCAGCATTAACAT 2520  
Db 5023 GATAGTTATAACCAATATAAAAAAATATGATATGGCATGAACCTTCTCTCATTTAACAAAT 5082



repeat_region	COVSNLKIKNIVASKNIARTNTTFFAGMSYLLQIGIDIT"		gene	PNGYI"		Query Match	26.2%; Score 765.8; DB 1; Length 14483;	
gene	complement (7277. .8607)			complement (13863. .14483)			Best Local Similarity 62.6%; Pred. No. 5.2e-102; Matches 1222; Conservative 0; Mismatches 725; Indels 4; Gaps 2;	
	/insertion_seq="IS2"			/gene="kpsr1"				
	complement (7288. .7944)			complement (13863. .>14483)				
	/gene="kfoIS"			/gene="kpsr"				
CDS	complement (7288. .7944)		/codon_start=1		167	ATCTTTCTGCTAAATAAAGAAGAAAAGTCAATGTTTTCGCATAGTCCGTTAGATATTGGCAA	226	
	/gene="kfoIS"		/transl_table=11					
	/codon_start=1		/product="ABC transporter"					
	/transl_table=11		/protein_id="BAC00526.1"					
gene	/product="IS hypothetical protein"		/db_xref="GI:2132678"		10558	ATCTTTCTGAAGAAGTTGATAAGTTAAATCGTAAAGCTGTTATTGTATTTGATTCGACGAA	10499	
	/protein_id="BAC00522.1"		/translation="RHYVFNKLNIEIPSGKSVAFIRGNHGAKSTLRLMIGGIDRRPDGS					
	/db_xref="GI:2132678"		/translatability="RHYVFNKLNIEIPSGKSVAFIRGNHGAKSTLRLMIGGIDRRPDGS					
	/db_xref="GI:2132678"		KIIITNKTIWPGVLGGFQCSLTGRENKVFARLYAKQEBKEKIEFVEFABELGYKF					
gene	complement (8637. .10697)		complement (8637. .10697)		227	CACAACCTGTTACTTTCCACCGGTAAAAAATTAGTACTTCTGACTCGGAAAAACACACGT	286	
	/gene="kfoC"		/gene="kfoC"					
	/codon_start=1		/codon_start=1					
	/transl_table=11		/product="chondroitin polymerase"					
CDS	/product="chondroitin polymerase"		/protein_id="BAC00523.1"		10498	CAAAAATAATGTTCTAAACGCCAAAGCAATTAGTCTGAACGAGGTTGAAAAAATGAAA	10433	
	/db_xref="GI:2132678"		/db_xref="GI:2132678"					
	/translation="MSILNQAINLYKNQVYRQALSLEKVAEIVDVSWVEANIKLCOT		/translation="MSILNQAINLYKNQVYRQALSLEKVAEIVDVSWVEANIKLCOT					
	ALNLSSEVDLNKRAVDIDAATKIMCSNAKATSLNVEKNEIISKREITAKKSEA		ALNLSSEVDLNKRAVDIDAATKIMCSNAKATSLNVEKNEIISKREITAKKSEA					
gene	ELKEVEPIPLDWPDLPLPESTNDYVWAGKELDDYPRKOLNIIDGLSIVIPYTN		ELKEVEPIPLDWPDLPLPESTNDYVWAGKELDDYPRKOLNIIDGLSIVIPYTN		347	TGCCTCTGTACAAAAGATCTTTCCAAAAGATCTGGTTTTCAGGCGCTTTTACCTGATCATG	406	
	RAKLTATLACLCHKQRTYDEVIVADDDGSKENETEEIVREFSLNIIKYRKQDYQY		RAKLTATLACLCHKQRTYDEVIVADDDGSKENETEEIVREFSLNIIKYRKQDYQY					
	LCVARNGLRAKNYVAIILDCDMPALVQSVYELLAVDNDVALIIPKRYIDTSKH		LCVARNGLRAKNYVAIILDCDMPALVQSVYELLAVDNDVALIIPKRYIDTSKH					
	TYLDFLSQSLNIEPIELIITNNQVAGKVEQNSVDWRIEHPKNTDNLRLNTPFRFS		TYLDFLSQSLNIEPIELIITNNQVAGKVEQNSVDWRIEHPKNTDNLRLNTPFRFS					
CDS	GQNVAFKKLFRAGDEEETHWGGSDNEFGYRLYREGCYFRSVEGAMAYHOEPPK		GQNVAFKKLFRAGDEEETHWGGSDNEFGYRLYREGCYFRSVEGAMAYHOEPPK		10378	TCGAACCCATTCCTTTAGATTGGCCCTAGTGATTAACTTTTACCGCGCTTACCTGAGACA	10313	
	ENEDRAAGNIITVQLQKQVPYFRKKEKIESATLRKPLVLSYIIPAYNSKYIVRC		ENEDRAAGNIITVQLQKQVPYFRKKEKIESATLRKPLVLSYIIPAYNSKYIVRC					
	VESALNQTITDLEVCICDGGSTDRLILQEHYANHPVRVFIISOKNKGIGSASNTAVR		VESALNQTITDLEVCICDGGSTDRLILQEHYANHPVRVFIISOKNKGIGSASNTAVR					
	LCRGFYIGOLDSDDFLPDVELCLDFRKLDSLACVYTTNRNIDRGNLISNGYNWP		LCRGFYIGOLDSDDFLPDVELCLDFRKLDSLACVYTTNRNIDRGNLISNGYNWP					
gene	IYSEKLTSMACHHFMPTARAKNLTEGFENESIENAVDYDMYLKLEVPGFHINKI		IYSEKLTSMACHHFMPTARAKNLTEGFENESIENAVDYDMYLKLEVPGFHINKI		10318	CAAACGATATGTTTGGCGGGGAAAAAGAAAAGAGCTTGATGATATATCCAGAAAACAGT	10255	
	CYNRVLGENTSIKKLDIQENHFKFVNESLSRLGIKKYKSPITNLNECRKYYTEKI		CYNRVLGENTSIKKLDIQENHFKFVNESLSRLGIKKYKSPITNLNECRKYYTEKI					
	complement (10995. .12635)		complement (10995. .12635)					
	/gene="kfoB"		/gene="kfoB"					
CDS	complement (10995. .12635)		complement (10995. .12635)		524	TTACATTTAGCCTGTTTAGTAAACCCAAAACACATTTACCCGTTTGAAGTTTTCGTGACAG	583	
	/gene="kfoB"		/gene="kfoB"					
	/codon_start=1		/codon_start=1					
	/transl_table=11		/transl_table=11					
gene	/product="kfoB hypothetical protein"		/product="kfoB hypothetical protein"		10198	TTACACTTCTGCTCTTTGTAACCCAAAAGACCATATACGACTATGAGTTATTGTTGCCG	10133	
	/protein_id="BAC00524.1"		/protein_id="BAC00524.1"					
	/db_xref="GI:2132678"		/db_xref="GI:2132678"					
	/translation="MNRILVGHPSNNVQIVVEILLHORGMNSLCPKRDNLSPODITQ		/translation="MNRILVGHPSNNVQIVVEILLHORGMNSLCPKRDNLSPODITQ					
CDS	TLRKAYQSPDIYTTDSADPEPLHVSTVWNGIALDLMSLNKLKCGSDPNALHTLE		TLRKAYQSPDIYTTDSADPEPLHVSTVWNGIALDLMSLNKLKCGSDPNALHTLE		584	ATGATCGTGTAGTCAGGAAGATCTATCACCGCATCATTCGCCAATATGAAAAATAAATTGGATA	643	
	YWKSVDENITPILYDHPKSLITNYFSDQNISSNYTSEHLIKNKLAYNTALLHFFLN		YWKSVDENITPILYDHPKSLITNYFSDQNISSNYTSEHLIKNKLAYNTALLHFFLN					
	RGRCLVSSSEQVKNADCTQQLQHLKLFGLFSNTINHSLEQSVNDFKTAESIT		RGRCLVSSSEQVKNADCTQQLQHLKLFGLFSNTINHSLEQSVNDFKTAESIT					
	LEKEHQIMSLSGDIDTGDIIIPKQSETEYLIIFNLVNDYDCKELYFELQSNANTPL		LEKEHQIMSLSGDIDTGDIIIPKQSETEYLIIFNLVNDYDCKELYFELQSNANTPL					
gene	RVLRKENVKPSFIWETPKQROIITLDVNGLYQSSKKIILDNELHLSKOLNAYQAILK		RVLRKENVKPSFIWETPKQROIITLDVNGLYQSSKKIILDNELHLSKOLNAYQAILK		644	TTGCGTCTAGCTCAGAAAAAGATTAACGGTTTTCAGACCACTGCCGCTCGGAATATCGGAT	703	
	ELSDSKEELQYDILIKNKTIOVELECAIENFESLLAKKQNKNELOOQRLKLSCEK		ELSDSKEELQYDILIKNKTIOVELECAIENFESLLAKKQNKNELOOQRLKLSCEK					
	ELLNLQHLVQOQLEQFIDNQRLEKQLPELYGAERIITQDIGRLGAVNVSRKTF		ELLNLQHLVQOQLEQFIDNQRLEKQLPELYGAERIITQDIGRLGAVNVSRKTF					
	LGLSIPFALISWEKRTKYDSEYQSLPSFIYADKHEARVKKHLSYQLGKLIIIN		LGLSIPFALISWEKRTKYDSEYQSLPSFIYADKHEARVKKHLSYQLGKLIIIN					
gene	QNHPPLGLISLPFSIYIRIQRFRTKNSQVGVKYCGK"		QNHPPLGLISLPFSIYIRIQRFRTKNSQVGVKYCGK"		10078	TAAATATGTACGTCAGAAAGGATTATGGAATATCAACTGTGTGCTGTAGAAAATCTTTGGGC	10011	
	complement (12822. .13841)		complement (12822. .13841)					
	/gene="kfoA"		/gene="kfoA"					
	complement (12822. .13841)		complement (12822. .13841)					
CDS	/gene="kfoA"		/gene="kfoA"		824	CAAGAAAATACATCGATACACAACATATTGACCCAAAAGACTTCTTAAATATACCGCAGTT	883	
	/codon_start=1		/codon_start=1					
	/transl_table=11		/transl_table=11					
	/product="UDP-glucose 4-epimerase"		/product="UDP-glucose 4-epimerase"					
gene	/protein_id="BAC00525.1"		/protein_id="BAC00525.1"		9898	CTAGAAAAATATATAGATACAAAGACGATACATATTTAGTATTCTTTTCCCAAAAATAC	9839	
	/db_xref="GI:2132678"		/db_xref="GI:2132678"					
	/translation="MNLIVTGAGYIGSHTSLCLLNKYNVVIIDNLINSSCESIRRI		/translation="MNLIVTGAGYIGSHTSLCLLNKYNVVIIDNLINSSCESIRRI					
	ELIAKKKVPFVELNINEKEVQILKKHKFDCIMHFAGAKSVAESLIIKPIFYDNNVS		ELIAKKKVPFVELNINEKEVQILKKHKFDCIMHFAGAKSVAESLIIKPIFYDNNVS					
CDS	GTQLINCAIKNDVLANIFSSSATVYGESKIMPTVEDCHIGGTLNPGYTSKYSIELMI		GTQLINCAIKNDVLANIFSSSATVYGESKIMPTVEDCHIGGTLNPGYTSKYSIELMI		943	RDLAKYSDTNLCVFNPTGSAHESGMIGESPADIPSNLVPYILOVAMGKLEKLVF	9779	
	GGDYPTKDGTVGRDYIHWMDLAEGHVAALSYPFRDNTNTHVFNLTGKGYSLVELVS		GGDYPTKDGTVGRDYIHWMDLAEGHVAALSYPFRDNTNTHVFNLTGKGYSLVELVS					
	TFEKISGVRIPFYEIVSRDGDIAESWSSPEKAYLNWKAKELELTMLEDAWRQMKN		TFEKISGVRIPFYEIVSRDGDIAESWSSPEKAYLNWKAKELELTMLEDAWRQMKN					
	complement (10995. .12635)		complement (10995. .12635)					





**THIS PAGE BLANK (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 04:18:45 ; Search time 1579 Seconds  
(without alignment)  
12324.827 Million cell updates/sec

Title: US-10-642-248-1  
Perfect score: 2920  
Sequence: 1 atgaatacattatcacaaac.....taatagataactctataaa 2920

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 21.\*  
1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2917.4	99.9	2937	2	Aax58857 Pasteurel
2	2917.4	99.9	2937	3	Aax35589 P. multoc
3	2917.4	99.9	2937	10	Adc77478 Pasteurel
4	2917.4	99.9	2937	10	Add93925 Pasteurel
5	2914.4	99.8	2916	9	Abt44090 Pasteurel
6	2271.2	77.8	2979	6	Aaa27449 P. multoc
7	2271.2	77.8	2979	6	Abao5097 Pasteurel
8	2271.2	77.8	2979	11	Adp75648 Pasteurel
9	2267.8	77.7	2271	11	Adp75667 Pasteurel
10	2266.4	77.6	2979	6	Abao5098 Pasteurel
11	2266.4	77.6	2979	11	Adp75650 Pasteurel
12	2266.4	77.6	2979	14	Aea04966 Chondroit
13	2110.4	72.3	2112	14	Aea04964 Hyaluron
14	2108.8	72.2	2112	3	Aaa27448 P. multoci
15	2108.8	72.2	2112	11	Adp75718 Pasteurel
16	2107.2	72.2	2112	11	Adp75665 Pasteurel
17	2107.2	72.2	2112	11	Adp75695 Pasteurel
18	2107.2	72.2	2112	11	Adp75658 Pasteurel
19	2107.2	72.2	2112	11	Adp75680 Pasteurel

20	2107.2	72.2	2112	11	Adp75681 Pasteurel
21	2107.2	72.2	2112	11	Adp75684 Pasteurel
22	2107.2	72.2	2112	11	Adp75689 Pasteurel
23	2107.2	72.2	2112	11	Adp75663 Pasteurel
24	2107.2	72.2	2112	11	Adp75686 Pasteurel
25	2107.2	72.2	2112	11	Adp75696 Pasteurel
26	2107.2	72.2	2112	11	Adp75687 Pasteurel
27	2107.2	72.2	2112	11	Adp75687 Pasteurel
28	2107.2	72.2	2112	11	Adp75690 Pasteurel
29	2107.2	72.2	2112	11	Adp75692 Pasteurel
30	2107.2	72.2	2112	11	Adp75659 Pasteurel
31	2107.2	72.2	2112	11	Adp75693 Pasteurel
32	2105.6	72.1	2112	11	Adp75664 Pasteurel
33	2105.6	72.1	2112	11	Adp75682 Pasteurel
34	2105.6	72.1	2112	11	Adp75688 Pasteurel
35	2105.6	72.1	2112	11	Adp75666 Pasteurel
36	2105.6	72.1	2112	11	Adp75694 Pasteurel
37	2105.6	72.1	2112	11	Adp75691 Pasteurel
38	2105.6	72.1	2112	11	Adp75697 Pasteurel
39	2105.6	72.1	2112	11	Adp75685 Pasteurel
40	2073.6	71.0	2136	11	Adp75698 Pasteurel
41	2057.4	70.5	2061	11	Adp75679 Pasteurel
42	2002.4	68.6	2007	11	Adp75678 Pasteurel
43	1975.4	67.7	1980	11	Adp75674 Pasteurel
44	1949.8	66.8	1953	11	Adp75657 Pasteurel
45	1898.4	65.0	1902	11	Adp75675 Pasteurel

ALIGNMENTS

RESULT 1  
AAX58857  
ID AAX58857 standard; DNA; 2937 BP.  
XX  
AC AAX58857;  
XX  
DT 16-AUG-1999 (first entry)  
XX  
DE Pasteurella multocida hyaluronate synthase pmHAS DNA.  
XX  
KW Hyaluronate synthase; pmHAS; hyaluronic acid; hyaluronan; ss.  
XX  
OS Pasteurella multocida.  
XX  
FH Key Location/Qualifiers  
FT CDS 19..2937  
FT FT /\*tag= a  
XX  
PN WO9923227-A2.  
XX  
PD 14-MAY-1999.  
XX  
PF 30-OCT-1998; 98WO-US023153.  
XX  
PR 31-OCT-1997; 97US-0064435P.  
PR 26-OCT-1998; 98US-00178851.  
XX  
PA (OKLA ) UNIV OKLAHOMA STATE.  
XX  
PI Weigel PH, Kumari K, Deangelis P;  
XX  
DR WPI: 1999-137486/28.  
XX  
DR P-PSDB; AAY06212.  
XX  
CC Nucleic acid encoding hyaluronate synthase for production of hyaluronic acid with controlled molecular weight and targeting specificity.  
XX  
CC Disclosure; Page 123-125; 125pp; English.  
XX  
CC This DNA sequence codes for the hyaluronate synthase (pmHAS, see AAY06212) of Pasteurella multocida Carter type A. The pmHAS enzyme has different kinetic optima with respect to pH and metal ion dependence, and

CC different Km values compared with the HAS enzymes of Streptococcus  
CC equisimilis (see AY06206) and Streptococcus pyogenes. Km values are  
CC about 2- to 3-fold lower for UDP sugars, and Vmax values are about 2-  
CC 3-fold higher. The invention provides recombinant vectors containing  
CC hyaluronate synthase DNA, especially S. equisimilis hyaluronate synthase  
CC DNA (see AA58841), and prokaryotic or eukaryotic host cells which  
CC produce the enzyme and its hyaluronic acid product, particularly a  
CC product with modified structure or molecular size. The hyaluronic acid  
CC produced this way is purer than that produced by conventional methods  
XX  
SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Query Match 99.9%; Score 2917.4; DB 2; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGAATACATATATCACAGCAATATAAGCATATATAACAGCAATGACTATCAATTAGCACTC	60
Db	19	ATGAATACATATATCACAGCAATATAAGCATATATAACAGCAATGACTATCAATTAGCACTC	78
Qy	61	AAATTATTTGAAAGTCGGCGGAATCTATGACGCGGAAATTTGTTGAATTTCAAATTACC	120
Db	79	AAATTATTTGAARAGTCGGCGGAATCTATGACGCGGAAATTTGTTGAATTTCAAATTACC	138
Qy	121	AAATGCAAGAAATCTCTAGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	180
Db	139	AAATGCCAAGAAATCTCTAGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	198
Qy	181	AAAGAAGAAAGTCAATGTTTGGATAGTCGTTTGTAGTATTTGCAACACACTGTTACTT	240
Db	199	AAAGAAGAAAGTCAATGTTTGGATAGTCGTTTGTAGTATTTGCAACACACTGTTACTT	258
Qy	241	TCCAACGTAAATAATTAGTACTTTCTGACTCGGAAATAAACAAGTAAATAATAATGG	300
Db	259	TCCAACGTAAATAATTAGTACTTTCTGACTCGGAAATAAACAAGTAAATAATAATGG	318
Qy	301	AAATTGCTCACTGAGAGAAATCTGAAATTCGGAGGTAAAGCGGTCGCCCTTGTACCA	360
Db	319	AAATTGCTCACTGAGAGAAATCTGAAATTCGGAGGTAAAGCGGTCGCCCTTGTACCA	378
Qy	361	AAAGATTTTCCAAAGATCTGGTTTACGCGCTTTTACTGATCATGTTAATGATTTTACA	420
Db	379	AAAGATTTTCCAAAGATCTGGTTTACGCGCTTTTACTGATCATGTTAATGATTTTACA	438
Qy	421	TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACATGTTGGCTT	480
Db	439	TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAAACATCAACATGTTGGCTT	498
Qy	481	TCTATTATCGTTAACAATTCGACCGACGCAATTTTATCGATTACATTTAGCCTGTTTA	540
Db	499	TCTATTATCGTTAACAATTCGACCGACGCAATTTTATCGATTACATTTAGCCTGTTTA	558
Qy	541	GTAACCAAAAACACATTTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Db	559	GTAACCAAAAACACATTTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	618
Qy	601	GATCTATCACCGATCATTCGCGCAATATGAAATAAAATTTGGAATTTTCGCTAGCTCAGCAA	660
Db	619	GATCTATCACCGATCATTCGCGCAATATGAAATAAAATTTGGAATTTTCGCTAGCTCAGCAA	678
Qy	661	AAAGATAACCGTTTTCAGGCGAGTCCGCTCGGAAATATGGGATATCGCTTAGGCAAAATAT	720
Db	679	AAAGATAACCGTTTTCAGGCGAGTCCGCTCGGAAATATGGGATATCGCTTAGGCAAAATAT	738
Qy	721	GACTTTATTCGCTTACTCGATGATATGGCCCAATCCATTTAGGGTTCACTTCTAT	780
Db	739	GACTTTATTCGCTTACTCGATGATATGGCCCAATCCATTTAGGGTTCACTTCTAT	798
Qy	781	GTTGCGAGCTATTAGAGAGATGATTTTAAACAATCATTTGGTCCAAAGAAATAACATCGAT	840
Db	799	GTTGCGAGCTATTAGAGAGATGATTTTAAACAATCATTTGGTCCAAAGAAATAACATCGAT	858
Qy	841	ACACAACATATTGACCCCAAGAGACTTTCTTAATAAATACCGGAGTTTGTGTAATCATATTACCA	900

Db	859	ACACAACATATTGACCCCAAGAGACTTCTTAATAACGCGAGTTTGTGTAATCATATTACCA	918
Qy	901	GAAGTGAAACCAATTAATAGTGTTCGCCCAAAAGGGGAAGAAACAGTTCTCTGGATTGG	960
Db	919	GAAGTGAAACCAATTAATAGTGTTCGCCCAAAAGGGGAAGAAACAGTTCTCTGGATTGG	978
Qy	961	CGTTTAGACAATTCGAAACCAAGAAATCTCCGCTTATCCGATTCGCTTCCGCTTTT	1020
Db	979	CGTTTAGACAATTCGAAACCAAGAAATCTCCGCTTATCCGATTCGCTTCCGCTTTT	1038
Qy	1021	TTTGGCGCGGTAAATGTTGCTTTTCCGCTTAAATAATGCTAAATAAATCCGCTTCTTTGAT	1080
Db	1039	TTTGGCGCGGTAAATGTTGCTTTTCCGCTTAAATAATGCTAAATAAATCCGCTTCTTTGAT	1098
Qy	1081	GAGGAATTTTAATCACTCGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGCTTAC	1140
Db	1099	GAGGAATTTTAATCACTCGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGCTTAC	1158
Qy	1141	GGTAGTTTCTTTAAACCTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCAGGTAAA	1200
Db	1159	GGTAGTTTCTTTAAACCTATTGATGGCATTTATGGCTTACCATCAAGAGCCACCAGGTAAA	1218
Qy	1201	GAATAATGAAACCGATCGTGAAGCGGAAATAATATTACGCTCGATATTTAGAGAGAAAAG	1260
Db	1219	GAATAATGAAACCGATCGTGAAGCGGAAATAATATTACGCTCGATATTTAGAGAGAAAAG	1278
Qy	1261	GTCCCTTATATCTATAGAAAATTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT	1320
Db	1279	GTCCCTTATATCTATAGAAAATTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT	1338
Qy	1321	TTAGTTTCAATTTATATCCAGCTTTAATCTGTCGAAATCTATATTCAACGTTGCGGTAGAT	1380
Db	1339	TTAGTTTCAATTTATATCCAGCTTTAATCTGTCGAAATCTATATTCAACGTTGCGGTAGAT	1398
Qy	1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGCTTGTATTTGTAAACAGTGGTTCAACA	1440
Db	1399	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGCTTGTATTTGTAAACAGTGGTTCAACA	1458
Qy	1441	GATAATACCTTTAGAAGTGATCAATAAGCTTTTATGGTAATAATCCTAGGGTACGCATCATG	1500
Db	1459	GATAATACCTTTAGAAGTGATCAATAAGCTTTTATGGTAATAATCCTAGGGTACGCATCATG	1518
Qy	1501	TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCCGCTTTCTTTTGTAAAGGT	1560
Db	1519	TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCCGCTTTCTTTTGTAAAGGT	1578
Qy	1561	TATTACATTCGGCAGTTAGATTTCAGATGATTATCTTGAGCTTGATGCAAGTTGAACCTGCT	1620
Db	1579	TATTACATTCGGCAGTTAGATTTCAGATGATTATCTTGAGCTTGATGCAAGTTGAACCTGCT	1638
Qy	1621	TTAAAGAAATTTTAAAGATATAAAGCTAGCTTGTGTTTATACCACTAAATAGAAACGTC	1680
Db	1639	TTAAAGAAATTTTAAAGATATAAAGCTAGCTTGTGTTTATACCACTAAATAGAAACGTC	1698
Qy	1681	AATCCGATGGTAGCTTTAATCGCTTAATGGTTTACAATTTGGCCGAGAAATTTTCAGAGAAAA	1740
Db	1699	AATCCGATGGTAGCTTTAATCGCTTAATGGTTTACAATTTGGCCGAGAAATTTTCAGAGAAAA	1758
Qy	1741	CTCAACACGCTATGATGCTCACCCTTTAGAAATGTTACGATTAGAGCTTGGCATTTTA	1800
Db	1759	CTCAACACGCTATGATGCTCACCCTTTAGAAATGTTACGATTAGAGCTTGGCATTTTA	1818
Qy	1801	ACTGATGGATTCATGAAAAAATTTGAAATATGCGGTAGACTATGACATGTTCTCTCAAACTC	1860
Db	1819	ACTGATGGATTCATGAAAAAATTTGAAATATGCGGTAGACTATGACATGTTCTCTCAAACTC	1878
Qy	1861	AGTGAAGTGGAAATTTTAAACATCTTTAATAAATCTGCTTATTAACCGTGTATTTACATGGT	1920
Db	1879	AGTGAAGTGGAAATTTTAAACATCTTTAATAAATCTGCTTATTAACCGTGTATTTACATGGT	1938
Qy	1921	GATAACACATCAATTAAGAAACTTGGCATTCAGAAAGAAACCACTTTTGTGTAGTCAAT	1980

Db 1939 GATAACACATCAATTAAGAAACCTTGGCATTCAAAAGAAAAACCAATTTTGGTTGTAGTCAAT 1998  
Qy 1981 CAGTCATTTAAATAGACAGGCATTAACCTATTATATATATGACGAATTTTGATGATTTAGAT 2040  
Db 1999 CAGTCATTTAAATAGACAGGCATTAACCTATTATATATATGACGAATTTTGATGATTTAGAT 2058  
Qy 2041 GAAAGTGAAGATATATTTTCAATAAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA 2100  
Db 2059 GAAAGTGAAGATATATTTTCAATAAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA 2118  
Qy 2101 AAAGATATTTAAATCATCCAGATTAAGATGCGCAAAATCGCAGTCAGTATTTTATATCCC 2160  
Db 2119 AAAGATATTTAAATCATCCAGATTAAGATGCGCAAAATCGCAGTCAGTATTTTATATCCC 2178  
Qy 2161 AATACATTTAAACGGCTTAGTGAAGAACTTAACCAATATTTTGAATATAAATAAATAATA 2220  
Db 2179 AATACATTTAAACGGCTTAGTGAAGAACTTAACCAATATTTTGAATATAAATAAATAATA 2238  
Qy 2221 TTCGTTATTTCTACATGTTGATGAAGATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2239 TTCGTTATTTCTACATGTTGATGAAGATCATCTTACACAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCTTCTATCATATAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTTAC 2340  
Db 2299 CTAGCCTTCTATCATATAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTTAC 2358  
Qy 2341 ACGAGTATAGATTAATAAAACTGAGGGCATTTTAAGTAAATTAATAAATTAAGTCAG 2400  
Db 2359 ACGAGTATAGATTAATAAAACTGAGGGCATTTTAAGTAAATTAATAAATTAAGTCAG 2418  
Qy 2401 TTAATATCTAAATTTGTAATACATCATCTTTTGAATATCATGACAGCCTATTCGTTAAAAAT 2460  
Db 2419 TTAATATCTAAATTTGTAATACATCATCTTTTGAATATCATGACAGCCTATTCGTTAAAAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAAAATATGATGTCGCATGAATTTCTCAGCATTAACAT 2520  
Db 2479 GACAGCTATGCTTATATGAAAAATATGATGTCGCATGAATTTCTCAGCATTAACAT 2538  
Qy 2521 GATTGATCGAAAAATCAATCGCATCCACCATTTTAAAGCTCATTAATACTTATTTT 2580  
Db 2539 GATTGATCGAAAAATCAATCGCATCCACCATTTTAAAGCTCATTAATACTTATTTT 2598  
Qy 2581 AATGCAATGACTTTAAAGATGATGAATGTAAGGGGCATCAAGGATGTTTATGAGC 2640  
Db 2599 AATGCAATGACTTTAAAGATGATGAATGTAAGGGGCATCAAGGATGTTTATGAGC 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCATCACATCTTGCAGTCA 2700  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCATCACATCTTGCAGTCA 2718  
Qy 2701 ATTGATAGTGCAGAAATATTAACACTGAGGATATTTGTTCCNATTTGCACTTTTAAATC 2760  
Db 2719 ATTGATAGTGCAGAAATATTAACACTGAGGATATTTGTTCCNATTTGCACTTTTAAATC 2778  
Qy 2761 TTAGAAAGAAACCGGCCATGTTATTTAATAAACAATCGACCTGACTTATATGCTCTGG 2820  
Db 2779 TTAGAAAGAAACCGGCCATGTTATTTAATAAACAATCGACCTGACTTATATGCTCTGG 2838  
Qy 2821 GAACGAAATTTCAATATGGAACAAATGAACAAATTTGAAGTGCACAAAGAGAGAAATATA 2880  
Db 2839 GAACGAAATTTCAATATGGAACAAATGAACAAATTTGAAGTGCACAAAGAGAGAAATATA 2898  
Qy 2881 CCGTTTAAACAGTTTCATTTAATAGTATTAATCTCTATAA 2919  
Db 2899 CCGTTTAAACAGTTTCATTTAATAGTATTAATCTCTATAA 2937

## RESULT 2

AAZ35589

ID AAZ35589 standard; DNA; 2937 BP.

XX

AC AAZ35589;

XX

DT 06-AUG-2003 (revised)  
DT 01-FEB-2000 (first entry)  
XX  
DE P. multocida hyaluronate synthase (PmHAS) nucleotide sequence.  
XX  
KW Hyaluronate synthase; PmHAS; hyaluronan; hyaluronic acid; HA; cosmetic;  
KW drug delivery; angiogenesis; wound healing; capsule synthesis;  
KW fowl cholera; shipping fever; ss.  
XX  
OS Pasteurella multocida.  
XX  
FH Key Location/Qualifiers  
FH CDS 19. .2937  
FT /\*tag= a  
FT /product= "PmHAS"  
FT /note= "Hyaluronate synthase"  
XX  
PW W09951265-A1.  
XX  
PD 14-OCT-1999.  
XX  
PF 01-APR-1999; 99WO-US007289.  
XX  
PR 02-APR-1998; 98US-0080414P.  
PR 26-OCT-1998; 98US-00178851.  
XX  
PA (OKLA ) UNIV OKLAHOMA.  
XX  
PI Deangelis P;  
XX  
DR WPI; 2000-013032/01.  
XX P-PSDB; AAY43099.  
PT New isolated hyaluronate synthase nucleic acids, used for the production  
PT of hyaluronic acid, for developing antibiotics and vaccines and for  
PT diagnostic applications.  
XX  
PS Claim 3; Page 113-114; 121pp; English.  
XX  
CC This is the Pasteurella multocida hyaluronate synthase (PmHAS) nucleic  
CC acid sequence. Hyaluronic acid (HA) or hyaluronan, is a polysaccharide  
CC that serves both structural and recognition roles in higher animals.  
CC Bacteria produce extracellular capsules of HA which mimic their host HA  
CC and aid escape from a host immune response. The invention includes a  
CC vector containing the PmHAS nucleotide sequence which can be used to  
CC express PmHAS in a foreign host. The HS nucleic acids can be used for the  
CC production of HA. Also, specific changes to the HS coding sequence can  
CC result in the production of HA having a modified size distribution or  
CC structural configuration and functional properties. The HA products can  
CC be used in e.g. drug delivery, angiogenesis and wound healing.  
CC stabilization of recombinant proteins and in cosmetics. The HS nucleic  
CC acids can also be used to develop agents to block capsule synthesis by  
CC pathogens and act as antibiotics. The avirulent P. multocida strains can  
CC be used as vaccines for fowl cholera or shipping fever. (Updated on 06-  
CC AUG-2003 to correct OS field.)  
XX  
SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Query Match 99.9%; Score 2917.4; DB 3; Length 2937;  
Best Local Similarity 100.0%; Fred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTTAGCACTC 60  
Db 19 ATGAATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTTAGCACTC 78  
Qy 61 AAATTTATTTTGAAGAGTCGCGGAAATCTATGAGCGGAAATTTGTTGAATTTCAATTACC 120  
Db 79 AAATTTATTTTGAAGAGTCGCGGAAATCTATGAGCGGAAATTTGTTGAATTTCAATTACC 138  
Qy 121 AAATGCAAGAAAGAACTCTCAGCACATCTTCTGTTAATTTACGACATCTTTCTGTAAT 180  
Db 139 AAATGCAAGAAAGAACTCTCAGCACATCTTCTGTTAATTTACGACATCTTTCTGTAAT 198

181 AAAGAGAAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACAACTGTACTTT 240  
199 AAAGAGAAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACAACTGTACTTT 258  
241 TCCAAAGTAAAAAAATTTAGTACTTTCTGACTCGCGAAAAAACAAGCTTTAAAAAATAAATGG 300  
259 TCCAAAGTAAAAAAATTTAGTACTTTCTGACTCGCGAAAAAACAAGCTTTAAAAAATAAATGG 318  
301 AAATTTGCTCAGTGAAGAGAAATCTGAAATTCGAGAGGTAAAGAGCGGTGCGCCCTTGTACCA 360  
319 AAATTTGCTCAGTGAAGAGAAATCTGAAATTCGAGAGGTAAAGAGCGGTGCGCCCTTGTACCA 378  
361 AAAGATTTTCCAAAGATCTGTTTTAGCGGCTTTTACCTGATCATGTTAATGATTTTACA 420  
379 AAAGATTTTCCAAAGATCTGTTTTAGCGGCTTTTACCTGATCATGTTAATGATTTTACA 438  
421 TGGTACAAAAGCGAAGAAAGACTTTGGCAATAAAACCTGAAACATCAACATGTTGGTCTT 480  
439 TGGTACAAAAGCGAAGAAAGACTTTGGCAATAAAACCTGAAACATCAACATGTTGGTCTT 498  
481 TCTATTATCGTTTACAAACATTTCAATCGACACAGCAATTTTATCGATTACATTAGCCCTGTTA 540  
499 TCTATTATCGTTTACAAACATTTCAATCGACACAGCAATTTTATCGATTACATTAGCCCTGTTA 558  
541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
601 GATCTATCACCGATCATTGCGCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 660  
619 GATCTATCACCGATCATTGCGCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 678  
661 AAAGATAACCGTTTTCAGCCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAAATAT 720  
679 AAAGATAACCGTTTTCAGCCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAAATAT 738  
721 GACTTTATGCGCTTACTCGCATGTGATGATGCGGCCAAATCCATTATGGGTTTCATCTTTAT 780  
739 GACTTTATGCGCTTACTCGCATGTGATGATGCGGCCAAATCCATTATGGGTTTCATCTTTAT 798  
781 GTTCAGAGCTATTAGAGATGATGATTTACAACTATTGCTCCAGAAATACATCGAT 840  
799 GTTCAGAGCTATTAGAGATGATGATTTACAACTATTGCTCCAGAAATACATCGAT 858  
841 ACACAACATATTGACCCCAAAAGACTTCTTAATAAACGCGAGTTTGTGTAATCATTACCA 900  
859 ACACAACATATTGACCCCAAAAGACTTCTTAATAAACGCGAGTTTGTGTAATCATTACCA 918  
901 GAAGTAAAAACCAATAATAGTGTGCGCCAAAGAGGAAAGGAAACAGTGTCTCGATGG 960  
919 GAAGTAAAAACCAATAATAGTGTGCGCCAAAGAGGAAAGGAAACAGTGTCTCGATGG 978  
961 CGCTTAGAACCAATTCGAAABAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020  
979 CGCTTAGAACCAATTCGAAABAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1038  
1021 TTTGCGGCGGTAAATGTTGCTTTTCGCTAAAAAATGGCTTAAATAAATCCGGTTTCTTTGAT 1080  
1039 TTTGCGGCGGTAAATGTTGCTTTTCGCTAAAAAATGGCTTAAATAAATCCGGTTTCTTTGAT 1098  
1081 GAGAAATTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1140  
1099 GAGAAATTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1158  
1141 GGTAGTTTCTTTAAACCTATTGATGGCAATTATGGCTTACCATCAAGACCCACAGGTAAA 1200  
1159 GGTAGTTTCTTTAAACCTATTGATGGCAATTATGGCTTACCATCAAGACCCACAGGTAAA 1218  
1201 GAAATGAACCGATCGTGAAGCGGGAAGAAATATTACGCTCGATATTATGAGAGAAAAG 1260  
1219 GAAATGAACCGATCGTGAAGCGGGAAGAAATATTACGCTCGATATTATGAGAGAAAAG 1278

1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTGCGATATCAATAGAGTACCT 1320  
1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTGCGATATCAATAGAGTACCT 1338  
1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1398  
1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGCTTCAACA 1440  
1399 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGCTTCAACA 1458  
1441 GATAATACCTTTAGAACTGATCAATAAGCTTTATGTTAAATCTTAGGGTACGCAATCATG 1500  
1459 GATAATACCTTTAGAACTGATCAATAAGCTTTATGTTAAATCTTAGGGTACGCAATCATG 1518  
1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCGAGCCGTTTCTTTTGTAAAGGT 1560  
1519 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCGAGCCGTTTCTTTTGTAAAGGT 1578  
1561 TATTACATTTGGGCACTTAGATTTCAGATGATTATCTTGAGCCTGATGCGAGTTGAACTGTGT 1620  
1579 TATTACATTTGGGCACTTAGATTTCAGATGATTATCTTGAGCCTGATGCGAGTTGAACTGTGT 1638  
1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
1639 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1698  
1681 AATCCGGATGTTAGCTTAAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCCAGAGAAAA 1740  
1699 AATCCGGATGTTAGCTTAAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCCAGAGAAAA 1758  
1741 CTCAACACGCTATGATGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1800  
1759 CTCAACACGCTATGATGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1818  
1801 ACTGATGGATTCATGAAATAAATTTGAAATGCGCTAGACTATGACATGTTTCTTCAAACTC 1860  
1819 ACTGATGGATTCATGAAATAAATTTGAAATGCGCTAGACTATGACATGTTTCTTCAAACTC 1878  
1861 AGTGAAAGTTGGAATAATTTAAACATCTTAAATAAATCTGCTTATAAACCCTGTATTACATGGT 1920  
1879 AGTGAAAGTTGGAATAATTTAAACATCTTAAATAAATCTGCTTATAAACCCTGTATTACATGGT 1938  
1921 GATAACACATCAATTTAAGAACTTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
1939 GATAACACATCAATTTAAGAACTTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1998  
1981 CAGTCATTAATAGAACGCATAAATTTATATAATTTATGACGAAATTTGTATGATTTAGAT 2040  
1999 CAGTCATTAATAGAACGCATAAATTTATATAATTTATGACGAAATTTGTATGATTTAGAT 2058  
2041 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAAGAGATTTGATATCTTA 2100  
2059 GAAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAAGAGATTTGATATCTTA 2118  
2101 AAAGATATTAATAATCATCCAGAAATAAGATGCCAAATATCGCAGTCAGTATTTTTTATCCC 2160  
2119 AAAGATATTAATAATCATCCAGAAATAAGATGCCAAATATCGCAGTCAGTATTTTTTATCCC 2178  
2161 AATACATTTAAACCGCTTAGTGAAAAAACTAAACAATATTATTGAAATATAATAAAAAATA 2220  
2179 AATACATTTAAACCGCTTAGTGAAAAAACTAAACAATATTATTGAAATATAATAAAAAATA 2238  
2221 TTTGTTATTTGTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280  
2239 TTTGTTATTTGTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2298  
2281 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
2299 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358  
2341 ACAGATTAATGATTTAATAAAAACTGAGGCGCATTTTAAAGTAAATATAATAATAAATAAGTCAG 2400



Db 2359 ACAGTAAATAGTAATAAATAAAGTACAGGCGCAATTTAAGTAATATTAATAAATTAAGTCAG 2418  
Qy 2401 TTAATCTTAATTTGTAATACATCATTTTTCATATCATGACAGCCTATTGTTAAATAAT 2460  
Db 2419 TTAATCTTAATTTGTAATACATCATTTTTCATATCATGACAGCCTATTGTTAAATAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAATTTTCTCAGCATTAACACAT 2520  
Db 2479 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAATTTTCTCAGCATTAACACAT 2538  
Qy 2521 GATTGATCGAGAAAAATCAATGCGCATCCACATTTTAAAAAGCTCATTTAAACCTTATTTT 2580  
Db 2539 GATTGATCGAGAAAAATCAATGCGCATCCACATTTTAAAAAGCTCATTTAAACCTTATTTT 2598  
Qy 2581 AATGACATGCTTAAAAAGTATGAATGTAAGAGGCGCATCAAGGTATGTTTATGACG 2640  
Db 2599 AATGACATGCTTAAAAAGTATGAATGTAAGAGGCGCATCAAGGTATGTTTATGACG 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTATCAACATCTTGCCAGTCA 2700  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGTATCAACATCTTGCCAGTCA 2718  
Qy 2701 ATTGATGCTGCCAGATATAAACAAGTATGATTTTGGTCCAAATTTGCACTTTTAAATC 2760  
Db 2719 ATTGATGCTGCCAGATATAAACAAGTATGATTTTGGTCCAAATTTGCACTTTTAAATC 2778  
Qy 2761 TTAGAAAAGAAAACCGGCATGATTTTAAACATGACCCCTGACCTATATGCTTGG 2820  
Db 2779 TTAGAAAAGAAAACCGGCATGATTTTAAACATGACCCCTGACCTATATGCTTGG 2838  
Qy 2821 GAACGAAATATCAATGACAAATCAACAAATTTGAAAGTGCAGAAAGAGGAGAAATATA 2880  
Db 2839 GAACGAAATATCAATGACAAATGACAAATTTGAAAGTGCAGAAAGAGGAGAAATATA 2898  
Qy 2881 CCTGTTAAAGTTCATTTAATTAAGTATACTCTATAA 2919  
Db 2899 CCTGTTAAAGTTCATTTAATTAAGTATACTCTATAA 2937

RESULT 3  
ADC77478  
ID ADC77478 standard; DNA; 2937 BP.  
XX AC ADC77478;  
XX AC ADC77478;  
XX 01-JAN-2004 (first entry)  
XX Pasteurella multocida hyaluronate synthase (HAS) gene sequence.  
XX hyaluronate synthase; HAS; streptococcal infection;  
XX streptococcal bacteria; phagocytic cell; foreign microorganism;  
XX polysaccharide capsule; hyaluronic acid capsule; HA capsule;  
XX antibacterial compound; bacterial infection; gene; ds.  
XX Pasteurella multocida.  
XX Pasteurella multocida.  
XX Key Location/Qualifiers  
FT CDS 19..2937  
FT /\*tag= a  
FT /product= "Pasteurella multocida hyaluronate synthase"  
XX US2003092118-A1.  
XX 15-MAY-2003.  
XX 13-JUN-2002; 2002US-00172527.  
XX 31-OCT-1997; 97US-0064435P.  
XX 26-OCT-1998; 98US-00178851.  
XX 21-DEC-1999; 99US-00469200.  
XX 13-JUN-2001; 2001US-0297744P.  
XX 13-JUN-2001; 2001US-0297788P.

XX (DEAN/) DEANGELIS P L.  
PA (WEIG/) WEIGEL P H.  
PA (KUMARI/) KUMARI K.  
XX Deangelis PL, Weigel PH, Kumari K;  
XX WPI; 2003-755179/71.  
DR P-PSDB; ADC77479.  
XX Recombinant host cell is a Bacillus cell comprising a recombinant vector  
PT having purified nucleic acid segment with a coding region encoding  
PT enzymatically active hyaluronan synthase.  
XX Claim 106; SEQ ID NO 9; 79pp; English.  
XX This invention relates to a recombinant Bacillus host cell containing a  
CC recombinant vector including a nucleic acid segment with a coding region  
CC encoding enzymatically active hyaluronate synthase (HAS), where the  
CC coding region is under control of a promoter. The incidence of  
CC streptococcal infections is a major health and economic problem  
CC worldwide. Streptococcal bacteria can grow undetected by the body's  
CC phagocytic cells which are responsible for recognising and engulfing  
CC foreign microorganisms. One way the bacteria evades these cells is by  
CC coating themselves with polysaccharide capsules, such as a hyaluronic  
CC acid (HA) capsule. As HA is non-immunogenic, the encapsulated bacteria do  
CC not illicit an immune response. The present invention provides a means of  
CC preparing HA which may prove useful for the identification of novel  
CC antibacterial compounds for the treatment of bacterial infection. The  
CC present sequence is the DNA sequence which encodes the hyaluronate  
CC synthase (HAS) of Pasteurella multocida, used in the method of the  
CC invention.  
XX SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Query Match 99.9%; Score 2917.4; DB 10; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGAATACATTTATCAAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC 60  
Db 19 ATGAATACATTTATCAAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC 78  
Qy 61 AAATTTATTTGAAAGTTCGCGGAAATCTATGACGCGGAAATTTGTTGAATTTCAATTTACC 120  
Db 79 AAATTTATTTGAAAGTTCGCGGAAATCTATGACGCGGAAATTTGTTGAATTTCAATTTACC 138  
Qy 121 AAATGCAAGAAAAAAGTCTGACGACATCTTCTGTTAATTCAGCACATCTTTCTGTAAT 180  
Db 139 AAATGCAAGAAAAAAGTCTGACGACATCTTCTGTTAATTCAGCACATCTTTCTGTAAT 198  
Qy 181 AAAGAAGAAAAAGTCAATGTTTTCGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 240  
Db 199 AAAGAAGAAAAAGTCAATGTTTTCGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 258  
Qy 241 TCCACGCTAAAAAATTTAGTACTTTTCTGACTCGGAAAAAACAACCTTAAAAAATAAATGG 300  
Db 259 TCCACGCTAAAAAATTTAGTACTTTTCTGACTCGGAAAAAACAACCTTAAAAAATAAATGG 318  
Qy 301 AAATGCTCACTGAGAAATCTGAAAAATGCGGAGGTAAAGCGGCTGCGCTTGTACCA 360  
Db 319 AAATGCTCACTGAGAAATCTGAAAAATGCGGAGGTAAAGCGGCTGCGCTTGTACCA 378  
Qy 361 AAAGATTTTCCCAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
Db 379 AAAGATTTTCCCAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACA 438  
Qy 421 TGGTACAAAAAGCGGAAAGAAAGACTTGGCATAAAAACCTGAAACATCAACATGTTGCTTT 480  
Db 439 TGGTACAAAAAGCGGAAAGAAAGACTTGGCATAAAAACCTGAAACATCAACATGTTGCTTT 498  
Qy 481 TCTATTATCGTTTACAACTTCAATCGACGAGCAATTTTATCGATTACATTAGCCTGTTTA 540

Db	499	TCATTATCGTTACAA	CATTCAATCGACGACCAGCRAATTTTATCGATTACATTAGCCTGTTA	558	
Qy	541	GTAACCAAAAAACA	ATTACCCGTTTGAAAGTTATCGTGACAGATGATGTGTAGTCAGGAA	600	
Db	559	GTAACCAAAAAACA	TATTACCCGTTTGAAAGTTATCGTGACAGATGATGTGTAGTCAGGAA	618	
Qy	601	GATCTATCACC	GATCAATCGCCCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA	660	
Db	619	GATCTATCACC	GATCAATCGCCCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA	678	
Qy	661	AAAGATAACCGG	TTTTCAAGCCAGTGC	CGCTCGGAATATGGGATTAACGCTTAGCAAAATAT	720
Db	679	AAAGATAACCGG	TTTTCAAGCCAGTGC	CGCTCGGAATATGGGATTAACGCTTAGCAAAATAT	738
Qy	721	GACTTTATGGCT	TATCGACTGTGATATGGCGCCAAATTCATATATGGGTTCAATCTTAT	780	
Db	739	GACTTTATGGCT	TATCGACTGTGATATGGCGCCAAATTCATATATGGGTTCAATCTTAT	798	
Qy	781	GTTCGACAGCT	TATAGAGATGATGATTTAACATCATTTGCTCCAGAAATACATCGAT	840	
Db	799	GTTCGACAGCT	TATAGAGATGATGATTTAACATCATTTGCTCCAGAAATACATCGAT	858	
Qy	841	ACACAAATATGA	CCCAAAAGACTTCTTAAATAACCGAGTTTGTCTTGAATCAATTACCA	900	
Db	859	ACACAAATATGA	CCCAAAAGACTTCTTAAATAACCGAGTTTGTCTTGAATCAATTACCA	918	
Qy	901	GAAGTAAACCA	ATAATAGTGTTCGCGCAAAAGGGGAAGGAAACAGTTTCTCTGGATGG	960	
Db	919	GAAGTAAACCA	ATAATAGTGTTCGCGCAAAAGGGGAAGGAAACAGTTTCTCTGGATGG	978	
Qy	961	CGCTTAGAAC	CAATTCGAAACACAGAAATCTCCGCTTATCCCGATTCGCTTCGCTTTT	1020	
Db	979	CGCTTAGAAC	CAATTCGAAACACAGAAATCTCCGCTTATCCCGATTCGCTTCGCTTTT	1038	
Qy	1021	TTTCGGCGGG	TAAATGTTGCTTTTCGCTTAAATAAGGGCTTAAATAATCCGTTTCTTTGAT	1080	
Db	1039	TTTCGGCGGG	TAAATGTTGCTTTTCGCTTAAATAAGGGCTTAAATAATCCGTTTCTTTGAT	1098	
Qy	1081	GAGAAATTTA	ATCATCGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC	1140	
Db	1099	GAGAAATTTA	ATCATCGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC	1158	
Qy	1141	GGTAGTTCTT	TAAACATATTGATGGCATTTATGCGCTTACCATCAAGACCCACAGGTAAA	1200	
Db	1159	GGTAGTTCTT	TAAACATATTGATGGCATTTATGCGCTTACCATCAAGACCCACAGGTAAA	1218	
Qy	1201	GAAATGAAC	CCGATCGTGAACGGGAAAAATATTACGCTCCGATATTATCAGAGAAAAAG	1260	
Db	1219	GAAATGAAC	CCGATCGTGAACGGGAAAAATATTACGCTCCGATATTATCAGAGAAAAAG	1278	
Qy	1261	GTCCCTTATAT	CTATAGAAAACTTTTACCAATAGAAATTCGCATATCAATAGAGTACCT	1320	
Db	1279	GTCCCTTATAT	CTATAGAAAACTTTTACCAATAGAAATTCGCATATCAATAGAGTACCT	1338	
Qy	1321	TTAGTTTCAAT	TATATCCGAGCTTATACTGTGCAACTATATTCAACGTTGCGGTAGAT	1380	
Db	1339	TTAGTTTCAAT	TATATCCGAGCTTATACTGTGCAACTATATTCAACGTTGCGGTAGAT	1398	
Qy	1381	AGTGACCTGA	ATCAGACTGTGTTGATCTCGAGGTTTGTATTTGTAAACGATGTTTCAACA	1440	
Db	1399	AGTGACCTGA	ATCAGACTGTGTTGATCTCGAGGTTTGTATTTGTAAACGATGTTTCAACA	1458	
Qy	1441	GATAATACCT	TAGAGTGATCAATAAGCTTTATGTTAATATTCCTAGGGTACGATCATG	1500	
Db	1459	GATAATACCT	TAGAGTGATCAATAAGCTTTATGTTAATATTCCTAGGGTACGATCATG	1518	
Qy	1501	TCTAAACCAAT	GGCGAATAGCCTCAGCATCAATATGCGCGTTTCTTTTGTCTTAAAGGT	1560	
Db	1519	TCTAAACCAAT	GGCGAATAGCCTCAGCATCAATATGCGCGTTTCTTTTGTCTTAAAGGT	1578	
Qy	1561	TATTACATTTG	GGCAGTTAGATTGATTTATCTTTGACGCTGATGACAGTTGAACTGTG	1620	
Db	1579	TATTACATTTG	GGCAGTTAGATTGATTTATCTTTGACGCTGATGACAGTTGAACTGTG	1638	

Qy	1621	TTAAAAAGAA	TTTTTAAAGATAAAACGCTAGCTTGTGTTTTATACCACCTAATAGAAACGTC	1680
Db	1639	TTAAAAAGAA	TTTTTAAAGATAAAACGCTAGCTTGTGTTTTATACCACCTAATAGAAACGTC	1698
Qy	1681	AATCCGGATGG	TAGCTTAATCGCTAATGGTTACAAATTTGGCCAGAAATTTTCAAGAGAAAA	1740
Db	1699	AATCCGGATGG	TAGCTTAATCGCTAATGGTTACAAATTTGGCCAGAAATTTTCAAGAGAAAA	1758
Qy	1741	CTCAACCGCT	ATGATTTGCTCAACACTTTTAGAATGTTTACGATTTAGAGCTTGGCATTTA	1800
Db	1759	CTCAACCGCT	ATGATTTGCTCAACACTTTTAGAATGTTTACGATTTAGAGCTTGGCATTTA	1818
Qy	1801	ACTGATGGAT	TTCAATGAAAAATTTGAAATGCGGTAGACTATGACATGTTTCTTCAAACTC	1860
Db	1819	ACTGATGGAT	TTCAATGAAAAATTTGAAATGCGGTAGACTATGACATGTTTCTTCAAACTC	1878
Qy	1861	AGTGAAGTTG	GAATAATTTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT	1920
Db	1879	AGTGAAGTTG	GAATAATTTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT	1938
Qy	1921	GATAACA	CATCAATTAAGAACTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT	1980
Db	1939	GATAACA	CATCAATTAAGAACTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT	1998
Qy	1981	CAGTCAATTA	ATAAGAGGCATAACTTATTATAATTTATGACGAATTTGATGATTTAGAT	2040
Db	1999	CAGTCAATTA	ATAAGAGGCATAACTTATTATAATTTATGACGAATTTGATGATTTAGAT	2058
Qy	2041	GAAAGTAGAA	AGTATATTTTCAATAAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA	2100
Db	2059	GAAAGTAGAA	AGTATATTTTCAATAAAAACCGCTGAATATCAAGAAGAGATTTGATATCTTA	2118
Qy	2101	AAAGATATTA	AAAAATCATCCAGAAATAAGATGCCAAATTCGACGTCAGTATTTTTTATCCC	2160
Db	2119	AAAGATATTA	AAAAATCATCCAGAAATAAGATGCCAAATTCGACGTCAGTATTTTTTATCCC	2178
Qy	2161	AATACATATTA	AAACCGCTTAGTGAATAAACTAAACATATTATTGAATATAATAAAATATA	2220
Db	2179	AATACATATTA	AAACCGCTTAGTGAATAAACTAAACATATTATTGAATATAATAAAATATA	2238
Qy	2221	TTCGTTATTG	CTTCTACATGTTGATAAGAATCATCTTACACAGATATCAAAAAAGAAATA	2280
Db	2239	TTCGTTATTG	CTTCTACATGTTGATAAGAATCATCTTACACAGATATCAAAAAAGAAATA	2298
Qy	2281	CTAGCCTTCT	ATCATAAACATCAAGTGAATATTTTTACTAAATTAATGATATCTCATATTAC	2340
Db	2299	CTAGCCTTCT	ATCATAAACATCAAGTGAATATTTTTACTAAATTAATGATATCTCATATTAC	2358
Qy	2341	ACGAGTAAT	AGATTTAATAAACTGAGGCGCATTTAAGTAAATTAATAAAATTAAGTCAG	2400
Db	2359	ACGAGTAAT	AGATTTAATAAACTGAGGCGCATTTAAGTAAATTAATAAAATTAAGTCAG	2418
Qy	2401	TTAAATCTAA	ATTGTGAATACATTTTTTTGATAATCATGACAGCCTTATTCGTTAAAAAT	2460
Db	2419	TTAAATCTAA	ATTGTGAATACATTTTTTTGATAATCATGACAGCCTTATTCGTTAAAAAT	2478
Qy	2461	GACAGCTATG	CTTATGAAAAAATATGATGTGGCATGAATTTCTCAGCATTTAACACAT	2520
Db	2479	GACAGCTATG	CTTATGAAAAAATATGATGTGGCATGAATTTCTCAGCATTTAACACAT	2538
Qy	2521	GATTGGATCG	AGAAAAATCAATGCGCATCCACCTTTTAAAAAGCTCATTTAAACCTTATTTT	2580
Db	2539	GATTGGATCG	AGAAAAATCAATGCGCATCCACCTTTTAAAAAGCTCATTTAAACCTTATTTT	2598
Qy	2581	AATGACAATG	CACTTAAAAAGTATGAATGTGAAAGGGGCATCACAAAGGTATGTTTATGACG	2640
Db	2599	AATGACAATG	CACTTAAAAAGTATGAATGTGAAAGGGGCATCACAAAGGTATGTTTATGACG	2658
Qy	2641	TATCGCTAGC	GCATGAGCTTCTGACGATTTATTAAGAAGTCATCACATCTTGCCAGTCA	2700
Db	2659	TATCGCTAGC	GCATGAGCTTCTGACGATTTATTAAGAAGTCATCACATCTTGCCAGTCA	2718

Qy 2701 ATTGATAGTGTGCAGAAATATAACACATGAGGATATTTGGTTCCAAATTTGACATTTTAAATC 2760  
Db |||||||  
Qy 2719 ATTGATAGTGTGCAGAAATATAACACATGAGGATATTTGGTTCCAAATTTGACATTTTAAATC 2778  
Db |||||||  
Qy 2761 TTAGAAAGAAAACCGGCATGTATTTAAATAAACATCGACCCCTGACTTATATGCTTGG 2820  
Db |||||||  
Qy 2779 TTAGAAAGAAAACCGGCATGTATTTAAATAAACATCGACCCCTGACTTATATGCTTGG 2838  
Db |||||||  
Qy 2821 GAACGAAATTTACATGACAAATGAACAAATTCGAAAGTGCAGAAAGGAGGAGAAATATA 2880  
Db |||||||  
Qy 2839 GAACGAAATTTACATGACAAATGAACAAATTCGAAAGTGCAGAAAGGAGGAGAAATATA 2898  
Db |||||||  
Qy 2881 CCTGTTAAAGATTCATTATTAATAGTATATACTCTATAA 2919  
Db |||||||  
Qy 2899 CCTGTTAAAGATTCATTATTAATAGTATATACTCTATAA 2937  
Db |||||||

## RESULT 4

ID ADD93925 standard; DNA; 2937 BP.  
XX  
AC ADD93925;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Pasteurella multocida hyaluronan synthase gene.  
XX  
KW hyaluronan synthase; HAS; Streptococcal infection;  
KW Streptococcal bacterium; phagocytic cell; macrophage;  
KW polymorphonuclear cell; PMN; polysaccharide capsule; hyaluronic acid;  
KW HA capsule; vaccine; gene; ds.  
XX  
OS Pasteurella multocida.  
XX  
PN WO2003048330-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 03-DEC-2002; 2002WO-US038596.  
XX  
PR 03-DEC-2001; 2001US-0336105P.  
PR 11-DEC-2001; 2001US-0001171.  
XX  
PA (WEIG/) WEIGEL P H.  
PA (KUMARI) KUMARI K.  
XX  
PI Weigel PH, Kumari K;  
XX  
DR WPI: 2003-482708/45.  
DR P-PSDB; ADD93926.  
XX  
PT Novel functionally active hyaluronan synthase having at least one  
PT modified amino acid residue in it as compared to a corresponding  
PT functionally active native hyaluronan synthase, useful for producing  
PT hyaluronic acid.  
XX  
PS Disclosure; SEQ ID NO 7; 362pp; English.  
XX  
CC This invention relates to a novel functionally active hyaluronan synthase  
CC (HAS) having at least one modified amino acid residue in it or having  
CC altered enzymatic activity as compared to a corresponding functionally  
CC active native hyaluronan synthase. Streptococcal infection is a major  
CC health and economic problem worldwide, particularly in developing  
CC countries. Streptococcal bacteria can grow undetected by the body's  
CC phagocytic cells (macrophages and polymorphonuclear cells; PMNs). The  
CC bacteria can evade detection by coating itself with polysaccharide  
CC capsules, such as a hyaluronic acid (HA) capsule. The invention is useful  
CC for producing hyaluronic acid and may aid the production of therapeutics  
CC and vaccines against Streptococcal infection. The present sequence is the  
CC HAS gene of Pasteurella multocida which is related to the invention.  
XX  
SQ Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 U; 0 Other;

Query Match 99.9%; Score 2917.4; DB 10; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGATATCATTTATCACAAGCAATAAAGCATATATAACAGCAATGACTATCAATTAGCACTC 60  
Db |||||||  
Qy 19 ATGATATCATTTATCACAAGCAATAAAGCATATATAACAGCAATGACTATCAATTAGCACTC 78  
Db |||||||  
Qy 61 AAATATTTTGAAGTGTGGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAATTACC 120  
Db |||||||  
Qy 79 AAATATTTTGAAGTGTGGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAATTACC 138  
Db |||||||  
Qy 121 AAATGCAAGAAAACCTCTCAGCACATCTCTGTTAATTCAGCACATCTTCTGTTAAAT 180  
Db |||||||  
Qy 139 AAATGCAAGAAAACCTCTCAGCACATCTCTGTTAATTCAGCACATCTTCTGTTAAAT 198  
Db |||||||  
Qy 181 AAAGAAGAAAAGTCAATGTTGGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 240  
Db |||||||  
Qy 199 AAAGAAGAAAAGTCAATGTTGGGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 258  
Db |||||||  
Qy 241 TCCAAACGTAAATAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300  
Db |||||||  
Qy 259 TCCAAACGTAAATAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 318  
Db |||||||  
Qy 301 AAATGTCTACTGAGAGAAAATCTGAAAAATCGCGAGGTAGAGCGGTGCGCCCTGTACCA 360  
Db |||||||  
Qy 319 AAATGTCTACTGAGAGAAAATCTGAAAAATCGCGAGGTAGAGCGGTGCGCCCTGTACCA 378  
Db |||||||  
Qy 361 AAAGATTTTCCAAAGATCTGTTTTTAGCGCCTTTTACCTGATCATGTTAAATGATTTTACA 420  
Db |||||||  
Qy 379 AAAGATTTTCCAAAGATCTGTTTTTAGCGCCTTTTACCTGATCATGTTAAATGATTTTACA 438  
Db |||||||  
Qy 421 TGGTACAAAAAGCGAAAAAGAAAGACTTTGGCATATAAAACCTGAAACATCAACATGTTGGTCTT 480  
Db |||||||  
Qy 439 TGGTACAAAAAGCGAAAAAGAAAGACTTTGGCATATAAAACCTGAAACATCAACATGTTGGTCTT 498  
Db |||||||  
Qy 481 TCTATATTCGTTACAAATTCATTCGACCAAGCAATTTTATCGATACATTTAGCCTGTTTA 540  
Db |||||||  
Qy 499 TCTATATTCGTTACAAATTCATTCGACCAAGCAATTTTATCGATACATTTAGCCTGTTTA 558  
Db |||||||  
Qy 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db |||||||  
Qy 559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
Db |||||||  
Qy 601 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGATATTCGCTACGTCAGACAA 660  
Db |||||||  
Qy 619 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGATATTCGCTACGTCAGACAA 678  
Db |||||||  
Qy 661 AAAGATAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATTTAGCGTTAGCAAAATAT 720  
Db |||||||  
Qy 679 AAAGATAACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATTTAGCGTTAGCAAAATAT 738  
Db |||||||  
Qy 721 GACTTTATGCTTACTCGACTGTGATATGGCCCAATCCATTTAGTGGTTTCATTTCTTAT 780  
Db |||||||  
Qy 739 GACTTTATGCTTACTCGACTGTGATATGGCCCAATCCATTTAGTGGTTTCATTTCTTAT 798  
Db |||||||  
Qy 781 GTTGACAGAGCTATTAGAGAGATGATTTTAAACATCATTTGGTCCAGAAAAATACATCGAT 840  
Db |||||||  
Qy 799 GTTGACAGAGCTATTAGAGAGATGATTTTAAACATCATTTGGTCCAGAAAAATACATCGAT 858  
Db |||||||  
Qy 841 ACACAAACATATGACCCCAAAAGACTTCTTAATAAACGGAGTTTCTGTTGAATCATTACCA 900  
Db |||||||  
Qy 859 ACACAAACATATGACCCCAAAAGACTTCTTAATAAACGGAGTTTCTGTTGAATCATTACCA 918  
Db |||||||  
Qy 901 GAAGTGAACCAATTAATAGTGTGTCGCAAAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
Db |||||||  
Qy 919 GAAGTGAACCAATTAATAGTGTGTCGCAAAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 978  
Db |||||||  
Qy 961 CGCTTTAGAACCAATTCGAAAAACAAAAATCTCCGCTTATCCGATTCGCTTTCCGCTTTT 1020  
Db |||||||  
Qy 979 CGCTTTAGAACCAATTCGAAAAACAAAAATCTCCGCTTATCCGATTCGCTTTCCGCTTTT 1038  
Db |||||||  
Qy 1021 TTTGCGGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATAAATTCGCTTTGAT 1080  
Db |||||||

Db 1039 TTTGGGGGGTAATGTTGCTTCCTTAAATAATGGCTAAATAAATCGGTTTCCTTGAT 1098  
Qy 1081 GAGGAATTAATCACTCGGGTGGAGAAGATGTGAAATTTGGATATCGCTTATTCGGTTAC 1140  
Db 1099 GAGGAAATTAATCACTCGGGTGGAGAAGATGTGAAATTTGGATATCGCTTATTCGGTTAC 1158  
Qy 1141 GGTAGTTTCTTTAAACCTATTGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200  
Db 1159 GGTAGTTTCTTTAAACCTATTGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1218  
Qy 1201 GAAATGAACCCGATCGTGAAGCGGGAAGAAATATTACGCTCGATATTATTGAGAGAAAAG 1260  
Db 1219 GAAATGAACCCGATCGTGAAGCGGGAAGAAATATTACGCTCGATATTATTGAGAGAAAAG 1278  
Qy 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
Db 1279 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1338  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATAA CTGTGCAAACTATATTCAACGTTGGTGTAGAT 1380  
Db 1339 TTAGTTTCAATTTATATCCAGCTTATAA CTGTGCAAACTATATTCAACGTTGGTGTAGAT 1398  
Qy 1381 AGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGATTTTCTGTAACGATGGTTCAACA 1440  
Db 1399 AGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGATTTTCTGTAACGATGGTTCAACA 1458  
Qy 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATATCTAGGGTACGCATATG 1500  
Db 1459 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAAATATCTAGGGTACGCATATG 1518  
Qy 1501 TCTAAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCGAGCGTTTCTTTGCTTAAAGGT 1560  
Db 1519 TCTAAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCGAGCGTTTCTTTGCTTAAAGGT 1578  
Qy 1561 TATTACATGGCGAGTTAGATTAGATGATGATCTTCTGAGCCTGATGCAAGTTGAACTGTG 1620  
Db 1579 TATTACATGGCGAGTTAGATTAGATGATGATCTTCTGAGCCTGATGCAAGTTGAACTGTG 1638  
Qy 1621 TTAAGAAGATTTTTTAAAGATAAAAACGCTAGCTTGTGTGTTATATACCACTTAATAGAAAACGTC 1680  
Db 1639 TTAAGAAGATTTTTTAAAGATAAAAACGCTAGCTTGTGTGTTATATACCACTTAATAGAAAACGTC 1698  
Qy 1681 AATCCGATGTAGCTTAAATCGCTAAATGGTTACAAATTTGGCCAGAAATTTTTCAGAGAAAAA 1740  
Db 1699 AATCCGATGTAGCTTAAATCGCTAAATGGTTACAAATTTGGCCAGAAATTTTTCAGAGAAAAA 1758  
Qy 1741 CTCAACAGGCTATGATGCTCACCACCTTTTAGAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
Db 1759 CTCAACAGGCTATGATGCTCACCACCTTTTAGAATGTTTACGATTTAGAGCTTGGCATTTA 1818  
Qy 1801 ACTGATGGATTCAAATGAAAAAATTTGAAAATGCCGTAGACATATGACATGTTCTCAAACTC 1860  
Db 1819 ACTGATGGATTCAAATGAAAAAATTTGAAAATGCCGTAGACATATGACATGTTCTCAAACTC 1878  
Qy 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAATCTGCTATAACCCGTGATTAACATGGT 1920  
Db 1879 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAATCTGCTATAACCCGTGATTAACATGGT 1938  
Qy 1921 GATAACACATCAATTAAGAACTTGGCATTTCAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Db 1939 GATAACACATCAATTAAGAACTTGGCATTTCAAAGAAAAACCAATTTTGTGTAGTCAAT 1998  
Qy 1981 CAGTCATTAAATAGACAGGCATTAATTTATTAATATATGCAAGATTTTGATGATTTAGAT 2040  
Db 1999 CAGTCATTAAATAGACAGGCATTAATTTATTAATATATGCAAGATTTTGATGATTTAGAT 2058  
Qy 2041 GAAAGTGAAGATTAATTTTCAATAAAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
Db 2059 GAAAGTGAAGATTAATTTTCAATAAAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2118  
Qy 2101 AAAGCATTAATAATCACCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2160

Db 2119 AAAGATATTAAATATCATCCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2178  
Qy 2161 AATAACATTAACCGCTTAGTGAATAAACTTAACAAATATTATTGAATATAATAAAATATA 2220  
Db 2179 AATAACATTAACCGCTTAGTGAATAAACTTAACAAATATTATTGAATATAATAAAATATA 2238  
Qy 2221 TTCGTTATTGCTTCTACATGTTGATAAGAATCATCTTACACCAAGATATCAAAAAAGAAATA 2280  
Db 2239 TTCGTTATTGCTTCTACATGTTGATAAGAATCATCTTACACCAAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCCTTCTATCATATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Db 2299 CTAGCCCTTCTATCATATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358  
Qy 2341 ACAGATTAATAGATTAATAAAAACTGAGGCGCATTTAAGTAAATATTAAATAATTAAGTCAG 2400  
Db 2359 ACAGATTAATAGATTAATAAAAACTGAGGCGCATTTAAGTAAATATTAAATAATTAAGTCAG 2418  
Qy 2401 TTAATCTAAATTTGTGAATACATCATTTTGTGAATATCATGACAGCCTATTTCGTTAAAAAT 2460  
Db 2419 TTAATCTAAATTTGTGAATACATCATTTTGTGAATATCATGACAGCCTATTTCGTTAAAAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2520  
Db 2479 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 2521 GATTGATCGAGAAAAATCAATGCGCATCCACATTTTAAAAAGCTCATTAAAACTTATTTT 2580  
Db 2539 GATTGATCGAGAAAAATCAATGCGCATCCACATTTTAAAAAGCTCATTAAAACTTATTTT 2598  
Qy 2581 AATGACAATGACTTAAAAAGTATGAATGTGAAGGGGCATCAAGAGTATGTTTATGACG 2640  
Db 2599 AATGACAATGACTTAAAAAGTATGAATGTGAAGGGGCATCAAGAGTATGTTTATGACG 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCAATCATCTTGCAGTCA 2700  
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCAATCATCTTGCAGTCA 2718  
Qy 2701 ATTGATAGTGTGCAGAAATATAACATGAGGATATTGTTGCCAATTTGCACTTTTAATC 2760  
Db 2719 ATTGATAGTGTGCAGAAATATAACATGAGGATATTGTTGCCAATTTGCACTTTTAATC 2778  
Qy 2761 TTAGAAAAGAAAAACCGCCCATGTATTATAAACAATCGACCCCTGACTTATATGCTTTGG 2820  
Db 2779 TTAGAAAAGAAAAACCGCCCATGTATTATAAACAATCGACCCCTGACTTATATGCTTTGG 2838  
Qy 2821 GAACGAAAATTTACAATCGACAAAATGAACAAATTTGAAAAGTCAAAAAAGAGGAGAAATATA 2880  
Db 2839 GAACGAAAATTTACAATCGACAAAATGAACAAATTTGAAAAGTCAAAAAAGAGGAGAAATATA 2898  
Qy 2881 CCTGTTAAACAAAGTTCAATTAATAATAGTATAACTCTATAA 2919  
Db 2899 CCTGTTAAACAAAGTTCAATTAATAATAGTATAACTCTATAA 2937  
  
RESULT 5  
ABT44090  
ID ABT44090 standard; DNA; 2916 BP.  
XX AC ABT44090;  
XX AC  
XX 17-OCT-2003 (first entry)  
XX DE  
XX Pasteurella multocida hyaluronan synthase DNA.  
KW Hyaluronic acid; glycosaminoglycan; hyaluronan synthase; antirheumatic;  
KW UDP-glucose 6-dehydrogenase; UDP-glucose pyrophosphorylase; orthopaedic;  
KW UDP-N-acetylglucosamine; ophthalmological; dermatological; joint surgery;  
KW eye; rheumatology; dermatology; adhesion; development; cell motility;  
XX cancer; angiogenesis; wound healing; de; gene.  
OS Pasteurella multocida.  
XX

```
PN WO2003054163-A2.
XX
PD 03-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US041067.
XX
PR 21-DEC-2001; 2001US-0342644P.
XX
PA (NOVO ) NOVOZYMES BIOTECH INC.
XX
PI Sloma A, Behr R, Widner W, Tang M, Sternberg D, Brown S;
XX
DR WPI; 2003-559139/52.
XX
PT P-PSDB; ABJ72189.
XX
PT Producing a hyaluronic acid (e.g. for use in eye and joint surgery,
PT orthopedics, rheumatology or dermatology) comprises cultivating a
PT Bacillus host cell and recovering the hyaluronic acid from the
PT cultivation medium.
XX
PS Claim 132; Page 186-190; 218pp; English.
XX
CC The invention relates to a novel method which comprises producing a
CC hyaluronic acid via cultivating a Bacillus host cell under conditions
CC suitable for production of the hyaluronic acid and subsequently
CC recovering the hyaluronic acid from the cultivation medium. The most
CC abundant heteropolysaccharides of the body are the glycosaminoglycans, of
CC which hyaluronic acid is an example. A number of enzymes are involved in
CC the biosynthesis of hyaluronic acid including hyaluronan synthase, UDP-
CC glucose 6-dehydrogenase, UDP-glucose pyrophosphorylase and UDP-N-
CC acetylglucosamine. The molecules of the invention demonstrate
CC ophthalmological, antirheumatic and dermatological activities, whilst the
CC method itself may be useful for producing a hyaluronan in a recombinant
CC host cell. The hyaluronan generated may be used in eye and joint surgery,
CC orthopaedics, rheumatology or dermatology and may exhibit further uses
CC within the fields of adhesion, development, cell motility, cancer,
CC angiogenesis and wound healing. The current sequence is that of the DNA
CC of the invention which encodes a protein that plays a role in the
CC synthesis of hyaluronic acid
XX
SQ Sequence 2916 BP; 1067 A; 481 C; 506 G; 862 T; 0 U; 0 Other;
Query Match 99.8%; Score 2914.4; DB 9; Length 2916;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
DB 1 ATGNATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
QY 61 AAATTTATTTGAAAGTCGGGGAATCTATGACGGAATAATTTGTAATTTCAAAATTACC 120
DB 61 AAATTTATTTGAAAGTCGGGGAATCTATGACGGAATAATTTGTAATTTCAAAATTACC 120
QY 121 AAATGCAAGAGAAACTCTCAGCACATCTTCTGTTAAATTCAGCACATCTTCTGTAAT 180
DB 121 AAATGCAAGAGAAACTCTCAGCACATCTTCTGTTAAATTCAGCACATCTTCTGTAAT 180
QY 181 AAAGAGAGAGAAAGTCAATGTTTTCGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 240
DB 181 AAAGAGAGAGAAAGTCAATGTTTTCGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 240
QY 241 TCCAACGTAAGAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAATAAATGCG 300
DB 241 TCCAACGTAAGAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAATAAATGCG 300
QY 301 AAATTCCTCCTCAGAGAGAAATCTGAAATTCGGAGGTAAAGACGGTTCGCCCTTGACCA 360
DB 301 AAATTCCTCCTCAGAGAGAAATCTGAAATTCGGAGGTAAAGACGGTTCGCCCTTGACCA 360
QY 361 AAAGATTTTCCCAAGAGATCTGGTTTTAGCGCCTTTTACCTGATCATGTTAATGATTTTACA 420
DB 361 AAAGATTTTCCCAAGAGATCTGGTTTTAGCGCCTTTTACCTGATCATGTTAATGATTTTACA 420
QY 421 TGGTACAAAAAGCGAAAGAAAAAGACTTTGGGCATAAAACTTGAACATCAACATGTTGGTCTT 480
DB 421 TGGTACAAAAAGCGAAAGAAAAAGACTTTGGGCATAAAACTTGAACATCAACATGTTGGTCTT 480
QY 481 TCTATTATCGTTTACAAATCAATTCGACCCAGCAATTTTATCGATTACATTTAGCCCTGTTTA 540
DB 481 TCTATTATCGTTTACAAATCAATTCGACCCAGCAATTTTATCGATTACATTTAGCCCTGTTTA 540
QY 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA 600
DB 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA 600
QY 601 GATCTATCACCGATCATTTGCGCAATATGAAATTAATTTGGATATTCGCTACGTACAGACAA 660
DB 601 GATCTATCACCGATCATTTGCGCAATATGAAATTAATTTGGATATTCGCTACGTACAGACAA 660
QY 661 AAGATAACGGTTTTTACAGCCAGTCCGCTCGGAATATGGGATTTACGTTTACCAAAATAT 720
DB 661 AAGATAACGGTTTTTACAGCCAGTCCGCTCGGAATATGGGATTTACGTTTACCAAAATAT 720
QY 721 GACTTTATTTGGCTTACTCGACTGTGATATGCGGCCAAATCCATTTATGGTTTCATTTCTAT 780
DB 721 GACTTTATTTGGCTTACTCGACTGTGATATGCGGCCAAATCCATTTATGGTTTCATTTCTAT 780
QY 781 GTTCAGAGCTATTAGAAAGATGATTTAAACAATCATTTGGTCCAAAGAAAATACATCGAT 840
DB 781 GTTCAGAGCTATTAGAAAGATGATTTAAACAATCATTTGGTCCAAAGAAAATACATCGAT 840
QY 841 ACACACATATTGACCCAAAAAGACTTCTTAATAACGCGAGTTTCTGTTGAATCATTACCA 900
DB 841 ACACACATATTGACCCAAAAAGACTTCTTAATAACGCGAGTTTCTGTTGAATCATTACCA 900
QY 901 GAAGTGAAAAACCAATAATAGTTTTCGCCGCAAAAGGGGAAGAACAGTTTCTCGGATTGG 960
DB 901 GAAGTGAAAAACCAATAATAGTTTTCGCCGCAAAAGGGGAAGAACAGTTTCTCGGATTGG 960
QY 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTTTT 1020
DB 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTTTT 1020
QY 1021 TTTGCGGCGGTAATTTGCTTTCGCTTAAATAATCGCTTAAATAAATCCGTTTTCTTTGAT 1080
DB 1021 TTTGCGGCGGTAATTTGCTTTCGCTTAAATAATCGCTTAAATAAATCCGTTTTCTTTGAT 1080
QY 1081 GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATTCGGTTAC 1140
DB 1081 GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATTCGGTTAC 1140
QY 1141 GGTAGTTTCTTTTAAAACTATTGATGGCATTTATGGCTACCATCAAGAGCCACAGGTAAA 1200
DB 1141 GGTAGTTTCTTTTAAAACTATTGATGGCATTTATGGCTACCATCAAGAGCCACAGGTAAA 1200
QY 1201 GAAATGAAACCGATCGTGAAGCGGAAAAATATTTACGCTCGATATTATGAGAGAAAAAG 1260
DB 1201 GAAATGAAACCGATCGTGAAGCGGAAAAATATTTACGCTCGATATTATGAGAGAAAAAG 1260
QY 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTTCGCATATCAATAGAGTACCT 1320
DB 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTTCGCATATCAATAGAGTACCT 1320
QY 1321 TTATGTTTCAATTTATATCCAGCTTATAA CTGTGCAAACTATTTCAAGCGTTCGCTAGAT 1380
DB 1321 TTATGTTTCAATTTATATCCAGCTTATAA CTGTGCAAACTATTTCAAGCGTTCGCTAGAT 1380
QY 1381 AGTGACCTGAATCAGACTGTTTGTGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA 1440
DB 1381 AGTGACCTGAATCAGACTGTTTGTGATCTCGAGGTTTGTATTGTAAACGATGGTTCAACA 1440
QY 1441 GATAATACCTTAGAGATGATCAATAGCTTTTATGGTAAATTAATCTTAGGGTACGCATCATG 1500
DB 1441 GATAATACCTTAGAGATGATCAATAGCTTTTATGGTAAATTAATCTTAGGGTACGCATCATG 1500
```

Qy 1501 TCTAAACCAATGGCGAATAGCCTCAGCATCAATGCAGCCGTTCTTTTGTCTAAGGT 1560  
Db 1501 TCTAAACCAATGGCGAATAGCCTCAGCATCAATGCAGCCGTTCTTTTGTCTAAGGT 1560  
Qy 1561 TATTACATTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCCTGATGCAAGTTGAACCTGTGT 1620  
Db 1561 TATTACATTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCCTGATGCAAGTTGAACCTGTGT 1620  
Qy 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTATATACCACTAATAGAAAAGTC 1680  
Db 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTGTGTGTATATACCACTAATAGAAAAGTC 1680  
Qy 1681 AATCCGATGTAGCTTAATCGCTAATGGTTACAAATTTGGCCAGAAATTTTCACGAGAAAA 1740  
Db 1681 AATCCGATGTAGCTTAATCGCTAATGGTTACAAATTTGGCCAGAAATTTTCACGAGAAAA 1740  
Qy 1741 CTCAACACGGCTATGATTGCTCACACCTTTAGAAATGTTTCAGATTTAGAGCTTTGGCATTTA 1800  
Db 1741 CTCAACACGGCTATGATTGCTCACACCTTTAGAAATGTTTCAGATTTAGAGCTTTGGCATTTA 1800  
Qy 1801 ACTGATGGATTCATGAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1801 ACTGATGGATTCATGAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Qy 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGGTGATTACATGGT 1920  
Db 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGGTGATTACATGGT 1920  
Qy 1921 GATAACACATCAATTAAGAAATCTGGCAATTCAAAAGAAAAACCAATTTTGGTTAGTCAAT 1980  
Db 1921 GATAACACATCAATTAAGAAATCTGGCAATTCAAAAGAAAAACCAATTTTGGTTAGTCAAT 1980  
Qy 1981 CAGTCATTAAATAGACAGGATCAATTTATTAATATATGACGAATTTGATGATTTAGAT 2040  
Db 1981 CAGTCATTAAATAGACAGGATCAATTTATTAATATATGACGAATTTGATGATTTAGAT 2040  
Qy 2041 GAAAGTAGAAAGTATATTTTCAATAAACCCTGAATATCAAGAGAGATTGATATCTTA 2100  
Db 2041 GAAAGTAGAAAGTATATTTTCAATAAACCCTGAATATCAAGAGAGATTGATATCTTA 2100  
Qy 2101 AAAGATATTAATAATCATCCAGATTAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 2160  
Db 2101 AAAGATATTAATAATCATCCAGATTAAGATGCCAAATCGCAGTCAGTATTTTATATCCC 2160  
Qy 2161 AATACATTAAACGGCTTAGTGAAGAACTAAACAATATTTTGAATATAATAAATAATA 2220  
Db 2161 AATACATTAAACGGCTTAGTGAAGAACTAAACAATATTTTGAATATAATAAATAATA 2220  
Qy 2221 TTCGTTATTGTTTACATGTTGATGAAGATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2221 TTCGTTATTGTTTACATGTTGATGAAGATCATCTTACACAGATATCAAAAAAGAAATA 2280  
Qy 2281 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Db 2281 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Qy 2341 ACGAGTAAATAGATTAAATAAAACTGAGCGCATTTTAAGTAAATTTAAATAATTAAGTCAG 2400  
Db 2341 ACGAGTAAATAGATTAAATAAAACTGAGCGCATTTTAAGTAAATTTAAATAATTAAGTCAG 2400  
Qy 2401 TTAATCTAAATTTGTAATACATCAATTTTGTGATATCATGACGCTATTGTTAAAAAT 2460  
Db 2401 TTAATCTAAATTTGTAATACATCAATTTTGTGATATCATGACGCTATTGTTAAAAAT 2460  
Qy 2461 GACAGTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTTAACACAT 2520  
Db 2461 GACAGTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTTAACACAT 2520  
Qy 2521 GATTGGATCGAGAAATCAATCGGCATCCACATTTAAAAAGCTCATTTAAACCTTATTTT 2580  
Db 2521 GATTGGATCGAGAAATCAATCGGCATCCACATTTAAAAAGCTCATTTAAACCTTATTTT 2580  
Qy 2581 AATGACATGACTTAAAAAGTATGATGTGAAGGGGCATCACAAGGTATGTTTATGACG 2640

Db 2581 AATGACATGACTTAAAAAGTATGATGTGAAGGGGCATCACAAGGTATGTTTATGACG 2640  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCATCATCTTGCCAGTCA 2700  
Db 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCATCATCTTGCCAGTCA 2700  
Qy 2701 ATTGATAGTGTGCAGAAATATAACACCTGAGGATATTTGGTTCCAAATTTGCACCTTTAATC 2760  
Db 2701 ATTGATAGTGTGCAGAAATATAACACCTGAGGATATTTGGTTCCAAATTTGCACCTTTAATC 2760  
Qy 2761 TTAGAAAAAGAAAAACCGCCCATGATTTTATAAAAAACATCGACCTGACTTATATGCTCTGG 2820  
Db 2761 TTAGAAAAAGAAAAACCGCCCATGATTTTATAAAAAACATCGACCTGACTTATATGCTCTGG 2820  
Qy 2821 GAACGAAAAATTTACAATGGACAAATGAACAAATTTGAAAGTCAAAAAGAGGAGAAATATA 2880  
Db 2821 GAACGAAAAATTTACAATGGACAAATGAACAAATTTGAAAGTCAAAAAGAGGAGAAATATA 2880  
Qy 2881 CCTGTTAAAGATTCATTATTATAGTATACTCTA 2916  
Db 2881 CCTGTTAAAGATTCATTATTATAGTATACTCTA 2916

RESULT 6  
AAA27449  
ID AAA27449 standard; cDNA; 2979 BP.  
XX  
AC AAA27449;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE P. multocida chondroitin synthase coding sequence.  
XX  
KW Chondroitin synthase; CS; enzyme; hyaluronic acid; ulcer;  
KW tissue abrasion; viscoelastic replacement; bioadhesive; ss.  
XX  
OS Pasteurella multocida.  
XX  
FH Key Location/Qualifiers  
CDS 61..2958  
FT /\*tag= a  
FT /product= "PmCS"  
XX  
FN W0200027437-A2.  
XX  
PD 18-MAY-2000.  
XX  
PF 10-NOV-1999; 99WO-US026501.  
XX  
PR 11-NOV-1998; 98US-0107929P.  
PR 01-APR-1999; 99US-00283402.  
XX  
PA (OKLA ) UNIV OKLAHOMA STATE.  
XX  
PI Deangelis PL;  
XX  
DR WPI; 2000-376319/32.  
DR P-PSDB; AAY96213.  
XX  
PT Novel method for the enzymatic transfer of sugar molecules to an  
acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or  
drug delivery systems, including hybrid molecules.  
XX  
PS Claim 16; Page 86; 86pp; English.  
XX  
CC The present sequence is the coding sequence of the Pasteurella multocida  
chondroitin synthase PmCS. PmCS catalyses glycosaminoglycan  
polymers to produce chondroitin: a linear polysaccharide which has  
viscoelastic properties which makes it useful for a number of  
applications. Chondroitin can be used with hyaluronic acid (HA) to coat  
medical devices e.g. catheters and sensors to reduce tissue abrasion. In  
addition, they can be used as bioadhesives for haemostatic sealing and



CC healing of wounds and surgical incisions; and as biomaterials that  
CC provide sustained delivery of encapsulated drugs, to wounds, ulcers,  
CC injuries or surgical sites  
XX

SQ Sequence 2979 BP; 1129 A; 466 C; 497 G; 887 T; 0 U; 0 Other;

Query Match 77.8%; Score 2271.2; DB 3; Length 2979;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;  
2Y 1 ATGAATACATTTATCACAAGCAATAAAGCATATATAACAGCAATAGACTATCAATTTAGCACTC 60  
Db 61 ATGAATACATTTATCACAAGCAATAAAGCATATATAACAGCAATAGACTATCAATTTAGCACTC 120  
2Y 61 AAATTTATTTGAAAGTCGGCGGAATCTATCGACGGAATTTGTTGAATTTCAATTTACC 120  
Db 121 AAATTTATTTGAAAGTCGCTGAAACCTACGGGCGAATAATCGTTGAATTTCAATTTATC 180  
2Y 121 AAATGCAAGAAATACTCTCAGCATCTCTCTGTTAATTCAGCACATCTTTCTGTTAAAT 180  
Db 181 AAATGTAAGAAATACTCTCGACCAATTC-----TTATGTAAGT 219  
2Y 181 AAAGAAGAAAGTCATTTTGGATAGTCGGTTAGATATATGCAACAACACTGTTACTT 240  
Db 220 GAAGATAAAAAAACAAGTGTGCGATAGCTCAITTAGATATCGCAACACAGCTCTTACTT 279  
2Y 241 TCCAAAGTTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATAAATGG 300  
Db 280 TCCAAAGTTAAAAAATTTAATCTCTATCCGAATCAGAAAAAACAAGTTAAAAAATAAATGG 339  
2Y 301 AAATGTCCTCAGTGAAGAAATCTGAAATGCGGAGGTAAAGAGCGTCCGCTTGTACCA 360  
Db 340 AAATCTATCAGTGGGAAAAAATTCGGAGAACGCAAGAAATCAGAAAGTGGAACTAGTACCC 399  
2Y 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTACCTGATCATGTTTAATGATTTTACA 420  
Db 400 AAAGATTTTCCTAAGATCTTGTCTGCTCCATTTGCCAGATCATGTTTAATGATTTTACA 459  
2Y 421 TGGTACAAAGCGGAAAGAAAGACTTGGCATATAAACCCTGAACATCAACATGTTGGTCTT 480  
Db 460 TGGTACAAAGAAATTCGAAAAAAGCTTAGGTATAAAGCGCTGTAAATTAAGATATCGGTCTT 519  
2Y 481 TCTATTTATCGTTTACAACTTCAATCGACGACCAATTTTATCGATTTACATTTAGCCCTGTTTA 540  
Db 520 TCTATTTATTTCTTACATTTTANTCGTAGCGGTAATTTTAGATATAAGCTTAGCCCTGTTTG 579  
2Y 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db 580 GTCAATCAGAAAAACAACTACCCATTTGAAGTCGTTGTCAGATGATGGTAGTAAGGAA 639  
2Y 601 GATCTATCACCGATCATTTGCGCAATATGAAATATAATTTGGATATATTCGCTACGTACAGCA 660  
Db 640 AACTTACTTACCATTGTGCAAAAAATACGAAACAAACAACTTGACATAAAGTATGTAAGACAA 699  
2Y 661 AAAGATACGGTTTTCAGCCAGTCGCGCTCGGAATATGGGATATACGCTTAGCAAAATAT 720  
Db 700 AAAGATATGGATATCAATTTGTGCGAGTCAGAACTTAGGTTTACGTACACGAAAGTAT 759  
2Y 721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCCAAATFCCAATTTATGGGTTCAATCTTAT 780  
Db 760 GATTTTGTCTCGATTTAGACTGCGATATGGCACCACACAAATTTATGGGTTCAATCTTAT 819  
2Y 781 GTTCGAGAGCTATTAAGAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT 840  
Db 820 CTTACAGAACTATTAGAGACAAATGATATTTGTTTAAITGGACCTAGAAAAATATGTGGAT 879  
2Y 841 ACACACATATTGACCCAAAGACTTCTTAATAAAGCGGAGTTTGTCTGAATCATTTACCA 900  
Db 880 ACTCAATATTATCCGCAAGACAAATTTCTTTACAGATCCCATATTTAATAGAAATCATTCT 939  
2Y 901 GAAAGTGAACCAATTAATAGTGTGCGGCAAAAGGGGAAGGAACAGTTTCTCTGGATTGG 960  
Db 940 GAAACCGCTTACAAATTAACAATCTCTCGATTATCATCAAAAGGAATATATATCGTTGGATTGG 999

961 CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCCGATTCGCTTCCGTTT 1020  
Db 1000 AGATTAGAACATTTCAAAAAAACCGATAATCTAGCTCTATGTGATTTCTCCGTTTCGTTAT 1059  
2Y 1021 TTTGCGGCGGTAATGTTGCTTAAATAATGGCTTAATAATCCGGTTTCTTTCGAT 1080  
Db 1060 TTTGTTGCGGTAATGTTGCTTAAATAATGGCTTAAATAATGGTTGTTGTTGAT 1119  
2Y 1081 GAGGAATTTAATCACTCGGGTGGAGAAGATGTGAAATTTGGATATCGCTTATTCGTTTAC 1140  
Db 1120 GAAGAAATTTAATCATTTGCGGGGCGAAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA 1179  
2Y 1141 GGTAGTTTCTTTTAAAACTATTGATGGCATTTATGCGCTTACCAATCAAGAGCCACCAAGGTAAA 1200  
Db 1180 GGCTGTTTTTTCAGAGTAATTTGACGGCGGAATGGCCATCCATCAAGAACCACCTGGTAAA 1239  
2Y 1201 GAAATGAACCGGATCGTGAAGCGGGAATAATATTAGCTCGATATTATGAGAGAAAG 1260  
Db 1240 GAAATGAACAGAACCGAGCTGGTAAAAAGTATTACGCTTAAATTTGTGAAAGAAAG 1299  
2Y 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCTATAGATACCT 1359  
2Y 1321 TTAGTTTCAATTTATATCCCAAGCTTTATAACTGTGCAAACTATATTTCAAAGTTGCGTAGAT 1380  
Db 1360 TTAGTTTCTATTTATATCCCGCTTTATAACTGTGCAAAATTTATTTCAAGATGTTGTAGAT 1419  
2Y 1381 AGTCACATGAATCAGACTGTTGTTGATCTCGAGGTTGTATTTGTAACGATGGTTCAACA 1440  
Db 1420 AGTCTCTTAATCAAACTGTTGTCGATCTCGAGGTTGTATTTGTAACGATGGTTCAACA 1479  
2Y 1441 GATTAATCTTTAGAGTGAATCAATAAGCTTTTATGTTAATAATCTTAGGGTAGCATCATG 1500  
Db 1480 GATAATACCTTTAGAGTGAATCAATAAGCTTTTATGTTAATAATCTTAGGGTAGCATCATG 1539  
2Y 1501 TCTAAACCAAAATGCGGAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGGT 1560  
Db 1540 TCTAAACCAAAATGCGGAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGGT 1599  
2Y 1561 TATTACATGCGGAGTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAG 1620  
Db 1600 TATTACATGCGGAGTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAG 1659  
2Y 1621 TTTAAAGATTTTAAAGATATAAAGCTAGCTGTTGTTTATACCACTAAATAGAAACGTC 1680  
Db 1660 TTTAAAGATTTTAAAGATATAAAGCTAGCTGTTGTTTATACCACTAAATAGAAACGTC 1719  
2Y 1681 AATCCGATGTTAGCTTAATCGCTTAATGTTTACAAATGGCCAGAAATTTTTCAGGAGAAAA 1740  
Db 1720 AATCCGATGTTAGCTTAATCGCTTAATGTTTACAAATGGCCAGAAATTTTTCAGGAGAAAA 1779  
2Y 1741 CTCACACGCTATGATTTGCTCACCACTTTTGAATGTTTACGATTTAGAGCTTTGGCATTTA 1800  
Db 1780 CTCACACGCTATGATTTGCTCACCACTTTTGAATGTTTACGATTTAGAGCTTTGGCATTTA 1839  
2Y 1801 ACTGATGATTTCAATGAAAAATTTGAAATGCGGTAGACTATGACATGTTTCTCTCAAACTC 1860  
Db 1840 ACGGATGATTTTAAACGAAAAATTTGAAACGCGGTGATTTAGACATGTTTCTTTAAACTC 1899  
2Y 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAAAAATCTGCTATAACCGGTGTTTATCATGGT 1920  
Db 1900 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAAAAATCTGCTATAACCGGTGTTTATCATGGT 1959  
2Y 1921 GATAACACATCAATTTAAGAAACTTTGGCATTTCAAAAAAGAAAAACATTTTGTGTAGTCAAT 1980  
Db 1960 GATAACACATCAATTTAAGAAACTTTGGCATTTCAAAAAAGAAAAACATTTTGTGTAGTCAAT 2019  
2Y 1981 CAGTCATTTAAATAGACAAAGGCATACCTTATTAATAATATGACGAATTTGATGATTTAGAT 2040  
Db 2020 CAGTCATTTAAATAGACAAAGGCATACCTTATTAATAATATGACAAATTTGATGATTTAGAT 2079

Qy 2041 GAAAGTAGAAGTATATTTTCAATAAACAACGCGTGAATATCAAGAAGAGATTGATATCTTA 2100  
Dy |||||||  
Qy 2080 GAAAGTAGAAGTATATCTTCATATAAACCCCTGAATATCAAGAAGAAATCGATATGTTA 2139  
Dy |||||||  
Qy 2101 AAAGATATTTAAATCATCCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTATCCC 2160  
Dy |||||||  
Qy 2140 AAAGATCTTAAACTCATTCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCC 2199  
Dy |||||||  
Qy 2161 AATACATAAAGCGGTAGTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2220  
Dy |||||||  
Qy 2200 AATACATAAAGCGGTAGTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2259  
Dy |||||||  
Qy 2221 TTGGTTATTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAGAAATA 2280  
Dy |||||||  
Qy 2260 TTGGTTATTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAGAAATA 2319  
Dy |||||||  
Qy 2281 CTAGCCTTCTATCATAAATCAATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2340  
Dy |||||||  
Qy 2320 TTGGCTTTCTATCATAGCACCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2379  
Dy |||||||  
Qy 2341 ACGAGTAATAGATAATAAATAAATAAAGCGGCAATTAAGTAATATTAATAAATAAAGTCAG 2400  
Dy |||||||  
Qy 2380 ACGAGTAATAGATAATAAATAAATAAAGCGGCAATTAAGTAATATTAATAAATAAAGTCAG 2439  
Dy |||||||  
Qy 2401 TTAATCTAAATCTGATATCATCATTTTTCATATCATGACAGCCTATTTCGTTAAAAAT 2460  
Dy |||||||  
Qy 2440 TTAATCTAAATCTGATATCATCATTTTTCATATCATGACAGCCTATTTCGTTAAAAAT 2499  
Dy |||||||  
Qy 2461 GACAGCTATGTTATATGAAAAATAATGATGTCGCGATGAATTTCTCAGCATTAACACAT 2520  
Dy |||||||  
Qy 2500 GACAGCTATGTTATATGAAAAATAATGATGTCGCGATGAATTTCTCAGCATTAACACAT 2559  
Dy |||||||  
Qy 2521 GATTGGATCGAGAAAAATCAATCGCGATCCACCATTTTAAAAAGCTCATTAATACTTATTTT 2580  
Dy |||||||  
Qy 2560 GATTGGATCGAGAAAAATCAATCGCGATCCACCATTTTAAAAAGCTCATTAATACTTATTTT 2619  
Dy |||||||  
Qy 2581 AATGACATGACTTAAAGATGATGAATGTAAGGCGCATCACAAGGTATGTTTATGACG 2640  
Dy |||||||  
Qy 2620 AATGACATGACTTAAAGATGATGAATGTAAGGCGCATCACAAGGTATGTTTATGAG 2679  
Dy |||||||  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCATCACAATCTTGCGAGTCA 2700  
Dy |||||||  
Qy 2680 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCATCACAATCTTGCGAGTCA 2739  
Dy |||||||  
Qy 2701 ATTGATAGTGCAGAAATATAAACAATGAGATATTTGGTTCCAAATTTGCACTTTTAAATC 2760  
Dy |||||||  
Qy 2740 ATTGATAGTGCAGAAATATAAACAATGAGATATTTGGTTCCAAATTTGCACTTTTAAATC 2799  
Dy |||||||  
Qy 2761 TTAGAAAAGAAAACCGGCCATGTTTAAATAAAACATCGACCCCTGACTTATATGCTTGG 2820  
Dy |||||||  
Qy 2800 TTAGAAAAGAAAACCGGCCATGTTTAAATAAAACATCGACCCCTGACTTATATGCTTGG 2859  
Dy |||||||  
Qy 2821 GAACGAAAATTAACATGAGCAAAATGAACAAATTTGAAAGTGAAGGAGGAGAGAAATATA 2880  
Dy |||||||  
Qy 2860 GAACGAAAATTAACATGAGCAAAATGAACAAATTTGAAAGTGAAGGAGGAGGAGAAATATC 2919  
Dy |||||||  
Qy 2881 CCTGTTAAAGGATCATTAATTAAGTATATACTCTATAA 2920  
Dy |||||||  
Qy 2920 CCCGTTAAAGGATCATTAATTAAGTATATACTCTATAA 2959  
Dy |||||||

RESULT 7  
ABA05097  
ID ABA05097 standard; DNA; 2979 BP.  
XX  
AC ABA05097;  
XX  
XX 22-FEB-2002 (first entry)  
XX Pasteurella multocida chondroitin synthase gene #1.  
DE Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer;  
XX eye application; joint application; moisturiser; drug delivery;  
KW

KW wound dressing; biocompatible film; ds.  
XX Pasteurella multocida.  
OS  
XX  
FH Key Location/Qualifiers  
FT 61..2945  
FT /\*tag= a  
FT /product= "chondroitin synthase"  
XX  
XX WO200180810-A2.  
XX  
XX 01-NOV-2001.  
XX  
XX 25-APR-2001; 2001WO-US013395.  
XX  
XX 25-APR-2000; 2000US-0199538P.  
XX  
XX (DANG/) DE ANGELIS P L.  
XX  
XX De Angelis PL;  
XX  
XX WPI; 2002-049237/06.  
DR P-PSDB; AAM47335.  
XX  
XX New chondroitin synthase gene obtained from Pasteurella multocida, useful  
PT as hyaluronan polysaccharide substitute in medial or cosmetic  
PT applications, e.g. for eye or joint applications, for moisturizer or  
PT wound dressings.  
XX  
XX Claim 4; Page 117-118; 125pp; English.  
XX  
XX The present invention relates to the coding sequence of the Pasteurella  
CC multocida chondroitin synthase. A chondroitin polysaccharide may be used  
CC as a hyaluronan polysaccharide substitute in medial or cosmetic  
CC applications, for example in eye or joint applications, for moisturiser  
CC or wound dressings. The enzyme may be used in covalently coupling  
CC specific drugs, proteins or toxins to the structurally modified  
CC chondroitin for general or targeted drug delivery or radiological  
CC procedures, covalently cross linking the hyaluronic acid itself or to  
CC other supports to achieve a gel or other three dimensional biomaterial  
CC with stronger physical properties, and covalently linking hyaluronic acid  
CC to a surface to create a biocompatible film or monolayer. The present  
CC sequence is one version of the coding sequence of the invention  
XX  
SQ Sequence 2979 BP; 1129 A; 466 C; 497 G; 887 T; 0 U; 0 Other;  
Query Match 77.8%; Score 2271.2; DB 6; Length 2979;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;  
Qy 1 ATGATATCATTTATCACAAGCAATAAAGCATATATACAGCAATGACTATCAATTAGCACTC 60  
Dy |||||||  
Qy 61 ATGATATCATTTATCACAAGCAATAAAGCATATATACAGCAATGACTATCAATTAGCACTC 120  
Dy |||||||  
Qy 61 AAATTATTTGAAAGTCCGCGGAAATCTATGAGCGGAAATTTGTTGAATTTCAAATATACC 120  
Dy |||||||  
Qy 121 AAATTATTTGAGAGTCTGCTGAAACCTAGCGGGAATAATCGTTGAATTCGAATATATC 180  
Dy |||||||  
Qy 121 AAATGCAAGAAAAAATCTTCAGCACATCTTCTGTTTAAATTCAGCACATCTTCTGTAAT 180  
Dy |||||||  
Qy 181 AAATGTAAGAAAAAATCTTCGACCAATTC-----TTATGTAAGT 219  
Dy |||||||  
Qy 181 AAAGAGAAAAAAGTCAATGTTTGGGATAGTCGTTAGATATTCGAACACACTGTTACTT 240  
Dy |||||||  
Qy 220 GAAGATAAAAAAAACAGTGTTCGATAGTCAATAGATATTCGCAACACAGCTCTTACTT 279  
Dy |||||||  
Qy 241 TCCAAAGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAAGCTTTAAAAAATAAATGG 300  
Dy |||||||  
Qy 280 TCCAAAGTAAAAAATTTAAGTACTTATCCGATCAGAAAAAACAAGCTTTAAAAAATAAATGG 339  
Dy |||||||  
Qy 301 AAATGCTCTAGAGAGAAATCTGAAATTCGAGAGGTAAAGAGCGGTCGCCCTTGTACCA 360  
Dy |||||||  
Qy 340 AAATCTATCACTCGGAAAAAATCGAGAACGCAAAATCAGAAAGGTGGAACCTAGTACCC 399  
Dy |||||||

QY 361 AAGATTTCCCAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
DB 400 AAGATTTTCTAAGATCTTGTTCTTGCTCCATGCGAGATCATGTTAATGATTTTACA 459  
QY 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAAACTGCAACATCAACATGTTGGTCTT 480  
DB 460 TGGTACAAAATCGAAAANAAGCTTAGGTATAAGCGCTGTAATAAGATAAGATATCGGTCTT 519  
QY 481 TCTATTATCGTTACAACTCAATCGAATCGACCAGCAATTTTATCGATTACATTTAGCCTGTTTA 540  
DB 520 TCTATTATTTCTTACATTTAATCGTAGCCGTATTTTAGATATAAOCGTTAGCCTGTTG 579  
QY 541 GTAACCAAAAACACATTTACCCTTTGGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
DB 580 GTCAATCAGAAAACAACTACCCATTTGNAAGTCGTTGTCAGATGATGGTAGTAGGAA 639  
QY 601 GATCTATCACCGATCATTTCCGCAATATGAAATAAATTTGGATATTTCCGCTACGTCAGACAA 660  
DB 640 AACTTACTTACCAATGTGCAAAAATACGAACAAAAACTTGACATAAAGTATGTAAGACAA 699  
QY 661 AAGATAACGGTTTCAAGCCAGTCCGCTCGGAATATGGGATTTAGCCTTAGCCTAGCAAAATAT 720  
DB 700 AAGATTTATGATATCAATTTGTGTCAGTCAGTACGAAACTTAGGTTTACGTACAGCAAAAGTAT 759  
QY 721 GACTTTATGGCTTACTCGATGATATGGCCCAATCCATTTATGTTGTTTCACTTCTTAT 780  
DB 760 GATTTTGTCTGATTTCTAGATGCGATATGGCACCACAAATATATGTTGTTTCACTTCTTAT 819  
QY 781 GTTGCGAGAGCTATTAGAAGATGATGATTTAAACAACTATTGGTCCAAAGAAAATACATCGAT 840  
DB 820 CTTACAGAACTATTAGAAGACAACTGATTTGTTTAAATGGACCTAGAAAATATGTCGAT 879  
QY 841 ACACAACATATTGACCCCAAGAGACTTCTTAAATAACGGGAGTTTCTGCTTGAATCATTACCA 900  
DB 880 ACTCATATATTACCGCCAGAACAACTTCTTAACGATCCATATTATTAAGAACTCACTACCT 939  
QY 901 GAAGTGAACCAATAATAGTGTGCGCAAGAGGGGAGGAACAGTTTCTCTGATTTGG 960  
DB 940 GAAACCGCTACAAATAACAACTCTTCGATTTACATCAAAAGGAAATATATCGTTGATTTGG 999  
QY 961 CGCTTAGAACAAATTCGAAAAACAGAAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020  
DB 1000 AGATTTAGAACATTTTCAAAAAACCGATATCTACGCTATGATGATTCCTCGTTTCGTTAT 1059  
QY 1021 TTTGCGCGGGTAAATGTTGCTTTCGCTAAAAATGGCTAAATTAATTCGCTTTCTTTGAT 1080  
DB 1060 TTTGTTGCGGGTAAATGTTGCAATTTCTAAAGAAATGGCTAAATAAAGTAGGTTGGTTTCGAT 1119  
QY 1081 GAGGAATTTAATCATTGGGGTGGAGAGATGGAATTTGGATATCGCTTATTTCCGTTTAC 1140  
DB 1120 GAAGAAATTTAATCATTGGGGGGGGGGAAGATGAGAAATTTGGTTTACAGATTTATTTGCCAAA 1179  
QY 1141 GGTAGTCTCTTTAAACTATTGATGGCAATTATGGCCTTACCATCAAGAGCCACCAGGTAAA 1200  
DB 1180 GGCTGTTTTTTCAGATATTGACGGCGGAATGGCCATCCATCAAGAACCACTGTGTAAA 1239  
QY 1201 GAAAATGAACCCGATCGTCAAGCGGGGAAAAATAATTACCGCTCGATATTATGAGAGAAAAG 1260  
DB 1240 GAAAATGAACAGACCGCAAGCTGTGTAAAGATATTACGCTTAAATAATTTGTGAAGAAAAG 1299  
QY 1261 GTCCCTTATATCTATAGAAAACCTTTTACCANTAGAGATTCGCNTATCAATAGAGTACCT 1320  
DB 1300 GTACCTTACATCTATAGAAAGCTTTTACCANTAGAAAGATTCACATATTCATAGAAATACCT 1359  
QY 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTTCAACGTTGCGTAGAT 1380  
DB 1360 TTAGTTTCTATTATTATCCCGCTTATTAATCTGTGCAAAATTAATTATCAAGAGATGTGTAGAT 1419  
QY 1381 AGTGCACTGAATCAGACTGTGTTGATCTCGAGGTTTGTATTTGTAAAGATGTTTCAACA 1440  
DB 1420 AGTGCTCTTAACTCAAACTGTGTCGATCTCGAGGTTTGTATTTGTAAAGATGTTTCAACA 1479

QY 1441 GATAATACTTTAGAGTGATCAATAAGCTTTATGGTAAATAATCCTAGGTAACGCATCATG 1500  
DB 1480 GATAATACTTTAGAGTGATCAATAAGCTTTATGGTAAATAATCCTAGGTAACGCATCATG 1539  
QY 1501 TCTAAACCAAAATCGCGAATAGCCTCAGCATCAAAATCAGCGCTTTCTTTTGTCTAAAGGT 1560  
DB 1540 TCTAAACCAAAATCGCGAATAGCCTCAGCATCAAAATCAGCGCTTTCTTTTGTCTAAAGGT 1599  
QY 1561 TATTACATTTGGCAGTTTAGATTTCAGATGATTTATCTTGAGCCTGATGAGTTGAACTGTGT 1620  
DB 1600 TATTACATTTGGCAGTTTAGATTTCAGATGATTTATCTTGAGCCTGATGAGTTGAACTGTGT 1659  
QY 1621 TTTAAAGAAATTTTAAAGATATAAACCGTAGCTTGTGTTTATACCACTAATAGAAAACGTC 1680  
DB 1660 TTTAAAGAAATTTTAAAGATATAAACCGTAGCTTGTGTTTATACCACTAATAGAAAACGTC 1719  
QY 1681 AATCCGAGTGTACTTAAATCGCTAAATGGTTTACAAATTTGGCCAGAAATTTTTCAGAGAAAAA 1740  
DB 1720 AATCCGAGTGTACTTAAATCGCTAAATGGTTTACAAATTTGGCCAGAAATTTTTCAGAGAAAAA 1779  
QY 1741 CTCAAAACGGCTATGATTTGCTCACCACTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1800  
DB 1780 CTCAAAACGGCTATGATTTGCTCACCACTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1839  
QY 1801 ACTGATGATTTCAATGAATAAAATTTGAAATGCTCCGCTAGACTATGACATGTTCTCTCAAACTC 1860  
DB 1840 ACGGATGATTTTAAACGAAAAATTTTAAACACCGCTGGATTTATGACATGTTCTCTTAAACTC 1899  
QY 1861 AGTGAAGTTGGAAAAATTTTAAACATCTTAAATAAAATCTGCTATAACCGGTGTTATACATGGT 1920  
DB 1900 AGTGAAGTTGGAAAAATTTTAAACATCTTAAATAAAATCTGCTATAACCGGTGTTATACATGGT 1959  
QY 1921 GATAACACATCAATTTAAGAAACTTTGGCAATTCAAAAGAAAAAACCAATTTTGTGTAGTCAAT 1980  
DB 1960 GATAACACATCCATTTAGAAACTCGCACTTCAAAGAAAAAACCAATTTTGTGTAGTCAAT 2019  
QY 1981 CAGTCATTTAAATAGAACAGGCAATCTTATTTATTAATGAGCAATTTGATGATTTAGAT 2040  
DB 2020 CAGTCATTTAAATAGAACAGGCAATCAATTTATTAATTAATTAATTAATTAATTAATTAATTAAT 2079  
QY 2041 GAAAGTAGAAAGTATTTTCAATAAAACCGCTGAATATCAAGAAGAGATGATATCTTTA 2100  
DB 2080 GAAAGTAGAAAGTATTTTCAATAAAACCGCTGATATCAAGAAGAGATGATATCTTTA 2139  
QY 2101 AAAGATATTTAAATCATCCAGAAATAAGATGCAAAATCGCAGTCAGTATTTTATCTCC 2160  
DB 2140 AAAGATCTTAACTCATTTCAAAATAAAGATGCAAAATCGCAGTCAGTATTTTATCTCC 2199  
QY 2161 AATACATTTAAACGGCTTAGTGAATAAACTAAACAATATTATTGAATATAATAAATAATA 2220  
DB 2200 AATACATTTAAACGGCTTAGTGAATAAACTAAACAATATTATTGAATATAATAAATAATA 2259  
QY 2221 TTCGTTATTTGTTTACATGTTGATGAATCATCTTTACACAGATATCAAAAAAGAAAAATA 2280  
DB 2260 TTCGTTATTTGTTTACATGTTGATGAATCATCTTTACACAGATATCAAAAAAGAAAAATA 2319  
QY 2281 CTAGCTTCTATCATATAAAACATCAAGTGAATTTTTTACTAAATTAATGATATCTCATATTAC 2340  
DB 2320 TTCGTTTCTATCATATAAGCAACCAAGTGAATTTTTTACTAAATAATGATATCTCATATTAC 2379  
QY 2341 ACGAGTAATAGATTTAATAAAAACTGAGGGCAATTTTAAAGTAATTTAATAAATTAAGTCAG 2400  
DB 2380 ACGAGTAATAGATTTAATAAAAACTGAGGGCAATTTTAAAGTAATTTAATAAATTAAGTCAG 2439  
QY 2401 TTAATCTTAAATTTGAATACATCATCTTTTGAATATCATGACAGCTATTCGTTAAAAAT 2460  
DB 2440 TTAATCTTAAATTTGAATACATCATCTTTTGAATATCATGACAGCTATTCGTTAAAAAT 2499  
QY 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGCGCATGAAATTTCTCAGCATTTAACACAT 2520  
DB 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCGCGCATGAAATTTCTCAGCATTTAACACAT 2559  
QY 2521 GATTGGATCGAGAAAAATCAATGGGCATCCACCAATTTTAAAAAGCTCATTTAAAACTTATTTT 2580



```
QY 961 CGCTTAGAACCAATTCGAAAAACAGAAAACTCTCGCTTATCGATTTCGCTTTTCGTTTT 1020
DB 1000 AGATTAGAACATTTCAAAAAAACCGATAATCTACGTCTATGTGATTCCTCGGTTGGTTAT 1059
QY 1021 TTTCGGGGGGTAAATGTTGCTTTTCGCTTAAAAAATCGCTAAATAATCGGTTTCTTTGAT 1080
DB 1060 TTTCGGGGTAAATGTTGCAATTTCTAAAGAAATGGCTAAATAAAGTAGGTGGTTTCGAT 1119
QY 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATTCGCTTATTCGTTAC 1140
DB 1120 GAAGAATTTAATCAATTTGGGGGGGCGAAGATGTAGAATTTGGTTACAGAAATTTTGCCAAA 1179
QY 1141 GGTAGTTCTTTTAAACATTTATCGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200
DB 1180 GGCTGTTTTTTTCAGAGTAATTTGACGGCGGAATGGCCATCCATCAAGAACCACTGGTAAA 1239
QY 1201 GAAAAATGAAACCGATCGTGAACGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260
DB 1240 GAAATGAAACAGAACGCGAAGCTGGTAAAGTATTACGCTTAAATTTGTGAAGAAAAG 1299
QY 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATGAGAAGATTCGCATATCAATAGACTACT 1320
DB 1300 GTACCTTACATCTATAGAAGCTTTTACCAATAGAAGATTCACATATTTCATAGAAATACCT 1359
QY 1321 TTAGTTTCAATTTATATCCAGCTTATTAACCTGTGCAAACTATATTCAAGTTGCGTAGAT 1380
DB 1360 TTAGTTTCTATTTATATCCCGCTTATTAACCTGTGCAAAATTAATTCAAGATGTGTAGAT 1419
QY 1381 AGTGCACTGAATCAGACTGTTGATCTCGAGGTTTGTATTGTGAACGATGGTTCAACA 1440
DB 1420 AGTGCTCTTAATCAAACTGTGTGCTGATCTCGAGGTTTGTATTGTGAACGATGGTTCAACA 1479
QY 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTAATAATCTTAGGGTAGCATCATG 1500
DB 1480 GATAATACCTTAGAAGTGATCAATAAGCTTTATGTTAATAATCTTAGGGTAGCATCATG 1539
QY 1501 TCTTAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACAGCGTTTCTTTGCTTAAAGGT 1560
DB 1540 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACAGCGTTTCTTTGCTTAAAGGT 1599
QY 1561 TATTACATTTGGGCGAGTTAGATTGAGATGATTTCTTTGAGCCTGATGACGTGAACGTGT 1620
DB 1600 TATTACATTTGGGCGAGTTAGATTGAGATGATTTCTTTGAGCCTGATGACGTGAACGTGT 1659
QY 1621 TTAAGAAATTTTAAAGATAAACGCTAGCTTGTGTTTATACCACTAATGAACGCTC 1680
DB 1660 TTAAGAAATTTTAAAGATAAACGCTAGCTTGTGTTTATACCACTAATGAACGCTC 1719
QY 1681 AATCCGGATGGTAGCTTAATCGCTAATGTTACNAATGGCCAGNAATTTTTCAGAGAAA 1740
DB 1720 AATCCGGATGGTAGCTTAATCGCTAATGTTACNAATGGCCAGNAATTTTTCAGAGAAA 1779
QY 1741 CTCACAACGGCTATGATGCTCACCACCTTTAGAAATGTTTCAAGATTAGAGCTTGGCATTTA 1800
DB 1780 CTCACAACGGCTATGATGCTCACCACCTTTAGAAATGTTTCAAGATTAGAGCTTGGCATTTA 1839
QY 1801 ACTGATGGATTCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTTCAAACTC 1860
DB 1840 ACGGATGGATTTAAACGAAATATTGAAAAACGCGGTGGATTTATGACATGTTCTTAAACTC 1899
QY 1861 AGTGAAGTTGGAAAAATTTTAAACATCTTAATAATCTGCTATTAACCGCTGATTACATGGT 1920
DB 1900 AGTGAAGTTGGAAAAATTTTAAACATCTTAATAATCTGCTATTAACCGCTGATTACATGGT 1959
QY 1921 GATAACACATCAATTAAGAAACTTTGGCAATTTCAAAAGAAAAAACCATTTTGTGTAGTCAAT 1980
DB 1960 GATAACACATCCATTTAGAAAACCTCGGCATTTCAAAAGAAAAAACCATTTTGTGTAGTCAAT 2019
QY 1981 CAGTCAATTAATAGAACGSCATCACTTATTAATAATTAATGAAGAAATTTGATGATTTAGAT 2040
DB 2020 CAGTCAATTAATAGAACGSCATCACTTATTAATAATTAATGAAGAAATTTGATGATTTAGAT 2079
```

```
QY 2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAAGAGATTGATATCTTA 2100
DB 2080 GAAAGTAGAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAAGAAATGATATGTTA 2139
QY 2101 AAGATATTAAAAATCAATCCAGAAATAAAGATGCCAAAAATCGCAGTCAGTATTTTATCCC 2160
DB 2140 AAGATCTTAAACTCAATTCAAAATAAAGATGCCAAAAATCGCAGTCAGTATTTTCTATCCC 2199
QY 2161 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAATATTTATTGAATATAATAAAAAATA 2220
DB 2200 AATACATTTAAACGGCTTAGTGAAAAAACTAAACAATATTTATTGAATAATAAAAAATA 2259
QY 2221 TTGCTTATTGTTTACATGTTGATAAGAAATCATCTTACACCAGATATCAAAAAAGAAATA 2280
DB 2260 TTGCTTATTATCTACATGTTGATAAGAAATCATCTTACACCAGATATCAAAAAAGAAATA 2319
QY 2281 CTAGCCTCTATCATAAACATCAAGATGAATATTTTACTAAAAATATGATATCTCATATTAC 2340
DB 2320 TTGGCTTTCTATCATAGCACCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2379
QY 2341 ACGAGTAATAGATTAAATAAAAACTGAGCGCATTTTAAGTAATATTTAAATAATAAGTCAG 2400
DB 2380 ACGAGTAATAGATTAAATAAAAACTGAGCGCATTTTAAGTAATATTTAAATAATAAGTCAG 2439
QY 2401 TTAATCTAAATTTGTAATACATCATTTTGTGATTAATCATGACAGCCTATTGTTAAAAAT 2460
DB 2440 TTAATCTAAATTTGTAATACATCATTTTGTGATTAATCATGACAGCCTATTGTTAAAAAT 2499
QY 2461 GACAGCTATGCTTATATGAAAAAATATGATCGGCATGAATTTCTCAGCATTAACACAT 2520
DB 2500 GACAGCTATGCTTATATGAAAAAATATGATCGGCATGAATTTCTCAGCATTAACACAT 2559
QY 2521 GATTGGATCGAGAAAAATCAATCGCATCCACCATTTTAAAAAGCTCATTTAAAACTTATTTT 2580
DB 2560 GATTGGATCGAGAAAAATCAATCGCATCCACCATTTTAAAAAGCTCATTTAAAACTTATTTT 2619
QY 2581 AATGCAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGAGGTATGTTTATGAGC 2640
DB 2620 AATGCAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGAGGTATGTTTATGAGC 2679
QY 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTATTAAGAAAGTCATCACATCTTGCAGTCA 2700
DB 2680 TATGCGCTAGCGCATGAGCTTCTGACGATTATTAAGAAAGTCATCACATCTTGCAGTCA 2739
QY 2701 ATTGATAGTGTGCCAGAAATATAACACTCAGGATATTTGTTCCAAATTTGCACTTTTAAATC 2760
DB 2740 ATTGATAGTGTGCCAGAAATATAACACTCAGGATATTTGTTCCAAATTTGCACTTTTAAATC 2799
QY 2761 TTAGAAAAAGAAAAACCGGCATGTATTTAATAAAACATCGACCTGACTTATATGCTTGG 2820
DB 2800 TTAGAAAAAGAAAAACCGGCATGTATTTAATAAAACATCGACCTGACTTATATGCTTGG 2859
QY 2821 GAACGAAATTTCAATGAGACAAATGAACAAATTTGAAGTGCAGAAAGAGGAGAAATATA 2880
DB 2860 GAACGAAATTTCAATGAGACAAATGAACAAATTTGAAGTGCAGAAAGAGGAGAAATATA 2919
QY 2881 CCGTGTAAACAAGTTCATATTATTAATAGTATACTTATAAA 2920
DB 2920 CCGTGTAAACAAGTTCATATTATTAATAGTATAACCTATAAA 2959
```

## RESULT 9

ADP75667

ID ADP75667 standard; DNA; 2271 BP.

XX ADP75667;

XX ADP75667;

DT 12-AUG-2004 (first entry)

XX Pasteurella multocida truncated hyaluronic acid synthase gene #11.  
DE polymer production; hyaluronic acid polymer; chondroitin polymer;  
KW hyaluronic acid synthase; gene; ds; enzyme.

XX	Pasteurella multocida.
OS	WO2003029261-A2.
XX	
PN	
XX	
PD	10-APR-2003.
XX	
PF	12-JUL-2002; 2002WO-US022386..
XX	
PR	13-JUL-2001; 2001US-0305263P.
PR	23-JAN-2002; 2002US-030642P.
PR	08-MAY-2002; 2002US-00142143..
XX	
PA	(DEAN/) DEANGELIS P L.
XX	
PI	Deangelis PL;
XX	
DR	WPI; 2003-532558/50.
XX	
PT	Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by providing a functional acceptor, a synthase capable of elongating the acceptor and sugars such that the synthase elongates the acceptor to provide polymer.
PT	
PT	
XX	
PS	Disclosure; SEQ ID NO 20; 538pp; English.
XX	
CC	The invention comprises a method for producing a polymer, especially a hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than 150 sugars. The method involves providing a functional acceptor, and providing a synthase capable of elongating the functional acceptor, and providing sugars such that the synthase elongates the functional acceptor to provide the polymer. The method of the invention is useful for producing a hyaluronic acid or chondroitin polymer composed of 1-150 sugars. The present DNA sequence encodes a truncated Pasteurella multocida hyaluronic acid synthase of the invention.
CC	
XX	
SQ	Sequence 2271 BP; 812 A; 384 C; 404 G; 671 T; 0 U; 0 Other;
	Query Match 77.7%; Score 2267.8; DB 11; Length 2271;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 2269; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1 ATGAATACATTATCACAAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
Db	1 ATGAATACATTATCACAAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
Qy	61 AAATTATTTGAAAAGTCGGCGGAAATCTATGACGGAATAATTTGTGAATTTCAAATTACC 120
Db	61 AAATTATTTGAAAAGTCGGCGGAAATCTATGACGGAATAATTTGTGAATTTCAAATTACC 120
Qy	121 AAATGCAAGAAAAAAGCTCTCAGCACATCTTCTGTTTAATTCAGCACATCTTTCTGTAAT 180
Db	121 AAATGCCAAGAAAAAAGCTCTCAGCACATCTTCTGTTTAATTCAGCACATCTTTCTGTAAT 180
Qy	181 AAAAGAAGAAAAAGCTCAATGTTTGCAGTAGTGCCGTTAGATATTGCAACAACACTGTACTT 240
Db	181 AAAAGAAGAAAAAGCTCAATGTTTGCAGTAGTGCCGTTAGATATTGCAACAACACTGTACTT 240
Qy	241 TCCAACGTAATAAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300
Db	241 TCCAACGTAATAAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300
Qy	301 AAATTGCTCACTCAGAGAAATCTGAAATGCGGAGGTAAAGCGGTCGCCCTCTGACCA 360
Db	301 AAATTGCTCACTCAGAGAAATCTGAAATGCGGAGGTAAAGCGGTCGCCCTCTGACCA 360
Qy	361 AAAAGATTTTCCCAGAAAGCTTGGTTTTAGCGCCCTTTTACCTGATCATGTTAAATGATTTACA 420
Db	361 AAAAGATTTTCCCAGAAAGCTTGGTTTTAGCGCCCTTTTACCTGATCATGTTAAATGATTTACA 420
Qy	421 TGGTACAAAAGCGAAAGAACACTTGGGCATATAAAACCTGGAACATCAACATGTTGGTCTT 480
Db	421 TGGTACAAAAGCGAAAGAACACTTGGGCATATAAAACCTGGAACATCAACATGTTGGTCTT 480



```
Qy 1561 TATTACATTGGCAGTTAGATTAGATTCAGATGATTAATCTTGAGCGCTGATGAGTGTGAAGTGTGT 1620
Db 1561 TATTACATTGGCAGTTAGATTAGATTCAGATGATTAATCTTGAGCGCTGATGAGTGTGAAGTGTGT 1620
Qy 1621 TTAAGAAGATTTTAAAGATATAAAGCGTAGCTGTGTGTATACCACTAATAGAAAAGTGC 1680
Db 1621 TTAAGAAGATTTTAAAGATATAAAGCGTAGCTGTGTGTATACCACTAATAGAAAAGTGC 1680
Qy 1681 AATCGGATGTCAGCTTAATCGCTAAATGGTTTACAAATGGCCAGAGAAATTTTACGAGAAAAA 1740
Db 1681 AATCGGATGTCAGCTTAATCGCTAAATGGTTTACAAATGGCCAGAGAAATTTTACGAGAAAAA 1740
Qy 1741 CTCACACGGCTATGATGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTGGCAATTTA 1800
Db 1741 CTCACACGGCTATGATGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTGGCAATTTA 1800
Qy 1801 ACTGATGATTCATGATGAAAAAATTTGAAATGCCGTAGACTATGACATGCTTCTCAACTC 1860
Db 1801 ACTGATGATTCATGATGAAAAAATTTGAAATGCCGTAGACTATGACATGCTTCTCAACTC 1860
Qy 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1920
Db 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1920
Qy 1921 GATAACATCAATTAAGAAATTTGGCAATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980
Db 1921 GATAACATCAATTAAGAAATTTGGCAATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980
Qy 1981 CAGTCATTAATAGACAGGCAATTAATTAATTAATGATGAGAAATTTGATGATTTAGAT 2040
Db 1981 CAGTCATTAATAGACAGGCAATTAATTAATTAATGATGAGAAATTTGATGATTTAGAT 2040
Qy 2041 GAAAGTGAAGATATATTTTCAATAAACCCTGATATCAAGAGAGATTTGATATCTTA 2100
Db 2041 GAAAGTGAAGATATATTTTCAATAAACCCTGATATCAAGAGAGATTTGATATCTTA 2100
Qy 2101 AAAGATATTAATAATCATCCAGATTAAGATGCAAAATCGCAGTCAAGTATTTTATCCC 2160
Db 2101 AAAGATATTAATAATCATCCAGATTAAGATGCAAAATCGCAGTCAAGTATTTTATCCC 2160
Qy 2161 AATACATTAACGGCTTGTAGTGAAGAACTAAACATATTTATGATATATAAATAATA 2220
Db 2161 AATACATTAACGGCTTGTAGTGAAGAACTAAACATATTTATGATATATAAATAATA 2220
Qy 2221 TTCGTTATTTCTACATGTTGATGAAGATCAATCTTACACAGATATCAAA 2271
Db 2221 TTCGTTATTTCTACATGTTGATGAAGATCAATCTTACACAGATATCTAA 2271
```

## RESULT 10

ABAO5098  
ID ABAO5098 standard; DNA; 2979 BP.

XX AC ABAO5098;

XX DT 22-FEB-2002 (first entry)

XX DE Pasteurella multocida chondroitin synthase gene #2.

XX KW Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer;  
XX KW eye application; joint application; moisturiser; drug delivery;  
XX KW wound dressing; biocompatible film; db.

XX OS Pasteurella multocida.

XX PH Key Location/Qualifiers  
XX FT 61..2958  
XX FT /tag= a  
XX FT /product= "chondroitin synthase"

XX WO200180810-A2.  
XX PN  
XX XX

PD 01-NOV-2001.

XX 25-APR-2001; 2001WO-US013395.

XX 25-APR-2000; 2000US-0199538P.

XX (DANG/) DE ANGELIS P L.

XX De Angelis PL;

XX WPI; 2002-049237/06.

XX P-PSDB; AAM47336.

XX New chondroitin synthase gene obtained from Pasteurella multocida, useful  
as hyaluronan polysaccharide substitute in medical or cosmetic  
applications, e.g. for eye or joint applications, for moisturizer or  
wound dressings.

XX Claim 4; Page 120-121; 125pp; English.

XX The present invention relates to the coding sequence of the Pasteurella  
multocida chondroitin synthase. A chondroitin polysaccharide may be used  
as a hyaluronan polysaccharide substitute in medical or cosmetic  
applications, for example in eye or joint applications, for moisturiser  
or wound dressings. The enzyme may be used in covalently coupling  
specific drugs, proteins or toxins to the structurally modified  
chondroitin for general or targeted drug delivery or radiological  
procedures, covalently cross linking the hyaluronic acid itself or to  
other supports to achieve a gel or other three dimensional biomaterial  
with stronger physical properties, and covalently linking hyaluronic acid  
to a surface to create a biocompatible film or monolayer. The present  
sequence is one version of the coding sequence of the invention

XX Sequence 2979 BP; 1130 A; 466 C; 495 G; 888 T; 0 U; 0 Other;

Query Match 77.6%; Score 2266.4; DB 6; Length 2979;

Best Local Similarity 86.4%; Pred. No. 0;

Matches 2523; Conservative 0; Mismatches 376; Indels 21; Gaps 1;

Qy 1 ATGAATACATTATCACAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC 60

Db 61 ATGAATACATTATCACAGCAATAAAGCATATTAACAGCAATGACTATGAATTAGCACTC 120

Qy 61 AAATTTATTTGAAAGTCTGGGCGAAATCTATGGACGGAATAATGTTGAAATTTCAATTACC 120

Db 121 AAATTTATTTGAAAGTCTGGTGAACCTTACGGCGGAAAAATCGTTGAATTTCCAAATATC 180

Qy 121 AAATGCAAGAAAAAATCTCAGACATCTTCTGTTAATTCAGCACATCTTTCTGTAAT 180

Db 181 AAATGTAAGAAAAAATCTCGACCAATTC-----TTATGTAAGT 219

Qy 181 AAAGAAGAAAAAATGCAATGTTTGGATAGTCCGTTAGATATTTGCAACACAACTGTACTT 240

Db 220 GAAGATAAAAAAATGCAATGTTTGGATAGTCTATGATATCGCAACACAGCTTACTT 279

Qy 241 TCCAAACGTAAAAAATTAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATTAATGG 300

Db 280 TCCAAACGTAAAAAATTAACCTATCCGAATCAGAAAAAACAAGTTAAAAAATTAATGG 339

Qy 301 AAATGCTCCTCAGAGAGAAATCTGAAATTCGGAGGTAAGAGCGGTCGCTCTGTACCA 360

Db 340 AAATCTATCACTGGGAAAAAATCGGAGAACGAGAAATCAGAAAGGTGGAACTAGTACCC 399

Qy 361 AAAGATTTTCCCAAGATCTGTTTACGCGCTTTTACCTGATCATGTTTAATGATTTTACA 420

Db 400 AAAGATTTTCCCTAAGATCTTGTCTGCTCATTTGCCAGATCATGTTAATGATTTTACA 459

Qy 421 TGGTACAAAAAGCGAAAAAGAAAGACTTGGGCATATAAAACCTGAACATCAACATGTTGGTCTT 480

Db 460 TGGTACAAAAATCGAAAAAAGCTTGGTATTAAGCCCTGTAATAAGAAATATCGGTCTT 519

Qy 481 TCTATTATCGTTACAACTTCAATCGACACAGCAATTTTATCGATTTACATTTAGCCCTGTTA 540

Db 520 TCTATTATTTCTTACATTTAATCGTAGCCGCTATTTTAGATATTAACGTTAGCCCTGTTT 579

Qy	541	GTAAACCAAAAAACACATTAACCGCTTTGAAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Dd	580	GTCAATCAGAAAAACAACACTACCCATTTTTGAAGTCGTTGTCAGATGATGGTAGTAAGGAA	639
Qy	601	GATCTATCACCGATCATTGCGCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA	660
Dd	640	AACCTTACTTACCATTTGTGCAAAAAATAGAAACAAAACTTGACATAAAGTATGTAAGCAA	699
Qy	661	AAAGATAACGGTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT	720
Dd	700	AAAGATTATGGATCAATCTGTGTGACAGTCAAGAACTTAGGTTACGTACAGCAAGTAT	759
Qy	721	GACTTTTATGGCTTACTCGACTGTGATATGATGCGGCAAAATCCATTAATGGGTTCACTTTAT	780
Dd	760	GATTTGTCTCGATTCTAGACTGCGATATGATGATGATGATGATGATGATGATGATGATGAT	819
Qy	781	GTTTCAGAGCTATTAGAGATGATGATTTAAACATCAATCTGTCACAGAAATACATCGAT	840
Dd	820	CTTACAGAACTATTAGAGACAAATGATATGTTTTAATTTGACCTAGAAAATATGTTGAT	879
Qy	841	ACACAAATATTGACCCAAAGACTTCTTAAATAACCGAGTTTGTGTTGAATCAATTACCA	900
Dd	880	ACTCATATATTACCGCAGAACATTCCTTAAACGATCCATATTTAATAGAACTACTACCT	939
Qy	901	GAACTGAAAAACCAATAATAGTGTGCGGCAAAAGGGGAAGGAAACAGTTTCTCTGGATTGG	960
Dd	940	GAAACCGCTACAAATTAACATCTTCGATTACATCAAAAGGAAATATATCCTGTTGGATTGG	999
Qy	961	CGCTTAGAACAAATTCGAAAAACAGAAATCTCGCTTATCCGATTCGCTTTCGGTTTTT	1020
Dd	1000	AGATTAGAACAAATTTCAAAAAAACCGATTAATCTACGCTATGATGATTTCTCGGTTTCGTTAT	1059
Qy	1021	TTTCGGCGGGTAATGTTGCTTTCGCTAAAAAATGGCTAAATAAATCCGGTTTCTTTGAT	1080
Dd	1060	TTTAGTTCGGGTATGTTGCAATTTCTTAAAGAAAGGCTTAATAAAGTAGGTTGGTTCGAT	1119
Qy	1081	GAGAAATTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATTCGCTTTATTCGGTTAC	1140
Dd	1120	GAGAAATTAATCAATTCGGGGGGGAGAGATGTAGAAATTTGGTTACAGATTAATTTGCCAAA	1179
Qy	1141	GGTAGTTTCTTTAAACCTAATTTGATGGCATTTATGGCTTACCATCAAGACCAACAGGTAAA	1200
Dd	1180	GGCTGTTTTTTCAGAGTAAATTTGACGGCGGAATGGCATCAAGAACCAACCTTGGTAAA	1239
Qy	1201	GAAATGAAACCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG	1260
Dd	1240	GAAATGAAACAGACCGGAGCTGGTAAAGTATTACGCTTAAAAATTTGTGAAGAAAAAG	1299
Qy	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT	1320
Dd	1300	GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAAGATTCACATATTATAGAAATACCT	1359
Qy	1321	TTAGTTTCAATTTATATCCAGCTTTAATCTGTGCAAACTATATCAAGTTGCGGTAGAT	1380
Dd	1360	TTAGTTTCTTATTTATATCCCGCTTATAAATCTGTGCAAAATTTATTTCAAGATGTTAGAT	1419
Qy	1381	AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTGAACGATGGTTCAACA	1440
Dd	1420	AGTGCTTTAATCAAACTGTTGTCATCTCGAGGTTTGTATTGTTGAACGATGGTTCAACA	1479
Qy	1441	GATAATACCTTAGAAGTATCAATAGCTTTTATGGTAAATATCTTAGGGTACGATCATG	1500
Dd	1480	GATAATACCTTAGAAGTATCAATAGCTTTTATGGTAAATATCTTAGGGTACGATCATG	1539
Qy	1501	TCTAAACCAATGGCGGATAGCTTCAGCATCAATGACCGGTTTCTTTTGGCTAAAGGT	1560
Dd	1540	TCTAAACCAATGGCGGATAGCTTCAGCATCAATGACCGGTTTCTTTTGGCTAAAGGT	1599
Qy	1561	TATTACATTTGGCAGTTAGATTAGATGATTTATCTTTGAGCTGTGATGAGTTGAACTGTGT	1620
Dd	1600	TATTACATTTGGCAGTTAGATTAGATGATTTATCTTTGAGCTGTGATGAGTTGAACTGTGT	1659

Qy	1621	TTAAAAAGAAATTTTTAAAAAGATAAAACGCTAGCTTGTGTTTATATACCACATAATAGAAACGTC	1680
Dd	1660	TTAAAAAGAAATTTTTAAAAAGATAAAACGCTAGCTTGTGTTTATATACCACATAATAGAAACGTC	1719
Qy	1681	AATCCGGATGGTAGCTTAATTCGCTAATGTTTCAATTTGGCCAGAAATTTTTCACGAGAAAAA	1740
Dd	1720	AATCCGGATGGTAGCTTAATTCGCTAATGTTTCAATTTGGCCAGAAATTTTTCACGAGAAAAA	1779
Qy	1741	CTCAACCGGCTATGATTTGCTCACCCTTTAGATGTTTACGATTTAGAGCTTGGCATTTTA	1800
Dd	1780	CTCAACCGGCTATGATTTGCTCACCCTTTAGATGTTTACGATTTAGAGCTTGGCATTTTA	1839
Qy	1801	ACTGATGGATTCAATCAAAAAATTTGAAATTCGCGTAGACTATGACATGTTTCTCAAACTC	1860
Dd	1840	ACGGATGGATTCAATCAAAAAATTTGAAATTCGCGTAGACTATGACATGTTTCTTAACTC	1899
Qy	1861	AGTGAAGTTGGAAAAATTTAAAACTTTAAATAAATCTGCTATAACCGTGTTTATACATGTT	1920
Dd	1900	AGTGAAGTTGGAAAAATTTAAAACTTTAAATAAATCTGCTATAACCGCGTATTACATGTT	1959
Qy	1921	GATAACACATCAATTTAAGAAACCTTGCGATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT	1980
Dd	1960	GATAACACATCCATTTAAGAAACCTTGCGATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT	2019
Qy	1981	CAGTCATTAATAAGACAGGCATACTTATTAATAATTCAGCAATTTTGTATGATTTAGAT	2040
Dd	2020	CAGTCATTAATAAGACAGGCATACTTATTAATAATTCAGCAATTTTGTATGATTTAGAT	2079
Qy	2041	GAAAGTAGAAAGTATATTTTCAATAAAAAACCGCTGAATATCAAGAAAGAGATTTGATATCTTA	2100
Dd	2080	GAAAGTAGAAAGTATATTTTCAATAAAAAACCGCTGAATATCAAGAAAGAGATTTGATATCTTA	2139
Qy	2101	AAAGATATTAAAAATCATCCAGAAATAAGATGCCAAAAATCGCAGTCAGTATTTTATATCCC	2160
Dd	2140	AAAGATCTTAAATCTATTCAAAAATAAGATGCCAAAAATCGCAGTCAGTATTTTATATCCC	2199
Qy	2161	AATACATTTAAACCGCTTAGTGAAGAACTAAAAAATAATTTAAATAATAATAAAAAATA	2220
Dd	2200	AATACATTTAAACCGCTTAGTGAAGAACTAAAAAATAATTTAAATAATAATAAAAAATA	2259
Qy	2221	TTGGTTATTGCTTACATGTTTGAAGAATCATCTTACACAGATATCAAAAAAGAAATA	2280
Dd	2260	TTGGTTATTATTCTACTGTTGATAGAAATCATCTTACACAGATATCAAAAAAGAAATA	2319
Qy	2281	CTAGCTTCTATCATAAAAATCAAGTGAATATTTTACTAAATTAATGATATCTCATATATAC	2340
Dd	2320	TTGGCTTTCTATCATAGACCAAGTGAATATTTTACTAAATTAATGATATCTCATATATAC	2379
Qy	2341	ACGAGTAATAGATTAAATAAACTGAGGCGCATTTTAAAGTAAATTAATAAAATTAAGTCAG	2400
Dd	2380	ACGAGTAATAGACTAAATAAACTGAGGCGCATTTTAAAGTAAATTAATAAAATTAAGTCAG	2439
Qy	2401	TTAAATCTAAATTTGTAATACATCATTTTGTATAATCATGACAGCTTATTCGTTTAAAAAT	2460
Dd	2440	TTAAATCTAAATTTGTAATACATCATTTTGTATAATCATGACAGCTTATTCGTTTAAAAAT	2499
Qy	2461	GACAGCTATGCTTATATGAAAAAATATGATGTGGCAATGAATTTTCTCAGCATTTAACAT	2520
Dd	2500	GACAGCTATGCTTATATGAAAAAATATGATGTGGCAATGAATTTTCTCAGCATTTAACAT	2559
Qy	2521	GATTGGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAGGCTCATTTAAACCTTATTTT	2580
Dd	2560	GATTGGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAGGCTCATTTAAACCTTATTTT	2619
Qy	2581	AATGACAATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCAACAAGGTATGTTTATGACG	2640
Dd	2620	AATGACAATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCAACAAGGTATGTTTATGACG	2679
Qy	2641	TATCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAAGTCATCATCTTGGCAGTCA	2700
Dd	2680	TATCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAAGTCATCATCTTGGCAGTCA	2739
Qy	2701	ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTTCCCAATTTTGCACCTTTTAAATC	2760

```
Db 2740 ATTGATAGTGGCCAGAAATAAACAACACACGAGATATTTGGTCCAAATTTGCACATTTTAATC 2799
Qy 2761 TTAGAAAAGAAAACCGGCCATGTATTTAATAAACAATCGACCTGACTTATATGCTTGG 2820
Db 2800 TTAGAAAAGAAAACCGGCCATGTATTTAATAAACAATCGACCTGACTTATATGCTTGG 2859
Qy 2821 GAACGAAATTTACAAATGACGACAAATGAACAAATTTGAAGTGCAGGAGGAGGAGAAATATA 2880
Db 2860 GAACGAAATTTACAAATGACGACAAATGAACAAATTTGAAGTGCAGGAGGAGGAGGAAATATC 2919
Qy 2881 CCTGTTAAAGTTCATTTAATAAGTATAACTCTATAA 2920
Db 2920 CCGGTTAAAGTTCATTTAATAAGTATAAGCTATAAA 2959

RESULT 11
ADP75650
ID ADP75650 standard; DNA; 2979 BP.
XX
XX ADP75650;
AC
XX
XX 12-AUG-2004 (first entry)
DT
XX
XX Pasteurella multocida chondroitin synthase coding sequence #1.
DE
XX polymer production; hyaluronic acid polymer; chondroitin polymer;
KW chondroitin synthase; gene; ds; enzyme.
XX
XX Pasteurella multocida.
OS
XX
XX WO2003029261-A2.
FN
XX
XX 10-APR-2003.
PD
XX
XX 12-JUL-2002; 2002WO-US022386.
XX
XX 13-JUL-2001; 2001US-0305263P.
PR
XX 22-JAN-2002; 2002US-0350642P.
PR
XX 08-MAY-2002; 2002US-00142143.
XX
XX (DEAN/) DEANGELIS P L.
PA
XX
XX Deangelis PL;
PI
XX
XX WPI; 2003-532558/50.
DR
XX P-PSDB; ADP75651.
XX
XX Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by
PT providing a functional acceptor, a synthase capable of elongating the
PT acceptor and sugars such that synthase elongates the acceptor to provide
PT polymer.
XX
XX Claim 86; SEQ ID NO 3; 538pp; English.
PS
XX
XX The invention comprises a method for producing a polymer, especially a
CC hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than
CC 150 sugars. The method involves providing a functional acceptor,
CC providing a synthase capable of elongating the functional acceptor, and
CC providing sugars such that the synthase elongates the functional acceptor
CC to provide the polymer. The method of the invention is useful for
CC producing a hyaluronic acid or chondroitin polymer composed of 1-150
CC sugars. The present DNA sequence encodes a Pasteurella multocida
CC chondroitin synthase of the invention.
XX
XX Sequence 2979 BP; 1130 A; 466 C; 495 G; 888 T; 0 U; 0 Other;
SQ

Query Match 77.6%; Score 2266.4; DB 11; Length 2979;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 2523; Conservative 0; Mismatches 376; Indels 21; Gaps 1;

Qy 1 ATCAATACATTATCAACGCAATATAAAGCATATAACAGCAATGACTATCAATAGCACATC 60
|||||
```

```
Db 61 ATGAATACATTATCAACGCAATATAAAGCATATAACAGCAATGACTATGAATTAGCACTC 120
Qy 61 AAATTTATTTGAAAGTCGGCGGAAATCTATGCGGAAATTTGTGTAATTTCAAATTAACC 120
|||||
Db 121 AAATTTATTTGAAAGTCGTCTGAAACCTACGGCGGAAATTCGTGTAATTTCAAATTAATC 180
|||||
Qy 121 AAATGCAAAAGAAAACCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTCTCTGTAAT 180
|||||
Db 181 AAATGTAAGAAAACCTCTCGAACCAATTC-----TTATGTAAGT 219
|||||
Qy 181 AAAGAAGAAAAGTCAATGTTTGGGATAGTCGTTAGATATTGCAACACAACTGTTACTT 240
|||||
Db 220 GAAGTAAAAAACAACAGTGTTCGATAGTCATAGATATCGCAACACAGCTCTTACTT 279
|||||
Qy 241 TCCAAACGTAAAAAATTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300
|||||
Db 280 TCCAAACGTAAAAAATTTAACTCTATCCGAATCAGAAAAAACAACGTTTAAAAAATAAATGG 339
|||||
Qy 301 AAATTGCTCACTGAGAGAAATCTGAAATTCGGAGGTAGAGCGGTCCGCTTGTACCA 360
|||||
Db 340 AAATCTATCACTGGGAAAAAATCGAGAACGAGAAATCAGAAAAGGTGGAACATAGTACCC 399
|||||
Qy 361 AAGATTTTCCCAAGATCTGGTTTGTAGCGCTTTTACTGATCATGTTAAATGATTTTACA 420
|||||
Db 400 AAGATTTTCCCAAGATCTGGTTTGTAGCGCTTTTACTGATCATGTTAAATGATTTTACA 459
|||||
Qy 421 TGGTACAAAAAGCGAAAAAGAAAGACTTGGCAATAAAACCTGAACATCAACATGTTGGTCTT 480
|||||
Db 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATAAAGCTGTAAATAAGAAATATCGGTCTT 519
|||||
Qy 481 TCTATTATCGTTTACAACATTCATTCGACCGACCAATTTTATCGATTACATTTAGCCCTGTTT 540
|||||
Db 520 TCTATTATTAATCTCTACATTTAATCGTAGCGCTATTTTAGATATAACGTTTAGCCCTGTTT 579
|||||
Qy 541 GTAACCAAAAAACACATTTACCGCTTTGAGCTTATTCGTGACAGATGATGGTAGTCAGGAA 600
|||||
Db 580 GTCAATCAGAAAAACAACCTCCCAATTTGAGCTGTTGTCAGATGATGGTAGTAAGNA 639
|||||
Qy 601 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGAATTTTCGCTACGTCAGACAA 660
|||||
Db 640 AACTTACTTACCAATTTGCAAAAATACGAAACAAAACCTTGACATAAAGTATGTAAGACAA 699
|||||
Qy 661 AAAGATAACGGTTTCAAGCCAGTCGCGCTCGGAATATGGGATTTACGCTTAGCAAAATAT 720
|||||
Db 700 AAAGATTATGATATCAATTTGTCAGCTCAGAACTTAGGTTTACGTACAGCAAAAGTAT 759
|||||
Qy 721 GACTTTATTTGCTTACTCGACTGTGATGATGGCCCAATCCATTTATGTTTCATCTTAT 780
|||||
Db 760 GATTTGCTCTCGATTTCTAGACTGGGATATGGCAACCAAAATTTATGGTTCAATCTTAT 819
|||||
Qy 781 GTTGACAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT 840
|||||
Db 820 CTTACGAACTATTAGAAGACAAATGATATTTGTTTAAATTTGGACCTAGAAAAATATGTTGAT 879
|||||
Qy 841 ACACAACATATTGACCCCAAGACTTCTTAATAAACGCGAGTTTTCCTTGAATCATATACCA 900
|||||
Db 880 ACTCATATAATTACCGCAGAACAAATTCCTTAACGATCCATATTTAATAAGAAATCACATCT 939
|||||
Qy 901 GAAGTGAACCAATAATAGTGTTCGCCCAAAAGGGAGGAAACAGTTTCTCTGATTCG 960
|||||
Db 940 GAAACCGGTACAAAATAACAAATTCGATTTACATCAAAAGGAAATATATCGTTGATTCG 999
|||||
Qy 961 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCTTTTCGCTTTT 1020
|||||
Db 1000 AGATTAGAACATTTCAAAAAAACCGATTAATCTACGCTATGTGATTTCCGTTTCGTTAT 1059
|||||
Qy 1021 TTTGCGCGGGTAATGTTGCTTTTCGCTTAAAAAATCGCTAAATAAATTCGCTTTCTTGTAT 1080
|||||
Db 1060 TTTAGTTGCGGTAATGTTGCAATTTCTAAAGAAATCGCTAAAATAAAGTAGTGGTTTCGAT 1119
|||||
Qy 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTTGGAATTTGGATATCGCTTATTCGCTTAC 1140
|||||
Db 1120 GAAGAATTTAATCATTTGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA 1179
|||||
```

1141 GGTAGTTCTTTAAACCTATTGATGGCATATTGSCCTACCAATCAAGACCCACCGAGTAA 1200  
1180 GGCTGTTTTTCAGAGTAAATTTGACGGCGGAATGGCATACCATCAAGAAACCACTGGTAAA 1239  
1201 GAAATGAAACCGATCGTGAACGGGAAATATATACGCTCGATATATATGAGRAAAG 1260  
1240 GAAATGAAACAGACCGGAGCTGGTAAAGTATTACGCTTAAATTTGTGAAGAAAG 1299  
1261 GTCCCTTATATCTATAGAAAATTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGATACCT 1359  
1321 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAAACGTTGCGTAGAT 1380  
1360 TTAGTTTCTATTTATATCCCGCTTATAAATGTGCAAAATATAATCAAGATGTGTAGAT 1419  
1381 AGTCACTGAATCAGATGTTGTTGATCTCAGGTTTGTATTTCTAAGATGTTTCAACA 1440  
1420 AGTGTCTTAAATCAAACTGTTTGTGATCTCGAGTTTGTATTTGTAACGATGGTTCAACA 1479  
1441 GATAATACCTTAGAAGTGAATCAATAAGCTTTATGTTAATAATCTTAGGGTACGCATCATG 1500  
1480 GATAATACCTTAGAAGTGAATCAATAAGCTTTATGTTAATAATCTTAGGGTACGCATCATG 1539  
1501 TCTAAACCAATGCGGGAATAGCCTCAGCATCAAAATGCGAGCGTTTCTTTGCTAAAGGT 1560  
1540 TCTAAACCAATGCGGGAATAGCCTCAGCATCAAAATGCGAGCGTTTCTTTGCTAAAGGT 1599  
1561 TATTACATTTGGGAGTTAGATTTCAGATGATTTATCTTGAGCCTGATGCAATTTGAATGTGT 1620  
1600 TATTACATTTGGGAGTTAGATTTCAGATGATTTATCTTGAGCCTGATGCAATTTGAATGTGT 1659  
1621 TTTAAAGAAATTTTAAAGAGATAAAACGCTAGCTGTGTTTATACCACTAATAGAAACGTC 1680  
1660 TTTAAAGAAATTTTAAAGAGATAAAACGCTAGCTGTGTTTATACCACTAATAGAAACGTC 1719  
1681 AATCCGGATGTTAGCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTTCACGAGAAAA 1740  
1720 AATCCGGATGTTAGCTTAATCGCTAATGTTTACAAATGGCCAGAAATTTTTCACGAGAAAA 1779  
1741 CTCACACGGCTATGATTTGCTCACCATTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
1780 CTCACACGGCTATGATTTGCTCACCATTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1839  
1801 ACTGATGATTTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCATAACTC 1860  
1840 ACGATGATTTTACGAAAAATTTGAAACGCGGTGATTTATGACATGTTCTTAAACTC 1899  
1861 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAAATCTGCTATAACCGGTGATTTACATGGT 1920  
1900 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAAATCTGCTATAACCGGTGATTTACATGGT 1959  
1921 GATAACACATCAATTTAAGAACTTTGGCATTTCAAGAAAAACCATTTTGTGTAGTCAAT 1980  
1960 GATAACACATCAATTTAAGAACTTTGGCATTTCAAGAAAAACCATTTTGTGTAGTCAAT 2019  
1981 CAGTCATTTAAATAGACAAGGATCACTTATATATTAATTTATGCAATTTTGTATGATTTAGAT 2040  
2020 CAGTCATTTAAATAGACAAGGATCACTTATATATTAATTTATGCAATTTTGTATGATTTAGAT 2079  
2041 GAAAGTAGAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAAAGATTTGATATCTTA 2100  
2080 GAAAGTAGAAGTATATCTTCAATAAAAACCGCTGAATATCAAGAAAGATTTGATATTTTA 2139  
2101 AAAGATTTAAATCATCTCAGAAATTAAGATGCGCAAAATCGCAGTCAGTATTTTATCCC 2160  
2140 AAAGATCTTAAACTCATTTCAAAATAAAGATGCGCAAAATCGCAGTCAGTATTTTATCCC 2199  
2161 AATACATTTAAACGGCTTAGTGAAAAAATCTTAAACATATTTATTTGAATATAAATAAATA 2220  
2200 AATACATTTAAACGGCTTAGTGAAAAAATCTTAAACATATTTATTTGAATATAAATAAATA 2259

2221 TTGCTTATTGTTCTACATGTTGATAGAATCATCTTACACGATATCAAAAAAGAAATA 2280  
2260 TTGCTTATTATTCTCATGTTGATAAGAATCATCTTACACGATATCAAAAAAGAAATA 2319  
2281 CTAGCCTTCTATCATAAAAATCAAGTGAATATTTTACTAAATTAATGATATCTCATATTAC 2340  
2320 TTGCTTCTTATCATTAAGCACCAGTGAATATTTTACTAAATTAATGATATCTCATATTAC 2379  
2341 ACAGTAATAGATTAATAAAAACTGAGGCGCATTTAAGTAAATTAATTAATTAAGTCAG 2400  
2380 ACAGTAATAGACTTAATAAAAACTGAGGCACATTTAAGTAAATTAATTAATTAAGTCAG 2439  
2401 TTTAAATCTAAATTTGCTGAATACATCATTTTGTGAATAATCATGACAGCCTATTTCGTTAAAAAT 2460  
2440 TTTAAATCTAAATTTGCTGAATACATCATTTTGTGAATAATCATGACAGCCTATTTCGTTAAAAAT 2499  
2461 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAAATTTCTCAGCATTAACACAT 2520  
2500 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAAATTTCTCAGCATTAACACAT 2559  
2521 GATTGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAAAGCTGATTTAAACCTATTTT 2580  
2560 GATTGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAAAGCTGATTTAAACCTATTTT 2619  
2581 AATGACAAATGACTTAAAAAGTATGAATGTGAAGGGGCATCAAGGTATGTTTATGACG 2640  
2620 AATGACAAATGACTTAAAAAGTATGAATGTGAAGGGGCATCAAGGTATGTTTATGACG 2679  
2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAAAGTATCATCATCTTGCAGTCA 2700  
2680 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAAAGTATCATCATCTTGCAGTCA 2739  
2701 ATTGATAGTGTCCGCAATATAACACAGGATTTTGGTTCGAATTTGCACTTTTAAATC 2760  
2740 ATTGATAGTGTCCGCAATATAACACAGGATTTTGGTTCGAATTTTAAATTTGCACTTTTAAATC 2799  
2761 TTAGAAAAAGAAACCGCCCATGTTTAAATAAACATCGACCTGACTTATATGSCCTTGG 2820  
2800 TTAGAAAAAGAAACCGCCCATGTTTAAATAAACATCGACCTGACTTATATGSCCTTGG 2859  
2821 GAACGAAAAATTTACAAATGGAACAAATGAACAAATTTGAAAGTGCAAAAAGGAGAAAAATATA 2880  
2860 GAACGAAAAATTTACAAATGGAACAAATGAACAAATTTGAAAGTGCAAAAAGGAGAAAAATATA 2919  
2881 CCTGTTAAACAGTTCATTTAATAAGTATTAATCTCTATAAA 2920  
2920 CCGTTAAACAGTTCATTTAATAAGTATTAATCTCTATAAA 2959

RESULT 12  
AEA04966

ID AEA04966 standard; DNA; 2979 BP.

XX AEA04966;

XX AC AEA04966;

XX DT 11-AUG-2005 (first entry)

XX DE Chondroitin synthase, PmCS, coding sequence, SEQ ID 4.

XX KW Chondroitin synthase; polysaccharide; gene; ds.

XX OS Pasteurella multocida.

XX FH Key Location/Qualifiers

XX FT CDS 61..2958

XX FT /\*tag= a

XX FT /product= "PmCS"

XX PN US2005124046-A1.

XX PD 09-JUN-2005.

XX PF 16-JUL-2002; 2002US-00197153.

XX 10-NOV-1999; 99US-00437277.  
XX (DEAN/) DEANGELIS P L.  
XX Deangelis PL;  
XX WPI: 2005-417007/42.  
DR P-PSDB; AEA04965.  
DR GENBANK; AF195517.  
XX  
PT Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin),  
PT useful in polysaccharide polymer grafting, comprises providing hyaluronic  
PT acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the  
PT functional acceptor.  
XX  
XX Disclosure; SEQ ID NO 4; 41pp; English.  
XX  
CC The present invention relates to a method for elongating a functional  
CC acceptor. The method comprises providing a hyaluronic acid (HA) synthase  
CC (PmHAS; AEA04963) capable of elongating the functional acceptor and  
CC providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid  
CC synthase elongates the functional acceptor. PmHAS adds sugars to the  
CC nonreducing end of a growing polymer chain. The PmHAS sequence is  
CC significantly different from the other known HA synthases; there appears  
CC to be only two short potential sequence motifs (AEA04967 and AEA04968) in  
CC common between PmHAS and the other HA synthases. The method is useful in  
CC polysaccharide polymer grafting, which may be utilized in the development  
CC of biotechnological medical improvements. These may be used for producing  
CC hybrid polysaccharides or for forming polysaccharide coatings. Also  
CC disclosed is chondroitin synthase (PmCS; AEA04965) and its coding  
CC sequence (AEA04966) from Pasteurella multocida. Type A P. multocida  
CC produces a HA capsule [GlcUA-GlcNAc repeats] and possesses the PmHAS  
CC enzyme. On the other hand, Type P. multocida produce a chondroitin or  
CC chondroitin-like polymer capsule [GlcUA-GalNAc repeats] using PmCS.  
CC Either HA or chondroitin chains can serve as acceptors for PmCS as both  
CC acceptors serve well for PmHAS.  
XX  
SQ Sequence 2979 BP; 1130 A; 466 G; 495 G; 888 T; 0 U; 0 Other;  
Query Match 77.6%; Score 2266.4; DB 14; Length 2979;  
Best Local Similarity 86.4%; Pred. No. 0;  
Matches 2523; Conservative 0; Mismatches 376; Indels 21; Gaps 1;  
QY 1 ATGAATACATTTATCAACGAATATAAGCATATAACAGCAATGACTATCAATAGCACTC 60  
DB 61 ATGAATACATTTATCAACGAATATAAGCATATAACAGCAATGACTATCAATAGCACTC 120  
QY 61 AAATTATTTCGAAGTCGGGAAATCTATGGACGGAAATTTGTAATTTCAATATACC 120  
DB 121 AAATTATTTCGAAGTCGCTGAAACCTACGGCGGAAATTCGTTGAAATTCNAATATC 180  
QY 121 AAATGCAAGAAATCTCTCAGCACATCTCTCTGTTTAATTCAGCACATCTTTCTGTAAT 180  
DB 181 AAATGTAAGAAATCTCTCGACCAATTC-----TTATGTAAGT 219  
QY 181 AAGAAGAAATAGTCAATGTTTCGGATAGTCGCTTAGATATTCGCAACACAACTGTTACTT 240  
DB 220 GAAGATAAATAAATACAGTGTTCGATAGCTCATTTAGATATCGCAACACAGCTCTTACTT 279  
QY 241 TCCAACGTAAAAAATAGTACTTTCTGACTCGGAAAAAACAACGTTTAAAAAATAATGG 300  
DB 280 TCCAACGTAAAAAATTAACCTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAATGG 339  
QY 301 AAATTGCTCACTCAGAAAGAAATCTGAAAAATGCGGAGGTAAAGCGGTTCGCCCTTGTAACA 360  
DB 340 AAATCTATCACTCGGAAAAAATCGGAGACGCAAGAAATCAGAAAGTGGAACTAGTACCC 399  
QY 361 AAGAATTTTCCAAAGATCTGGTTTATAGCGCCCTTTACCTGATCATGTTAATGATTTTACA 420  
DB 400 AAGAATTTTCCAAAGATCTGGTTTATAGCGCCCTTTACCTGATCATGTTAATGATTTTACA 459  
QY 421 TGGTACAAAGCAAGAAAGAAAGACTTTGGCATAAAAACCTGAACATCAACATGTTGCTCTT 480

DB 460 TGGTACAAATTCGAAAAAAGCTTAGGTATAAAGCCTGTAAATAAGAAATATCGGTCTT 519  
QY 481 TCTATTATCGTTTACAACATTCATTCGACCCAGCAATTTTATCGATTACATTAGCCCTGTTTA 540  
DB 520 TCTATTATATTCCTACATTTAATCGTAGCCGTATTTAGATATAACCGTTAGCCCTGTTTG 579  
QY 541 GTAAACCAAAAAACAATTTACCCGTTTGAAGTTATCGTGAAGATGATGGTAGTCAGAA 600  
DB 580 GTCAATCAGAAAAACAATTCACCATTTGAAGTCGTTGTTGAGATGATGGTAGTAAAGAA 639  
QY 601 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGAATATTCGCTACGTACAGCAA 660  
DB 640 AACTTACTTACCATTTGCAAAAAATACGAAACAAAACTTGACATAAAGTATGTAAGACAA 699  
QY 661 AAAGATACGGTTTTCAGCCAGTCGCCCTCGGAATATGGGATTAACGTTAGCAAAATAT 720  
DB 700 AAAGTATGATATCAATTTGTCAGTCAGAACTTAGGTTTACGTACAGCAAGTAT 759  
QY 721 GACTTTATTTGGCTTACTCGACTGTGATATGCGGCAAAATCCATTTATGGTTTCATCTTAT 780  
DB 760 GATTTTGTCTCGATTTCTAGACTGCGATATGCGCACCAACAATTTATGGGTTTCATCTTAT 819  
QY 781 GTTCAGAGCTATTAGAAAGATGATTAACAATCATTTGGTCCCAAGAAATACATCCGAT 840  
DB 820 CTTACAGAACTATTAGAAAGACATGATTTGTTTAAATTGGACCTAGAAAAATATGTGGAT 879  
QY 841 ACACAACATATTGACCCAAAAAGACTTCTTAATAACGGGAGTTTCTTGAATCATATACCA 900  
DB 880 ACTCATAATATTACCGCAGAACATTTCTTAACGATCCATATTATTAAGATCCTACTCCT 939  
QY 901 GAAATGAAAAACAATAATAGTTGTTGCCCAAAAGGGGAAGAAAGTTTCTCTGGAATGG 960  
DB 940 GAAACCGCTACAAATTAACAATCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999  
QY 961 CGCTTAGAACCAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCTTTCGCTTTT 1020  
DB 1000 AGATTAGAACATTTTCAAAAAAACCAGTAATCTACGCTCTATGTTGATTTCCCGTTTCT 1059  
QY 1021 TTTTCGCGGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAAAATTCGGTTTCTTTTAT 1080  
DB 1060 TTTAGTTGCGGTAATGTTGCTATTTTCTTAAGAAATGCTGCTAAATTAAGTAGTTGGTTG 1119  
QY 1081 GAGGAATTTAATCACTCGGGGGTGGAGAAGATGTGAATTTGGATATCGCTTATTCGGTTAC 1140  
DB 1120 GAAGAAATTTAATCATTTGGGGGGCGAAGATGTAGAATTTGGTTACAGATTTATTTGCCAAA 1179  
QY 1141 GGTAAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATTCAAGAGCCACAGGTAAA 1200  
DB 1180 GGCTGTTTTTTCAGAGTAATTTGACGGCGGAATGGCATACCATCAAGAACCACTCGTAAA 1239  
QY 1201 GAAATGAACCGATCGTGAAGCGGAAAAAATATTTAGCTCGATATTATGAGAGAAAAAG 1260  
DB 1240 GAAATGAACAGACGCGGAAGCTGTTAAAGTATTACGCTTAAATTTGTTGAAGAAAAAG 1299  
QY 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
DB 1300 GTACCTTACATCTATAGAAGCTTTTACCAATAGAAGATTCACATATTTCATAGAAATCCT 1359  
QY 1321 TTAGTTTCAATTTATATCCAGCTTATAAATCTGTGNAACATATATTCACAGTTGCGTAGAT 1380  
DB 1360 TTAGTTTCTTATTTATATATCCCGCTTATAACTGTGCAAAATTTATTTCAAAAGATGTGTAGAT 1419  
QY 1381 AGTGCACTGAATCAGACTGTTGTTGCTCGAGGTTTGTATTTGTAAACGATGTTTCAACA 1440  
DB 1420 AGTGCTTTAAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAAACGATGTTTCAACA 1479  
QY 1441 GATAATACCTTAGAAGTGTATCAATAGCTTTTATGGTAATAATCTTAGGGTAGCATCATG 1500  
DB 1480 GATAATACCTTAGAAGTGTATCAATAGCTTTTATGGTAATAATCTTAGGGTAGCATCATG 1539  
QY 1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACGCGGTTTCTTTGCTAAAGGT 1560

Db 1540 TCTAAACCAATGGCGNATAGCCTCAGCATCAAAATGCAGCGGTTCTTTTGCTAAAGGT 1599

Qy 1561 TATTACATTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCGAGTTGAACGTGT 1620

Db 1600 TATTACATTGGCGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCGAGTTGAACGTGT 1659

Qy 1621 TTTAAAGNATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTTAATAGAAAAGTC 1680

Db 1660 TTTAAAGNATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTTAATAGAAAAGTC 1719

Qy 1681 AATCCGGATGTAGCTTAATCGCTAAATGGTTTACAATTGGCCAGAGAAATTTTACAGAGAAAA 1740

Db 1720 AATCCGGATGTAGCTTAATCGCTAAATGGTTTACAATTGGCCAGAGAAATTTTACAGAGAAAA 1779

Qy 1741 CTCAACACGGCTATGATTGCTCACCACTTTTGAATGTTTCAAGATTTAGAGCTTGGCATTTA 1800

Db 1780 CTCAACACGGCTATGATTGCTCACCACTTTTGAATGTTTCAAGATTTAGAGCTTGGCATTTA 1839

Qy 1801 ACTGATGATTCAATGAAAAAATTTGAAAAATCGCGTAGACTATGACATGTTCTCAAACTC 1860

Db 1840 ACGGATGGAATTTAAACGAAAAATTTGAAAAACCGCGTAGACTATGACATGTTCTTTAAACTC 1899

Qy 1861 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTACATGGT 1920

Db 1900 AGTGAAGTTGAAAAATTTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTACATGGT 1959

Qy 1921 GATAACACATCAATTAAGAAAACTTGGCATTCAAAAGAAAAACCAATTTTGGTTGTAGTCAAT 1980

Db 1960 GATAACACATCAATTAAGAAAACTGCGCATTCAAAAGAAAAACCAATTTTGGTTGTAGTCAAT 2019

Qy 1981 CAGTCATTAATATAGCAAGGATACCTTATTATTAATATGACGAATTTGATGATTTAGAT 2040

Db 2020 CAGTCATTAATATAGCAAGGATCAATTTATTATTAATATGACAAATTTGATGATTTAGAT 2079

Qy 2041 GAAAGTACAAAGTATATTTTCAATAAACCCTGAAATCAAGAAAGAGATTGATATCTTA 2100

Db 2080 GAAAGTACAAAGTATATCTTCAATAAACCCTGAAATCAAGAAAGAAATGATATTTTA 2139

Qy 2101 AAAGATTTAAATCATCAGAAATAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2160

Db 2140 AAAGATCTTAAATCATCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCC 2199

Qy 2161 AATACATTAACCGCTTAGTGAATAAACTAAACAATTTATTGATATATAATAAAAAATA 2220

Db 2200 AATACATTAACCGCTTAGTGAATAAACTAAACAATTTATTGATATATAATAAAAAATA 2259

Qy 2221 TTGCTTATTTGTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2280

Db 2260 TTGCTTATTTGTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATA 2319

Qy 2281 CTAGCCTTCTATCAATAACATCAAGTGAATTTTTTACTAAATATGATATCTCATATTTAC 2340

Db 2320 TTGGCTTTCTATCAATAAGCACCAGTGAATTTTACTTAAATATGACATCTCATATTTAC 2379

Qy 2341 ACGAGTAATAGATTAAATAAACTGAGCGGCAATTTAAGTAATATTAATAAATTAAGTCAG 2400

Db 2380 ACGAGTAATAGACTAATAAAAACTGAGGCACATTTTAAGTAATATTAATAAATTAAGTCAG 2439

Qy 2401 TTTAAATCTAAATTTGTAATACATCATCTTTTGTATATCATGACGCTATTCGTTAAAAAT 2460

Db 2440 TTTAAATCTAAATTTGTAATACATCATCTTTTGTATATCATGACGCTATTCGTTAAAAAT 2499

Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCCGCATGAATTTTCTCAGCATTTAACAT 2520

Db 2500 GACAGCTATGCTTATATGAAAAAATATGATGTCCGCATGAATTTTCTCAGCATTTAACAT 2559

Qy 2521 GATTGGATCGAGAAAAATCAATCGCGATCCACCATTTTAAAGCTCATTTAAACCTTATTTT 2580

Db 2560 GATTGGATCGAGAAAAATCAATCGCGATCCACCATTTTAAAGCTCATTTAAACCTTATTTT 2619

Qy 2581 AATGACATGACTTTAAAGATGATGAATGTGAAAGGGGATCACAGGTGATGTTTATGACG 2640

Db 2620 AATGACATGACTTTAAAGATGATGAATGTGAAAGGGGATCACAGGTGATGTTTATGAG 2679

Qy 2641 TATCGCTAGCGCATGAGCTTCTGAGATTATTTAAAGNAGTCAATCATCTTGCCAGTCA 2700

Db 2680 TATCGCTACCGCATGAGCTTCTGAGATTATTTAAAGNAGTCAATCATCTTGCCAAATCA 2739

Qy 2701 ATTGATAGTGTGCGAGAAATAACACTGAGGATATTTGGTTCCAAATTTGCACATTTTAATC 2760

Db 2740 ATTGATAGTGTGCGAGAAATAACACTGAGGATATTTGGTTCCAAATTTGCACATTTTAATC 2799

Qy 2761 TTAGAAAAAGAAAAACCGGCCATGTATTTAATAAACATCGACCTGACTTTATATGCTTTGG 2820

Db 2800 TTAGAAAAAGAAAAACCGGCCATGTATTTAATAAACATCGACCTGACTTTATATGCTTTGG 2859

Qy 2821 GAACGAAATTTACAATGAGCAAAATGAACAAATTTGAAAGTGCAAAAGAGAGGAAATATA 2880

Db 2860 GAACGAAATTTACAATGAGCAAAATGAACAAATTTGAAAGTGCAAAAGAGGAAATATA 2919

Qy 2881 CCTGTTAAACAAGTTTCATTATTATAGTATATACTTATAA 2920

Db 2920 CCGTTAAACAAGTTTCATTATTATAGTATATAACGCTATAA 2959

RESULT 13

AEA04964

ID AEA04964 standard; DNA; 2112 BP.

XX AEA04964;

AC AC

XX 11-AUG-2005 (first entry)

DT

XX Hyaluronic acid synthase, PmHAS, coding sequence, SEQ ID 2.

DE Hyaluronic acid synthase; polysaccharide; gene; ds.

XX

XX Pasteurella multocida.

OS

XX Key Location/Qualifiers

FT CDS 1..2112

FT /\*tag= a

FT /product= "PmHAS"

XX

PN US2005124046-A1.

XX

PD 09-JUN-2005.

XX

PF 16-JUL-2002; 2002US-00197153.

XX

PR 10-NOV-1999; 99US-00437277.

XX

PA (DEAN/) DEANGELIS P L.

XX

XX Deangelis PL;

XX

XX WPI; 2005-417007/42.

DR P-FSDB; AEA04963.

DR GENBANK; AF036004.

XX

XX Elongating a functional acceptor (e.g. hyaluronic acid or chondroitin), useful in polysaccharide polymer grafting, comprises providing hyaluronic acid synthase, UDP-GlcUA and/or UDP-GlcNAc sugars to elongate the functional acceptor.

PT

PT

PT

XX

PS Claim 4; SEQ ID NO 2; 4lpp; English.

XX

XX The present invention relates to a method for elongating a functional acceptor. The method comprises providing a hyaluronic acid (HA) synthase (PmHAS; AEA04963) capable of elongating the functional acceptor and providing UDP-GlcUA and UDP-GlcNAc sugars such that the hyaluronic acid synthase elongates the functional acceptor. PmHAS adds sugars to the nonreducing end of a growing polymer chain. The PmHAS sequence is significantly different from the other known HA synthases: there appears to be only two short potential sequence motifs (AEA04967 and AEA04968) in common between PmHAS and the other HA synthases. The method is useful in



CC polysaccharide polymer grafting, which may be utilized in the development  
CC of biotechnological medical improvements. These may be used for producing  
CC hybrid polysaccharides or for forming polysaccharide coatings. The  
CC present sequence is the coding sequence for PmH5.

XX	SQ	Sequence 2112 BP; 746 A; 358 C; 387 G; 621 T; 0 U; 0 Other;	
		Query Match 72.3%; Score 2110.4; DB 14; Length 2112;	
		Best Local Similarity 100.0%; Pred. No. 0;	
		Matches 2111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	ATGATAATATATCAAGCAATATAAGCATATAACAGCAATGACTATCAATTAGCACTC 60	
Db	1	ATGATAATATATCAAGCAATATAAGCATATAACAGCAATGACTATCAATTAGCACTC 60	
Qy	61	AAATATTGAAAGTCGGCGGAATCTATGAGCGGAAATTTGTTGAATTTCAAAATACC 120	
Db	61	AAATATTGAAAGTCGGCGGAATCTATGAGCGGAAATTTGTTGAATTTCAAAATACC 120	
Qy	121	AAATGCAAGAAAACTCTCAGCACATCTCTGTTAAATTCAGCACATCTTCTGTAAT 180	
Db	121	AAATGCAAGAAAACTCTCAGCACATCTCTGTTAAATTCAGCACATCTTCTGTAAT 180	
Qy	181	AAAGAAAGAAAAAGTCAATGTTTGCATAGTCCTGTTAGATATTGCAACACAACTGTACTT 240	
Db	181	AAAGAAAGAAAAAGTCAATGTTTGCATAGTCCTGTTAGATATTGCAACACAACTGTACTT 240	
Qy	241	TCCAAAGTAAAAAATAGTAGTCTTCTGACTGCTGGAAAAAACAAGTAAAAAATAATGG 300	
Db	241	TCCAAAGTAAAAAATAGTAGTCTTCTGACTGCTGGAAAAAACAAGTAAAAAATAATGG 300	
Qy	301	AAATTCCTCAGTGAAGAAATCTGAAATGCGAGGTAAAGAGCGCTGCTGTACCA 360	
Db	301	AAATTCCTCAGTGAAGAAATCTGAAATGCGAGGTAAAGAGCGCTGCTGTACCA 360	
Qy	361	AAAGATTTTCCAAAGATCTGGTTTGTAGCGCTTTTACCTGATCATGTTAAATGATTACA 420	
Db	361	AAAGATTTTCCAAAGATCTGGTTTGTAGCGCTTTTACCTGATCATGTTAAATGATTACA 420	
Qy	421	TGGTACAAAAGCGGAAAGAAAGCTTGGCATATAAACCTCGAAATCAATGCTGCTT 480	
Db	421	TGGTACAAAAGCGGAAAGAAAGCTTGGCATATAAACCTCGAAATCAATGCTGCTT 480	
Qy	481	TCTATATCGTTACACATTCATCGACGAGCAATTTTATCGATTACATTTAGCCTGTTTA 540	
Db	481	TCTATATCGTTACACATTCATCGACGAGCAATTTTATCGATTACATTTAGCCTGTTTA 540	
Qy	541	GTAAACCAAAAAACATTTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600	
Db	541	GTAAACCAAAAAACATTTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600	
Qy	601	GATCTATCACCGATCATTCGCCAATATGAAATAAATTTGGATATTGCGTACGTCAGACAA 660	
Db	601	GATCTATCACCGATCATTCGCCAATATGAAATAAATTTGGATATTGCGTACGTCAGACAA 660	
Qy	661	AAAGATAACCGGTTTCAAGCCAGTGGCTCGGAAATATGGATATAGCTTACGCAAAATAT 720	
Db	661	AAAGATAACCGGTTTCAAGCCAGTGGCTCGGAAATATGGATATAGCTTACGCAAAATAT 720	
Qy	721	GACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCCAATATGGGTTCAATCTTAT 780	
Db	721	GACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCCAATATGGGTTCAATCTTAT 780	
Qy	781	GTTCGAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT 840	
Db	781	GTTCGAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT 840	
Qy	841	ACACACATATTGACCCAAAGACTTTTAAATAACCGGATTTGCTTGAATCATTTACCA 900	
Db	841	ACACACATATTGACCCAAAGACTTTTAAATAACCGGATTTGCTTGAATCATTTACCA 900	
Qy	901	GAAGTCAAAACCAATATAGTGTGCGGCAAAAGGGAAGAACAGTTCTCTGGATTGG 960	
Db	901	GAAGTCAAAACCAATATAGTGTGCGGCAAAAGGGAAGAACAGTTCTCTGGATTGG 960	

Db	901	GAAGTCAAAACCAATATAGTGTGCGGCAAAAGGGAAGAACAGTTCTCTGGATTGG 960	
Qy	961	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020	
Db	961	CGCTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020	
Qy	1021	TTTCGGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATTAATCCGGTTCTTTTCAT 1080	
Db	1021	TTTCGGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATTAATCCGGTTCTTTTCAT 1080	
Qy	1081	GAGGAATTTAATCACTCGGGTGGAGAGATCTGGAATTTGGATATCGCTTATTCGGTTAC 1140	
Db	1081	GAGGAATTTAATCACTCGGGTGGAGAGATCTGGAATTTGGATATCGCTTATTCGGTTAC 1140	
Qy	1141	GGTAGTTTCTTTAAAACTATTGATGGCAATTATGCCCTACCAAGACCCACAGGTAAA 1200	
Db	1141	GGTAGTTTCTTTAAAACTATTGATGGCAATTATGCCCTACCAAGACCCACAGGTAAA 1200	
Qy	1201	GAAATGAAACCGATCGTGAAACGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260	
Db	1201	GAAATGAAACCGATCGTGAAACGGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260	
Qy	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTGCGCATATCAATAGAGTACCT 1320	
Db	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTGCGCATATCAATAGAGTACCT 1320	
Qy	1321	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380	
Db	1321	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380	
Qy	1381	AGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAACGATGTTCAACA 1440	
Db	1381	AGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTAAACGATGTTCAACA 1440	
Qy	1441	GATAATACCTTAGAGTGCATCAATAGCTTTATGCTTAATATCTTAGGGTACGCATCATG 1500	
Db	1441	GATAATACCTTAGAGTGCATCAATAGCTTTATGCTTAATATCTTAGGGTACGCATCATG 1500	
Qy	1501	TCTAAACCAAAATGGCGGAATAGCCCTCAGCATCAAAATGCAGCGGTTTCTTTGCTAAAGT 1560	
Db	1501	TCTAAACCAAAATGGCGGAATAGCCCTCAGCATCAAAATGCAGCGGTTTCTTTGCTAAAGT 1560	
Qy	1561	TATTAATGCGGAGTTAGATTGATGATTAATCTTGAGCCCTGATGCGATGAACTGTGT 1620	
Db	1561	TATTAATGCGGAGTTAGATTGATGATTAATCTTGAGCCCTGATGCGATGAACTGTGT 1620	
Qy	1621	TTAAAGAAATTTTAAAGATAAAGCGCTAGCTGTTTATACCACTAATAGAACGCTC 1680	
Db	1621	TTAAAGAAATTTTAAAGATAAAGCGCTAGCTGTTTATACCACTAATAGAACGCTC 1680	
Qy	1681	AATCCGGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTACAGAGAAA 1740	
Db	1681	AATCCGGATGGTAGCTTAATCGCTAATGGTTACAAATGGCCAGAAATTTTACAGAGAAA 1740	
Qy	1741	CTCACACCGGCTATGTTGCTCACCATTTAGAAATGTTTACCGATTAGAGCTTGGCATTTA 1800	
Db	1741	CTCACACCGGCTATGTTGCTCACCATTTAGAAATGTTTACCGATTAGAGCTTGGCATTTA 1800	
Qy	1801	ACTGATGATTCATGAAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTTCAAACTC 1860	
Db	1801	ACTGATGATTCATGAAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTTCAAACTC 1860	
Qy	1861	AGTGAAGTTTGGAAAAATTTAAACATCTTAAATAAAATCTGCTATAACCGTGTATTACATGGT 1920	
Db	1861	AGTGAAGTTTGGAAAAATTTAAACATCTTAAATAAAATCTGCTATAACCGTGTATTACATGGT 1920	
Qy	1921	GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACATTTTGTGTAGTCAAT 1980	
Db	1921	GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACATTTTGTGTAGTCAAT 1980	
Qy	1981	CAGTCAATTAATAGACAGGCATACCTTATTATTAATGACGAATTTGATGATTAGAT 2040	
Db	1981	CAGTCAATTAATAGACAGGCATACCTTATTATTAATGACGAATTTGATGATTAGAT 2040	



Db 1021 TTTGCGGGTAAATGTTGCTTTCGCTAAATAAATGGCTAAATAAATCGGTTTCTTTGAT 1080  
Qy 1081 GAGGAATTTAATCACTGGGTTGGAGAGATGAGAAATTTGGATATCGCTTATTCGGTTAC 1140  
Db 1081 GAGGAATTTAATCACTGGGTTGGAGAGATGAGAAATTTGGATATCGCTTATTCGGTTAC 1140  
Qy 1141 GGTAGTTTCTTTAAATCTATTGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200  
Db 1141 GGTAGTTTCTTTAAATCTATTGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200  
Qy 1201 GAAATGAAACCGATCGTGAAGCGGAAAAAATAATTACGCTCGATATTATGAGAGAAAAG 1260  
Db 1201 GAAATGAAACCGATCGTGAAGCGGAAAAAATAATTACGCTCGATATTATGAGAGAAAAG 1260  
Qy 1261 GTCCCTTATATCTATAGAAACTTTTACCAATAGAGATTGCGATATCAATAGAGTACCT 1320  
Db 1261 GTCCCTTATATCTATAGAAACTTTTACCAATAGAGATTGCGATATCAATAGAGTACCT 1320  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATAAATGCTGCAAACTATATTCAACGTTTGGCTAGAT 1380  
Db 1321 TTAGTTTCAATTTATATCCAGCTTATAAATGCTGCAAACTATATTCAACGTTTGGCTAGAT 1380  
Qy 1381 AGTGCACTGAATCAGACTGTTGTCATCTCGAGTTTGTATTTGTAAACGATGTTTCAACA 1440  
Db 1381 AGTGCACTGAATCAGACTGTTGTCATCTCGAGTTTGTATTTGTAAACGATGTTTCAACA 1440  
Qy 1441 GATAATACCTTAGAAGTATCAATAGCTTTATGTTATGTTATTAATCTTAGGTCAGCATATG 1500  
Db 1441 GATAATACCTTAGAAGTATCAATAGCTTTATGTTATGTTATTAATCTTAGGTCAGCATATG 1500  
Qy 1501 TCTAACCAAAATGGCGGAATACGCTCAGCATCAAAATGCAAGCGGTTCTTTTGTCTAAAGGT 1560  
Db 1501 TCTAACCAAAATGGCGGAATACGCTCAGCATCAAAATGCAAGCGGTTCTTTTGTCTAAAGGT 1560  
Qy 1561 TATTACATTTGGCAGTTAGATTGATGATGATGATGATGATGATGATGATGATGATGATG 1620  
Db 1561 TATTACATTTGGCAGTTAGATTGATGATGATGATGATGATGATGATGATGATGATGATG 1620  
Qy 1621 TTTAAAGAAATTTTAAAGATATAAAGCTGATGATGATGATGATGATGATGATGATGATG 1680  
Db 1621 TTTAAAGAAATTTTAAAGATATAAAGCTGATGATGATGATGATGATGATGATGATGATG 1680  
Qy 1681 AATCCGATGTTAGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 1740  
Db 1681 AATCCGATGTTAGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 1740  
Qy 1741 CTCACACCGCTATGATGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTGGCAATTA 1800  
Db 1741 CTCACACCGCTATGATGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTGGCAATTA 1800  
Qy 1801 ACTGATGGATTCATGAAATAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1801 ACTGATGGATTCATGAAATAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Qy 1861 AGTGAAGTTGGAATTTTAAACATCTTAAATAAATCTGCTATAAACCGCTGATTACATGCT 1920  
Db 1861 AGTGAAGTTGGAATTTTAAACATCTTAAATAAATCTGCTATAAACCGCTGATTACATGCT 1920  
Qy 1921 GATAACACATCAATTAAGAAACTTTGGCATTTCAAAAGAAACCAATTTTGTGTAGTCAAT 1980  
Db 1921 GATAACACATCAATTAAGAAACTTTGGCATTTCAAAAGAAACCAATTTTGTGTAGTCAAT 1980  
Qy 1981 CAGTCATTAATAATAGACAAAGCATAACTTATTATTAATTAATGACGAATTTGATGATTTAGAT 2040  
Db 1981 CAGTCATTAATAATAGACAAAGCATAACTTATTATTAATTAATGACGAATTTGATGATTTAGAT 2040  
Qy 2041 GAAAGTAGAAGTATTTTCAATTAACCGCTGAAATATCAAGAGAGATTTGATATCTTAA 2100  
Db 2041 GAAAGTAGAAGTATTTTCAATTAACCGCTGAAATATCAAGAGAGATTTGATATCTTAA 2100  
Qy 2101 AAAGATATTAAA 2112  
Db 2101 AAAGATATTAAA 2112

RESULT 15

ADP75718

ID ADP75718 standard; DNA; 2112 BP.

XX

AC ADP75718;

XX

DT 12-AUG-2004 (first entry)

XX

DE Pasteurella multocida polymer production method-related DNA sequence #2.

XX

KW polymer production; hyaluronic acid polymer; chondroitin polymer; enzyme; gene; ds.

XX

OS Pasteurella multocida.

XX

PN WO2003029261-A2.

XX

PD 10-APR-2003.

XX

PF 12-JUL-2002; 2002WO-US022386.

XX

PR 13-JUL-2001; 2001US-0305263P.

PR

22-JAN-2002; 2002US-0350642P.

PR

08-MAY-2002; 2002US-00142143.

XX

PA (DEAN/) DEANGELIS P L.

XX

PI Deangelis PL;

XX

WPI; 2003-532558/50.

XX

PT Producing polymer, e.g. hyaluronic acid or chondroitin polymer, by providing a functional acceptor, a synthase capable of elongating the acceptor and sugars such that synthase elongates the acceptor to provide polymer.

XX

PS Disclosure; SEQ ID NO 71; 538pp; English.

XX

CC The invention comprises a method for producing a polymer, especially a hyaluronic acid (HA) or chondroitin (CD) polymer composed of less than 150 sugars. The method involves providing a functional acceptor, CC providing a synthase capable of elongating the functional acceptor, and CC providing sugars such that the synthase elongates the functional acceptor to provide the polymer. The method of the invention is useful for CC producing a hyaluronic acid or chondroitin polymer composed of 1-150 CC sugars. The present Pasteurella multocida DNA sequence was used in the CC exemplification of the invention.

XX

SQ Sequence 2112 BP; 745 A; 359 C; 387 G; 621 T; 0 U; 0 Other;

Query Match 72.2%; Score 2108.8; DB 11; Length 2112;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1 ATGAATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60

Db

1 ATGAATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60

Qy

61 AAATATTTTGAAGTCGCGGAAATCTATGACGGAATAATTTGTAATTCAAATTACC 120

Db

61 AAATATTTTGAAGTCGCGGAAATCTATGACGGAATAATTTGTAATTCAAATTACC 120

Qy

121 AAATGCAAGAAAACTCTCAGCACATCTCTGTTTAAATTCAGCACATCTTTCTGTAAT 180

Db

121 AAATGCAAGAAAACTCTCAGCACATCTCTGTTTAAATTCAGCACATCTTTCTGTAAT 180

Qy

181 AAGAGAGAAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACACACTGTTACTT 240

Db

181 AAGAGAGAAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACACACTGTTACTT 240

Qy

241 TCCAACGTAAAAAATTTAGTACTTCTGACTCGGAAAAAACACGTTAAAAAATAATG 300

|||||  
241 TCCAACTGTAATAAATTTAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATAAATGG 300  
Qy |||||  
301 AAATTTGCTCACTGAGAGAAATCTGAATAATCGGAGGTGAAGAGCGGTGCGCCCTTTGTACCA 360  
Db |||||  
301 AAATTTGCTCACTGAGAGAAATCTGAATAATCGGAGGTGAAGAGCGGTGCGCCCTTTGTACCA 360  
Qy |||||  
361 AAAGATTTTCCAAAGATCTGGTTTTAGCGCCTTTTACCTGATCATGTTAATGATTTTACA 420  
Db |||||  
361 AAAGATTTTCCAAAGATCTGGTTTTAGCGCCTTTTACCTGATCATGTTAATGATTTTACA 420  
Qy |||||  
421 TGGTACAAAAAGCGAAGAAAGACTTGGCATATAAACTGAACTCAACATGTTGGTCTT 480  
Db |||||  
421 TGGTACAAAAAGCGAAGAAAGACTTGGCATATAAACTGAACTCAACATGTTGGTCTT 480  
Qy |||||  
481 TCTATTATCGTTACAACAATTCAAATCGACCAAGCAATTTTATCGATTTACATTTAGCCTGTTA 540  
Db |||||  
481 TCTATTATCGTTACAACAATTCAAATCGACCAAGCAATTTTATCGATTTACATTTAGCCTGTTA 540  
Qy |||||  
541 GTAAACCAAAAAACACATTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db |||||  
541 GTAAACCAAAAAACACATTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Qy |||||  
601 GATCTATCACCGATCATTCGCGCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 660  
Db |||||  
601 GATCTATCACCGATCATTCGCGCAATATGAAATAAATTTGGATATTCGCTACGTCAGACAA 660  
Qy |||||  
661 AAAGATAACCGTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 720  
Db |||||  
661 AAAGATAACCGTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTACGCTTAGCAAAATAT 720  
Qy |||||  
721 GACTTTATTTGCGTTACTCGACTGTGATATGCGCCAAATCCATTTAGGGTTCAATCTTAT 780  
Db |||||  
721 GACTTTATTTGCGTTACTCGACTGTGATATGCGCCAAATCCATTTAGGGTTCAATCTTAT 780  
Qy |||||  
781 GTTCGAGAGCTATTAGAAGATGATGTTTAAACAATCATTTGGTCCAAAGAAAATACATCGAT 840  
Db |||||  
781 GTTCGAGAGCTATTAGAAGATGATGTTTAAACAATCATTTGGTCCAAAGAAAATACATCGAT 840  
Qy |||||  
841 ACACAACATATTGACCCAAAAGACTTCTTAATAAACGCGAGTTTGTGGAATCATTTACCA 900  
Db |||||  
841 ACACAACATATTGACCCAAAAGACTTCTTAATAAACGCGAGTTTGTGGAATCATTTACCA 900  
Qy |||||  
901 GAAGTGAACCAATAATAGTTGTCGCGCAAAAGGGGAAGAACAGTTTCTCTGGATTGG 960  
Db |||||  
901 GAAGTGAACCAATAATAGTTGTCGCGCAAAAGGGGAAGAACAGTTTCTCTGGATTGG 960  
Qy |||||  
961 CGCTTAGAACCAATTCGAAAAACAGAAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020  
Db |||||  
961 CGCTTAGAACCAATTCGAAAAACAGAAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020  
Qy |||||  
1021 TTTGCGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTTAAATAAATCCGGTTTCTTTGAT 1080  
Db |||||  
1021 TTTGCGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTTAAATAAATCCGGTTTCTTTGAT 1080  
Qy |||||  
1081 GAGGAATTTAATCACTGGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGTTTAC 1140  
Db |||||  
1081 GAGGAATTTAATCACTGGGGTGGAGAAGATGTGGAATTTGGATATCGCTTATTCGTTTAC 1140  
Qy |||||  
1141 GGTAGTTTCTTTTAAACATATTGATGGCATTTATGGCTTACCATTCAAGAGCCACCGGTAAA 1200  
Db |||||  
1141 GGTAGTTTCTTTTAAACATATTGATGGCATTTATGGCTTACCATTCAAGAGCCACCGGTAAA 1200  
Qy |||||  
1201 GAAATGAACCGGATCGTGAAGCGGAAAAAATAATTACCGCTCGATATTATGAGAGAAAAG 1260  
Db |||||  
1201 GAAATGAACCGGATCGTGAAGCGGAAAAAATAATTACCGCTCGATATTATGAGAGAAAAG 1260  
Qy |||||  
1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTGCGATATCAATAGAGTACCT 1320  
Db |||||  
1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTGCGATATCAATAGAGTACCT 1320  
Qy |||||  
1321 TTAGTTTCAAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
Db |||||

Db |||||  
1321 TTAGTTTCAAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
Qy |||||  
1381 AGTGCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTGTAACGATGGTTCAACA 1440  
Db |||||  
1381 AGTGCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTGTAACGATGGTTCAACA 1440  
Qy |||||  
1441 GATAATACCTTTAGAAGTGATCAATAGCTTTATGTTAATCTTAGGGTACGTCATCATG 1500  
Db |||||  
1441 GATAATACCTTTAGAAGTGATCAATAGCTTTATGTTAATCTTAGGGTACGTCATCATG 1500  
Qy |||||  
1501 TCTAAACCAAAATCGCGAATAGCCTCAGCATCAAAATGACGCGCTTTCTTTGCTTAAAGGT 1560  
Db |||||  
1501 TCTAAACCAAAATCGCGAATAGCCTCAGCATCAAAATGACGCGCTTTCTTTGCTTAAAGGT 1560  
Qy |||||  
1561 TATTACATTTGGGAGTTAGATTGATGATTATCTTGAGCCTGATGAGCTTGAACCTGCT 1620  
Db |||||  
1561 TATTACATTTGGGAGTTAGATTGATGATTATCTTGAGCCTGATGAGCTTGAACCTGCT 1620  
Qy |||||  
1621 TTTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTAATAGAAAACGTC 1680  
Db |||||  
1621 TTTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTAATAGAAAACGTC 1680  
Qy |||||  
1681 AATCCGGATGCTAGCTTTAATCGCTTAATGTTTACAATTTGGCCAGAAATTTTCAAGAGAAAA 1740  
Db |||||  
1681 AATCCGGATGCTAGCTTTAATCGCTTAATGTTTACAATTTGGCCAGAAATTTTCAAGAGAAAA 1740  
Qy |||||  
1741 CTCAACACGCTATGATGCTCACCACCTTTAGAAATGTTTCAAGATTAGAGCTTGGCATTTA 1800  
Db |||||  
1741 CTCAACACGCTATGATGCTCACCACCTTTAGAAATGTTTCAAGATTAGAGCTTGGCATTTA 1800  
Qy |||||  
1801 ACTGATCGATTCAATGAAAAAATTTGAAAAATGCGCTAGACTATGACATGTTCTCTCAAACTC 1860  
Db |||||  
1801 ACTGATCGATTCAATGAAAAAATTTGAAAAATGCGCTAGACTATGACATGTTCTCTCAAACTC 1860  
Qy |||||  
1861 AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAATCTGCTATAACCGTGTATTACATGGT 1920  
Db |||||  
1861 AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAATCTGCTATAACCGTGTATTACATGGT 1920  
Qy |||||  
1921 GATAACACATCAATTAAGAAAACCTTGGCATTTCAAAAGAAAAAACCCATTTTGTGTAGTCAAT 1980  
Db |||||  
1921 GATAACACATCAATTAAGAAAACCTTGGCATTTCAAAAGAAAAAACCCATTTTGTGTAGTCAAT 1980  
Qy |||||  
1981 CAGTCATTAAATAGACAAGGCATAAATTTATTAATAATTATGACGAAATTTGATGATTTAGAT 2040  
Db |||||  
1981 CAGTCATTAAATAGACAAGGCATAAATTTATTAATAATTATGACGAAATTTGATGATTTAGAT 2040  
Qy |||||  
2041 GAAAGTAGAAAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAGAGAGATTGATATCTTA 2100  
Db |||||  
2041 GAAAGTAGAAAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAGAGAGATTGATATCTTA 2100  
Qy |||||  
2101 AAAGATATTAAA 2112  
Db |||||  
2101 AAAGATATTAAA 2112

Search completed: January 8, 2006, 06:07:35  
Job time : 1590 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 05:23:16 ; Search time 10317 Seconds  
(without alignments)  
13242.055 Million cell updates/sec

Title: US-10-642-248-1  
Perfect score: 2920  
Sequence: 1 atgaatacatatcacaagc.....taatagataactctataaa 2920

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues  
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hc:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gss1:  
10: gb\_gss2:  
11: gb\_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101.8	3.5	1101	10	CNS00EVL
2	100.6	3.4	1380	1	AJ928744
3	100.2	3.4	891	10	CW952279
4	96.6	3.3	889	10	CW973509
5	96.4	3.3	1378	10	AG350209
6	94.2	3.2	2157	10	CL081966
7	92	3.2	1060	10	CW937448
8	90.6	3.1	1324	10	AG376784
9	90.2	3.1	1313	7	CK997149
10	89.8	3.1	1239	10	CW953278
11	89.8	3.1	1539	10	AG340947
12	89.4	3.1	1390	10	AG347224
13	87.6	3.0	1260	10	CL491610
14	87.4	3.0	735	10	CW960936
15	87.4	3.0	1268	10	AG347098
16	87	3.0	1017	10	CL101048
17	86.8	3.0	1335	10	CL546802
18	86.6	3.0	641	9	AQ946120
19	86.6	3.0	1169	11	CNS06KHQ
20	86.6	3.0	1608	10	CL118721
21	86.2	3.0	1238	1	AJ925855
22	86.2	3.0	1981	10	CL082000

23	86	2.9	844	10	BX139987
24	86	2.9	994	11	CNS04NOJ
25	86	2.9	1350	10	CG744271
26	85.8	2.9	1015	10	CL135318
27	85.8	2.9	1095	1	AJ926415
28	85.8	2.9	1542	10	AG386981
29	85.4	2.9	829	10	BX173672
30	85.4	2.9	1116	1	AJ925982
31	85	2.9	1272	1	AJ927522
32	84.8	2.9	1056	8	DN572905
33	84.8	2.9	1147	1	AJ928334
34	84.8	2.9	1599	10	CL083840
35	84.6	2.9	1163	1	AJ927129
36	84	2.9	1191	10	CL104745
37	83.6	2.9	505	10	CW270542
38	83.6	2.9	1193	1	AJ926364
39	83.6	2.9	1896	10	CG753083
40	83.2	2.8	707	10	CG403581
41	83.2	2.8	1365	1	AJ927702
42	83.2	2.8	1404	10	CL055132
43	83.2	2.8	1493	10	CL078589
44	83.2	2.8	1503	10	AG346761
45	83.2	2.8	1626	6	CF238805

ALIGNMENTS

RESULT 1  
CNS00EVL  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999  
Drosophila melanogaster genome survey sequence T7 end of BAC:  
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly); genomic survey sequence.  
AL069706  
GI:4949849  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Osoegawa and Aaron Mammosier at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source

1. .1101  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR29B23"  
/clone\_lib="RPCI-98"  
/note="end : T7"

ORIGIN

```
Query Match      3.5%; Score 101.8; DB 10; Length 1101;
Best Local Similarity 35.5%; Pred. No. 3.1e-10;
Matches 237; Conservative 122; Mismatches 301; Indels 7; Gaps 2;

Qy 1947 CATTCAAAAGAAAAACCAATTTTGTGTAGTCACATCAGTCATTAAATAGACAGGCAATAC 2006
Db 442 CMMMMHMAATYCTCAHTTMMMMMMWAAATWTWAAAWAAATTTATWAAATWAAAW 501

Qy 2007 TTATTATAATATGACGAATTTGATGATTTAGATGAAGTAGAAGTATATTTTCAATAA 2066
Db 502 AWWWWTTTTTTWWWWTTTWTWTTTWTWTTWAAAAAATAAAATTTAAAAAAT 561

Qy 2067 AACCGCTCAATATCAAGAGAGATTTGATCTTAAAGATATTAATATCATCCAGATAA 2126
Db 562 AWATTAATAATTTAAWAAWTTATATTAATWTA-TAAATWTWTTATATAAAAAATATTT 620

Qy 2127 AGATGCCAAATCGCAGTCAGTATTTTATCCCAATACATTAACCGCTTAGTGAAAAA 2186
Db 621 TTTWATAAATTTTAAATAATTTAAATTAATTTATTAATAATWTTWWTTAAATATAA 680

Qy 2187 ACTAAACAATATTTGAATATAAATAATATATTCGTTATTCGTTCTACATGTTGATAA 2246
Db 681 TTTWAAATATAAAAAAATAAAAAATAAAATWAAWATWATAAAATTTAAAAAATAAAW 740

Qy 2247 GAATCATCTTACACCGAGTATCAAAAAGAAATACTAGCCTTCTATCATAAACATCAAGT 2306
Db 741 AAWAATWAAWATAATATWNAATATATWTTTAAWNAWTTWNAWTTATATAWATAWAAW 800

Qy 2307 GAATATTTTACTAAATATGATCTCATATATACACGAGTAGATTAATAAAAACTGA 2366
Db 801 AAWNA-----TAAATAWATAWATAWAAWATAWATAWATAWATAWATAWATAWATAW 854

Qy 2367 GCGCGATTTAAGTAAATATAAATAAATTAAGTCAGTTAAATCTAAATTTGTAATCATCAT 2426
Db 855 ATWTAATATWAAATWATAWAAAAAATAWAAWTTTWTWTTTWTWNAWATAWAAWATAW 914

Qy 2427 TTTTGAATATCATGACAGCCTATTTCGTTAAAAATGACAGCTATGCTTATATGAAAAATA 2486
Db 915 AAWAAAAAATAAAATAAAWNAWTTATTTTATTTAAATWTTATWNAWTTWNAWTT 974

Qy 2487 TGATGTGGCGATGAATTTCTCAGCATTAACACATGATTCGAGAGAAAAATCAATGGCA 2546
Db 975 WTATATWTTATATATATATWTTATWATAWATAATTTATTAWNAWTTATTTTAAWNAW 1034

Qy 2547 TCCACCATTTAAAAAGCTCATTAATAAATTTTAAATGACAAATGACGCTTAAAAAGTATGAA 2606
Db 1035 TATATWATAWTTWATAWATAWAAWAAATTAATTTATATATATWTAWATAWAAAAAATAW 1094

Qy 2607 TGTGAAA 2613
Db 1095 ATAWAA 1101
```

```
RESULT 2
AJ928744
LOCUS AJ928744 1380 bp mRNA linear EST 10-JUN-2005
DEFINITION AJ928744 Theileria annulata merozoite Theileria annulata cDNA clone
tam022c08_glk, mRNA sequence.
```

```
ACCESSION AJ928744
VERSION AJ928744.1 GI:67499132
```

```
KEYWORDS EST.
```

```
SOURCE Theileria annulata
```

```
ORGANISM Theileria annulata
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
Theileria.
```

```
REFERENCE 1 (bases 1 to 1380)
AUTHORS Pain,A., Renaud,H., Berriman,M., Murphy,L., Yeates,C.A., Weir,W.,
Kerhornou,A., Aslett,M., Bishop,R., Bouchier,C., Cochet,M.,
Coulson,R.M.R., Cronin,A., de Villiers,E., Fraser,A., Foster,N.,
Gardner,M., Goble,A., Griffiths-Jones,S., Harris,D.E., Katzer,F.,
Larke,N., Lord,A., Maser,P., McKellar,S., Mooney,P., Morton,F.,
Nene,V., O'Neil,S., Price,C., Quail,M.A., Rabinowitz,E.,
Rawlings,N.D., Rutter,S., Saunders,D., Seeger,K., Shah,T.,
```

```
Squares,R., Squares,S., Tivey,A., Walker,A.R., Woodward,J.,
Dobbelare,D.A.E., Langsley,G., Rajandream,M.-A., McKeever,D.,
Shields,B., Tait,A., Barrell,B. and Hall,N.
The genome of the host-cell transforming parasite Theileria
annulata and a comparison with T. parva
Unpublished (2005)
Contact: Pain A
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Campus, CB10 1SA, UNITED KINGDOM
Merozoite cDNA library: Frank Katzer and Brian Shields, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
FEATURES
source
1..1380
/organism="Theileria annulata"
/mol_type="mRNA"
/isolate="Ankara (clone D7)"
/db_xref="taxon:5874"
/clone="tam022c08_glk"
/dev_stage="merozoite"
/lab_host="Bos taurus (cow)"
/clone_lib="Theileria annulata merozoite"
/notes="country: Turkey;Ankara"
```

## ORIGIN

```
Query Match      3.4%; Score 100.6; DB 1; Length 1380;
Best Local Similarity 40.9%; Pred. No. 5.5e-10;
Matches 444; Conservative 0; Mismatches 633; Indels 8; Gaps 3;

Qy 1813 AATCAAAAAATTCGAAATCGGTAGACTATGACATGTTCTCAAACTCAGTGAAGTTGGA 1872
Db 282 AATNAAAAATTAATAAAAAAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 341

Qy 1873 AAATTTAAACATCTTAATAAAAACTGCTATAACCGTGTATTATCATGGTGATACACATCA 1932
Db 342 TAAATATAAAATAAAATAAAAAAATAATAAAAAATAAAATATAAAAAATAATAT 401

Qy 1933 ATTAAGAACTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCATCAGTCATTAAT 1992
Db 402 TAAATATAAAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAT 461

Qy 1993 AGACAAGGCATACTTATTATAATATGACGAATTTGATGATTTAGATGAAGTAGAAAG 2052
Db 462 TAAAAAATAATTAATTAATAAAAAAATAAAAAAATAAAAAAATAAAAAATAATAA 521

Qy 2053 TATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTTAAAAAGATTTAAA 2112
Db 522 AAAAATAAAAAAATAAAAAATAAAAAAATAAAAAATAAAAAATAAAAAATAAAAAAT 581

Qy 2113 ATCATCCAGATTAAGATGCGAAATCGCAGTCAGTATTTTATCCCAATACATTAAC 2172
Db 582 AATAATAAAAAAATAAAAAATAAAATAAAATAAAATAAAATAAAAAATAAAAAATAA 641

Qy 2173 GGCTTAGTGAATAAACTAAAAATAATTTATTGAATAATAATAA---AAATATATTCGTTATT 2229
Db 642 AATAAAAAATTAATAAAAAAATAAAAAATAAAATAATTAATTAATTAATTAATAAATA 701

Qy 2230 GTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAGAAATCTAGCCTTC 2289
Db 702 ATAAANNAATTAATAAAAAATNAATAAATAAATAAANAANAANAANAATAATAATATAT 761

Qy 2290 TATCATAAACATCAAGTGAATATTTTACTAAATAAGTATATCTCATATTACACAGGTAAT 2349
Db 762 AAAAAAATAAAAAATAAATAATTTATTAATTAATAAAAAAATAAAAAATAAATAATAT 821

Qy 2350 AGATTATAAAAACTGAGGCGCATTTAAGTAATATTAAATAATTAATTAAGTCAGTTAAATCTA 2409
Db 822 AATTAAAAAATTAATAATAAAAAATAAAATAAATAAATAAATAAANAANAANAATAAATA 881

Qy 2410 AAT---TGCGAATACATCATTTTGTGTAATCATGACAGCCTATTCGTTAAAAAATGACAGC 2466
Db 882 AATAAAAAATTAATATAAAAAATAAAAAAATAAAAAATAAATAAATAAATAAATAAATAA 941
```





Fax: 314 286 1810  
Email: nenatode@watson.wustl.edu  
Genomic DNA provided by John Hawdon (mtmjmh@gwumc.edu) DNA  
sequenced by Washington University Genome Sequencing Center  
Class: shotgun.

FEATURES  
    source  
        1..889  
            /organism="Ancylostoma caninum"  
            /mol\_type="genomic DNA"  
            /strain="Baltimore"  
            /db\_xref="taxon:29170"  
            /dev\_stage="Adult"  
            /lab\_host="GS10"  
            /clone\_lib="Ancylostoma caninum whole genome shotgun  
            library (A1AAGSS 001)"  
            /note="vector: pOTW13; Site 1: BstX1; Site 2: BstX1;  
            Ancylostoma caninum genomic DNA was randomly sheared,  
            end-repaired and size fractionated to enrich for 2-4 kb  
            fragments. Genomic DNA was provided by John Hawdon  
            (mtmjmh@gwumc.edu) at George Washington University.  
            Sequencing by Washington University Genome Sequencing  
            Center, St. Louis, MO."

ORIGIN  
    Query Match 3.3%; Score 96.6; DB 10; Length 889;  
    Best Local Similarity 46.5%; Pred. No. 3.6e-09;  
    Matches 312; Conservative 0; Mismatches 359; Indels 0; Gaps 0;  
  
Qy 1813 AATGAAAAATTTGAAATCGCGTAGACATATGACATGTTCCCTCAAACTCAGTGAAGTTGGA 1872  
Db 14 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 73  
  
Qy 1873 AAATTTAAACATCTTAATAAAATCGCTATAACCGGTGATTTACATGGTGATAACACATCA 1932  
Db 74 AGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 133  
  
Qy 1933 ATTAAGAACTTGGCATTCAAAGAAACCATTTTGTGTGAGTCAATCGATCAATTAAT 1992  
Db 134 AAT 193  
  
Qy 1993 AGACAAGGCATACTATTATAATTTATGACGAATTTTGATGATTTAGATGAAGTAGAAAG 2052  
Db 194 AAT 253  
  
Qy 2053 TATATTTTCAATAAAACCGGTGAATATCAAGAAGATTTGATATCTTTAAAGATATTAAA 2112  
Db 254 AAT 313  
  
Qy 2113 ATCATCCAGATAAGATGCCAAATCGCAGTCAGTATTTTTTATCCCAATACATTTAAAC 2172  
Db 314 AAT 373  
  
Qy 2173 GGCTTAGTGAATAAATAAATAATTTATGAAATATAATAATAATAATAATAATAATAATTTGTT 2232  
Db 374 GATAATAATAATAACATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 433  
  
Qy 2233 CTACATGTTGATAGAATCATCTTACACCATATCAAAAAGAAATCTAGCCCTCTAT 2292  
Db 434 AAT 493  
  
Qy 2293 CATTAACATCAAGTGAATTTTACTAATAATATGATCTCATATTACACAGTAATAAGA 2352  
Db 494 AAT 553  
  
Qy 2353 TTAATAAAACCTGAGGCCCATTTAAGTAATAATAATAATAATAATAATAATAATAATAAT 2412  
Db 554 AGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 613  
  
Qy 2413 TGTGAATACATCATTTTGTGATAATCATGACAGCCATTTTGGTTAAAAATGACAGCTATGCT 2472  
Db 614 AAT 673  
  
Qy 2473 TATATGAAAA 2483

Db 674 AATAATAATAA 684

RESULT 5  
AG350209/c 1378 bp DNA linear GSS 18-DEC-2004  
LOCUS Mus musculus molossinus DNA, Clone.MSMg01-146M02.TJ, genomic survey  
DEFINITION Mus musculus molossinus (Japanese wild mouse)  
ACCESSION AG350209  
VERSION AG350209.1 GI:47923519  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus (Japanese wild mouse)  
ORGANISM Mus musculus molossinus  
    Bukaryoka; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
    Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
    Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and  
    Shiroishi, T.  
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to  
    genomic constitution of strain C57BL/6J, as defined by BAC-end  
    sequence-SNP analysis  
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)  
PUBMED 15574823  
REFERENCE 2 (bases 1 to 1378)  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
    and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
    1-7-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
    (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,  
    Tel:81-45-503-9111, Fax:81-45-503-9170)  
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC  
    library availability, please contact Kunya Abe (abe@tc.riken.jp).  
    Taikuba Institute, Bio Resource Center.  
    The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
    Koyadai, Tsukuba, 305-0074 Japan  
    phone: 81-298-36-9189, fax: 81-298-36-9199  
    e-mail: abe@tc.riken.jp  
PRIMERS  
Sequencing : T U  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.  
FEATURES  
    source  
        1..1378  
            /organism="Mus musculus molossinus"  
            /mol\_type="genomic DNA"  
            /sub\_species="molossinus"  
            /db\_xref="taxon:57486"  
            /clone="MSMg01-146M02.TJ"  
            /sex="male"  
            /tissue\_type="mixture of kidney and spleen"  
            /clone\_lib="MSMg01 Mouse Male BAC Library"  
ORIGIN  
    Query Match 3.3%; Score 96.4; DB 10; Length 1378;  
    Best Local Similarity 47.7%; Pred. No. 4e-09;  
    Matches 350; Conservative 0; Mismatches 376; Indels 8; Gaps 2;  
  
Qy 1873 AAATTTAAACATCTTATAAAATCTGCTATAACCGGTATATTACATGGTGATACACATCA 1932  
Db 1178 AAATTTAAAAATAAAAAATTAATAATAATAAAAAATATATAAAAAATATAAAAAATAAA 1119  
  
Qy 1933 ATTAAGAACTTGGCATTCAAAGAAACCATTTTGTGTGAGTCAATCATTAAT 1992  
Db 1118 AAAATAATAATAATAAAAAATAAAAAATCAATAATAATAATAATAATAATAATTAATTA 1059  
  
Qy 1993 AGACAAGGCATACTATTATAATAATTTGATGATTTAGATGAAGTAGAAAG 2052

Db 1058 AAAAAAAAAATAAAAAAAAAATTTAA-----AAATTAATAATAATAATAATAATAATAATA 1006

Qy 2053 TATATTTTCAATAAAACCGCTGATATACAGACAGATTCATATCTTTAAAGATATTAAA 2112

Db 1005 AAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAA 946

Qy 2113 ATCATCCAGATAAAGATGCCAAATCGCAGTCAGTATTTTTTATCCCAATACATTAAC 2172

Db 945 AATAATAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 886

Qy 2173 GGCTTAGTGAATAAACTAAACATATTATTGAAATATAATAAAAAATAATTTCGTTATTGTT 2232

Db 885 AATAAAAAATATAAATTTATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAATA 826

Qy 2233 CTACATGTTGATAGAATCATCTTACACCAGATATCAAAAAGAAATACTAGCCTTCTAT 2292

Db 825 AAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 766

Qy 2293 CATAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTACACGAGTAATAGA 2352

Db 765 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAAT 706

Qy 2353 TTAATAAAAACTGAGCGCATTTAAGTAAATATTATAATAATTAAGTCAGTTAAATCTAAAT 2412

Db 705 ATATAAAAAATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAA 646

Qy 2413 TGTGAATACATCATTTTGTGATATCATGCACGCTTTCGTTAAATAATGACAGCTATGCT 2472

Db 645 AAAAAATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA-T 587

Qy 2473 TATATGAAATAATGATGTCGGCATGAATTTCTCAGCATTAACACATGATGGATCGAG 2532

Db 586 AAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 527

Qy 2533 AAAATCAATGCCATCCACCATTTAAAAAGCTCATTAAAACTTATTTTAAATGACAAATGAC 2592

Db 526 AAAAAATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 467

Qy 2593 TTAATAAGTATGAA 2606

Db 466 TTAATAATAATAA 453

RESULT 6

CL081966/c

LOCUS

DEFINITION

CH216-165D13 Sp5.1 CH216 Xenopus tropicalis genomic clone

CH216-165D13, genomic survey sequence.

ACCESSION

CL081966

VERSION

CL081966.1 GI:40537879

SOURCE

GSS.

ORGANISM

Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE

1 (bases 1 to 2157)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)

CONTACT

Contact: Richard K Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 175000 Std Error: 0.00

Seq primer: Sp5 atctgccgttcgatcct

Class: BAC ends

High quality sequence start: 341

High quality sequence stop: 412.

FEATURES

Location/Qualifiers

1..2157

/organism="Xenopus tropicalis"

/mol\_type="genomic DNA"

/strain="Nigerian frog"

/db\_xref="taxon:8364"

/clone="CH216-165D13"

/sex="male"

/cell\_line="Stock 248 F7A2, inbred N7"

/clone\_lib="CH216"

/notes="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"

ORIGIN

Query Match 3.28; Score 94.2; DB 10; Length 2157;

Best Local Similarity 47.1%; Pred. No. 1.2e-08;

Matches 384; Conservative 0; Mismatches 428; Indels 3; Gaps 3;

Qy 1801 ACTGATCGATCAATGAAAAAATTTGAAAAATGCCGTAGCATATGACATGTTCTCTCAAACTC 1860

Db 1583 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1524

Qy 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAATCTGCTATAACCGTGTATTACATGGT 1920

Db 1523 AATAAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAATATA 1464

Qy 1921 GATTAACATCAATTAAGAAACTTGGCATTCAGAAAGAA-AAACCATTTTGTGTAGTCAA 1979

Db 1463 TAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1404

Qy 1980 TCAGTCATTAATAAGACAGGCATAACTTATTATAATTTATGACGAATTTGATGATTTAGA 2039

Db 1403 TATATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1344

Qy 2040 TGAAGTAGAAGATATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTT 2099

Db 1343 CAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1284

Qy 2100 AAAAGATATTA-AAATCATCCAGATTAAGATGCCAAATCGCAGTCAGTATTTTTTATC 2158

Db 1283 AAAAAATAACATAAAAAAATAACAAAAAATAAAAAAATAATAACAAAAAATAAAAAAT 1224

Qy 2159 CCAATACATTAACCGCTTAGTGAATAAATAAACAATATTATTGAATATATAATAAAAA 2218

Db 1223 AAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAAAA 1164

Qy 2219 TATTGTTATTGTTCTACATGTTGATAAGAATCATCTTTACACGAGATATCAAAAAAGAA 2278

Db 1163 ACTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAAAAACAA 1104

Qy 2279 TACTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATT 2338

Db 1103 AAATAATAAAAAATAAAAAAATAAATAATAATAATAATAATAATAATAATAAAAAA 1045

Qy 2339 ACACGAGTAATAGATTAATAAAAACTGAGGCGCATTTAAGTAATATTATAATAATTAAAGTC 2398

Db 1044 AAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAAAAATA 985

Qy 2399 AGTTAAATCTAAATTTGTGAATACATCATTTTGTGATAATCATGACAGCCTTATCGTTAAAA 2458

Db 984 ATAAAAATAAAAAATAATAAAAAATAATAATAATAATAATAATAATAATAATAAAAA 925

Qy 2459 ATGACAGCTATGCTTATATGAAAAAATAATGATGTGGCGATGAATTTCTCAGCATTAACAC 2518

Db 924 AAAAAATAAAAAATAAAAAAATAAATAATAATAATAATAATAATAATAAAAAAATAATAC 865

Qy 2519 ATGATTGGATCGAGAAATCAATGCGCATCCACCATTTTAAAAAGCTCATTTAAACCTTATT 2578

Db 864 AAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAAAAATA 805

Qy 2579 TTAATGACAAATGACTTTAAAAAGTATGAATGTGAAA 2613

Db 804 TATAATAAAAAATAATAAAAAATAAAAAATAAAAAATAATAATAATAATAA 770

CW937448	CW937448	1060 bp	DNA	linear	GSS 20-DEC-2004
LOCUS	TCB16.2_H03_SP6 Tribolium BAC library Tribolium castaneum genomic,				
DEFINITION	genomic survey sequence.				
ACCESSION	CW937448				
VERSION	CW937448.1	GI:56720061			
KEYWORDS	GSS.				
SOURCE	Tribolium castaneum (red flour beetle)				
ORGANISM	Tribolium castaneum				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
	Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;				
	Tenebrionidae; Tribolium.				
	1 (bases 1 to 1060)				
REFERENCE	Savard, J. and Tautz, D.				
AUTHORS	Tribolium castaneum BAC-ends sequencing project				
TITLE	Unpublished (2003)				
JOURNAL	Contact: Savard, J.				
COMMENT	Abteilung für Evolutionsgenetik, AG Tautz Institut für Genetik, Universitat zu Köln Weyertal 121, 50931 Köln, Germany Tel: 49 221 470 6911 Fax: 49 221 470 5975 Email: savard@uni-koeln.de Class: BAC ends.				
FEATURES	Location/Qualifiers				
source	1..1060				
	/organism="Tribolium castaneum"				
	/mol_type="genomic DNA"				
	/strain="GA-2"				
	/db_xref="taxon:7070"				
	/clone_lib="Tribolium BAC library"				
	/note="vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Library constructed by Exelixis Inc."				
ORIGIN					
	Query Match 3.2%; Score 92; DB 10; Length 1060;				
	Best Local Similarity 44.5%; Pred. No. 3.2e-08;				
	Matches 470; Conservative 0; Mismatches 572; Indels 15; Gaps 3;				
QY	1872 AAAATTAAACATCTTAATAAAATCTGCTATAACCGTGATTACATGGTGATAACACATC	1931			
DB	10 AAAAAAAAAAATAAAAAAAAAATAAAAAATATATAAAAAAAAAATAAAAAATAAATAAATA	69			
QY	1932 AATTAAAGAACTTGGCATTCACAAAGAAAAACCAATTTGTGTAGTCAATCAGTCATTTAA	1991			
DB	70 AATAATAAAAAAGAAAAAATTTAAAAAAGATAAATGAAAAAATTAATCAATWAATTC	129			
QY	1992 TAGACAAGGCATACTTATTATAATATGACGAATTTGTAGATTTAGATGAAGTAGAAA	2051			
DB	130 AACAAAAAATAAAAAAANNNT	189			
QY	2052 GTATATTTTCAAT-----AAAACCGCTGAATATCAAGAAGCATTTGATCTTTAAAG	2104			
DB	190 ATAATAATAAAAAATAATAAAAAATAATAAAAAATAAAAAATAAAAAATAAAAAATA	249			
QY	2105 ATATTAAAAATCATCCAGAAATAAGATGCAAAATCGCAGTCAGTATTTTTTATCCCAAT	2164			
DB	250 AATATATAATTAATAAAAAATAATAAAAAATAAAAAATAAAAAATAAAAAATAAA	309			
QY	2165 CATTAACCGCTTAGTGAAAAAACTAAACAATATATTGTAATATAATAAAAAATATATTCG	2224			
DB	310 AAAAAAAAAAATAAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAA	369			
QY	2225 TTATTGTTTACATGTTGATAAAGATCATCTTTACACAGATATCATAAAGAAATACTAG	2284			
DB	370 ATAATAATAAAAAAATAAAAAAAGATAAATAAAAAATAAAAAATAAAAAATAAAA	429			
QY	2285 CCTTCTATCAAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTACACGA	2344			
DB	430 AATAAATGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	489			
QY	2345 GTAATAGATTAATAAAACCTGAGCGCATTTTAAGTAATATTTAATAAATTAAGTCAGTTAA	2404			

Db	490	AAAATATAGATAATTAACAACAATAAAAAATTAAGAAAAAGAAAAAAGAAAAAAGAAAAAAGAA	549
Qy	2405	ATCTAAATGTGAATACATCATTTTTTGATTAATCATGACAGCCTATTGTTTAAATAATGACA	2464
Db	550	AAAAATTAATAAAAAAATAAAAAATATATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	609
Qy	2465	GCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACATGATT	2524
Db	610	AAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	669
Qy	2525	GGATCGAGAAAAATCAATGCGCATCCACCTTTTAAAAAGAGCTCATTAACAACTTATTTTAATG	2584
Db	670	ATAAAAAATAAAAAAATAATATTAATAAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	723
Qy	2585	ACAATGACTTTAAAAAGTATGAATGTGAAGGGGCATCACAAGGTATGTTTATGACGTATG	2644
Db	724	AAAGATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	783
Qy	2645	CGTAGGGCATGAGCTTCTGCAGCATTTATTAAGAAGTCATCACAATCTTGGCAGTCATTTG	2704
Db	784	AAGAAAAAATAATAGATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	843
Qy	2705	ATAGTGGCCAGAAATATAACACTGAGGATATTTGGTTCCTCAATTTGCACTTTTAACTCTTAG	2764
Db	844	TAAAAATAAAAAATAATTAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	903
Qy	2765	AAAAAGAAACCGCCCATGTATTTTAATAAAAAACATCGACCCCTGACTTATATGCTTTGGGAAC	2824
Db	904	TAAAAAATAAAAAAATAATTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	963
Qy	2825	GAAAAATTACAATGGACAAATGAACA--AATTGAAAGTGCAAAAAAGGAGGAAAAATATATACC	2882
Db	964	GAATAAAAATTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	1023
Qy	2883	TGTTTACAAGTTCATTATTAATAGTAACTCTATAA	2919
Db	1024	AAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	1060
RESULT 8	AG376784/c		
LOCUS	AG376784	1324 bp	DNA linear GSS 21-DEC-2004
DEFINITION	Mus musculus molossinus DNA, clone:MSMg01-184I09.T7, genomic survey sequence.		
ACCESSION	AG376784		
VERSION	AG376784.1	GI:47987989	
KEYWORDS	GSS.		
SOURCE	Mus musculus molossinus (Japanese wild mouse)		
ORGANISM	Mus musculus molossinus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Shira, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and Shiroishi, T.		
TITLE	Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis		
JOURNAL	Genome Res. 14 (12), 2439-2447 (2004)		
PUBMED	15574823		
REFERENCE	2 (bases 1 to 1324)		
AUTHORS	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan, 305-8565, Japan (e-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)		
COMMENT	Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1		

Koyadai, Teukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp

## PRIMERS

Sequencing : T7

## LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1..1324

/organism="Mus musculus molossinus"

/mol\_type="genomic DNA"

/sub\_species="molossinus"

/db\_xref="taxon:57486"

/clone="MSMg01-184109.T7"

/sex="male"

/tissue type="mixture of kidney and spleen"

/clone\_lib="MSMg01 Mouse Male BAC Library"

FEATURES  
source

## ORIGIN

Query Match 3.1%; Score 90.6; DB 10; Length 1324;  
Best Local Similarity 45.9%; Pred. No. 6.2e-08;  
Matches 345; Conservative 0; Mismatches 402; Indels 5; Gaps 1;

QY 1853 TCARACTCAGTGAAGTGGAAATTTAAACATCTTTAAATAAAATCTGCTATACCGTGAT 1912  
DB 1268 TAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1209  
QY 1913 TACATGGTGATACACATCAATTAAGAACTTTGGCATTCAGAAAGAAACCCATTTGTTG 1972  
DB 1208 AATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1149  
QY 1973 TAGTCAATCAGTCATTAATAGACAGGCAATCACTTTATTAATTTATGACGATTTGATG 2032  
DB 1148 AAAAAAATACATCAAAATATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 1089  
QY 2033 ATTTAGATGAAGTAGAAGTATATTTCAATAAAACCGCTCAATATCAAGAAGAGATG 2092  
DB 1088 TCATAAAAAATAAAAAAATAATAATAATAATAATAATAATAATAATAATAATA 1029  
QY 2093 ATATCTTTAAAGATATTTAAATCATCCAGAAATAAGATGCCAAAATCGCAGTCAGTATTT 2152  
DB 1028 ATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 969  
QY 2153 TTTATCCCAATACATTAACCGGCTTAGTGAAAAAATAAACAATATTTATGATATATA 2212  
DB 968 TAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 909  
QY 2213 AAAATATATTCGTTATTTGTTCTACATGTTGTAAGAATCATCTTACACCAGATATCAAAA 2272  
DB 908 AATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 849  
QY 2273 AAGAATACTAGCCTTCTA-----TCATAAACATCAAGTGAATATTTTACTAAATAATGA 2327  
DB 848 AATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 789  
QY 2328 TATCTCATATTAACAGAGTAATAGATTAATAAATACTAGGCGCATTTAAGTAATATTA 2387  
DB 788 TAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 729  
QY 2388 TAAATTAAGTCAGTTAAATCTAAATTTGTAATACATCAATTTTGATAATCATGACAGCCT 2447  
DB 728 AAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 669  
QY 2448 ATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATAATGATGTCGGCATGAATTTCTC 2507  
DB 668 AATAAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 609  
QY 2508 AGCATTTAACACATGATTTGGATCGAGAAAAATCAATGCGCATCCACCATTAAAAAGCTCAT 2567  
DB 608 AATAAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 549

QY 2568 TAAAACTATTTTAAATGACAAATGACTTAAAAA 2599  
DB 548 AAAAAATATATTTAAAAAATAAAAAAATAAAAA 517

## RESULT 9

CK997149

LOCUS

DEFINITION

CK997149

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)

Canis familiaris

Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

Canis.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1313)

Baliya, V., Nascimento, L.U. and McCombie, W.R.

ESTs from Canis familiaris cerebellum (dog)

Unpublished (2004)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: ip15 row: c column: 02

High quality sequence stop: 1313.

Location/Qualifiers

1..1313

/organism="Canis familiaris"

/mol\_type="mRNA"

/db\_xref="taxon:9615"

/clone="ip15c02"

/sex="Unknown"

/tissue type="Cerebellum"

/dev\_stage="3 month old normal canine"

/lab\_host="XL10 Gold"

/clone\_lib="Brain - Cerebellum Library (DOGS8T8)"

/note="Organ: Brain; Vector: pBluescript II SK; Site 1:

EcoRI; Site 2: XhoI; Library constructed using pBluescript

XR kit from Stratagene. Cloned cDNA was size selected

between 1-3 kb. Mark Haskins VMD, PhD, Pathology and

Medical Genetics, School of Veterinary Medicine,

University of Pennsylvania, 3800 Spruce Street,

Philadelphia, PA 19104-6051"

## ORIGIN

Query Match

Best Local Similarity 3.1%; Score 90.2; DB 7; Length 1313;

Matches 312; Conservative 0; Mismatches 336; Indels 5; Gaps 2;

QY 1796 ATTTAACTGATGATTCATGAAAAAATTTGAAAAATCGCGTAGACATGATGATGCTCTCA 1855

DB 434 ATAAAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 493

QY 1856 AACTCAGTGAAGTTGGAAAAATTTAAACATCTTTAAATAATCTGCTATTAACCGTGTATTAC 1915

DB 494 TATAATTTTAATTTAAATAATTTAATTAATTTAATTTAATTTAATTTAATTAATTAATA 553

QY 1916 ATGGTGATTAACACATCA-ATTAAGAACTTGGCATTCAAGAAAAACCAATTTTGTGTA 1974

DB 554 AATTAATTAATTAATTAATTAATTAATTAATTAATTTTNTTATTAATTAATTAATTAATA 613

QY 1975 GTCAATCAGTCAATTAATAGACAGGCATTAATTAATTAATTAATTAATTAATTAATTAAT 2034

DB 614 ATAAAAAANTTTTAAATAAAAAAATAAAATTTTAAANTTTTAAATAAAAAAATTTTATT 673

QY 2035 TTAGATGAAGTAGAAGTATATTTTCAATAAAACCGGTGAATATATCAAGAGATTTGAT 2094

Db 674 TAATATTATAATAATAAATTTTATTTATTTATTAATTAATTTATTTATTTATTTATTTA 733  
Qy 2095 ATCTTAAAGATATTAAATCATCCAGAATAAGATGCCAAAATPCGAGTCAGTATTTTT 2154  
Db 734 TTATAAATTAATTTAAATTTTATTTATTTATTTTAAATATAAATAAATAAAT 793  
Qy 2155 TATCCCAATACATTAAGCGGCTTAGTGAAATAAATAAATAAATAAATAAATAAATAA 2214  
Db 794 AAAATTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 853  
Qy 2215 AATATATTTCGTTATTTCTACATGTTGATAAGAAATCATCTTACACAGATAT---CAA 2270  
Db 854 TATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 913  
Qy 2271 AAAAGAAATACAGCTCTTATCATATAAATCAAGTGAATATTTTACTAAATAATGATAT 2330  
Db 914 ATAAATAATTAATAATAATTTTAAATAAATAAATTTATTTATTTTAAATTTAAATAA 973  
Qy 2331 CTCAATATACAGAGTAAATAGATTAATAAATAAATAAATAAATAAATAAATAAATAA 2390  
Db 974 TATATATTATATTATTTTANNTTTTAAATAAATAAATAAATAAATAAATAAATAAATA 1033  
Qy 2391 ATTAAGTCAGTTAAATCTAAATCTGATACATCATTTTGTGATATCATGACA 2443  
Db 1034 TTTATTTTAAATATAATTTTAAATAAATAAATTTTNTTTTATTTAA 1086

RESULT 10  
LOCUS CW953278 1239 bp DNA linear GSS 20-DEC-2004  
DEFINITION TCB39.2\_C10\_SP6 Tribolium BAC library Tribolium castaneum genomic,  
genomic survey sequence.

ACCESSION CW953278  
VERSION CW953278.1 GI:56736315  
KEYWORDS GSS.  
SOURCE Tribolium castaneum (red flour beetle)  
ORGANISM Tribolium castaneum  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
Tenebrionidae; Tribolium.  
1 (bases 1 to 1239)

Savard, J. and Tautz, D.  
Tribolium castaneum BAC-ends sequencing project  
Unpublished (2003)  
Contact: Savard, J.

Abteilung fur Evolutionsgenetik, AG Tautz  
Institut fur Genetik, Universitat zu Koln  
Weyertal 121, 50931 Koln, Germany  
Tel: 49 221 470 6911  
Fax: 49 221 470 5975  
Email: savard@uni-koeln.de  
Class: BAC ends.

FEATURES  
source Location/Qualifiers  
1..1239

/organism="Tribolium castaneum"  
/mol\_type="genomic DNA"  
/strain="GA-2"  
/db\_xref="taxon:7070"  
/clone\_lib="Tribolium BAC library"  
/note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Library constructed by Exelixis Inc."

## ORIGIN

Query Match 3.1%; Score 89.8; DB 10; Length 1239;  
Beet Local Similarity 46.0%; Pred. No. 9,1e-08;  
Matches 341; Conservative 0; Mismatches 397; Indels 3; Gaps 1;  
Qy 1873 AAATTTAAACATCTTAATAAATCTGCTATTAACCGTGATTACATGGTGATAACACATCA 1932  
Db 469 AAAAAATAAAGATAAATAATAATAAAGAAATAAATTTTAAATAATAAATAAATAAATA 528  
Qy 1933 ATTAAGAACTGGCATTCAAAGAAACCAATTTTGTGTAGTCATCATTAAT 1992

Db 529 TATAAATAAATTTTAAATAAATAATGAAAATCATATAAACTGATCAAAAAATAAT 588  
Qy 1993 AGACAAGGCATTAATTTATTTATTAATTAATGACGAATTTTGATGATTTAGATGAAAGTAGAAG 2052  
Db 589 AAAAAATAAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 648  
Qy 2053 TATATTTTCAATAAACCCTGATATCAAGAGAGATTTGATATCTTTAAAGATATTTAA 2112  
Db 649 TACATTTAAATTTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 705  
Qy 2113 ATCATCCAGAATAAAGATGCCAAAATCGCAGTCAGTATTTTATCCCAATACATTAAC 2172  
Db 706 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 765  
Qy 2173 GGCTTAGTGAAAAAATCTAAACAATATTTGAATATAATAAATAAATAAATAAATAA 2232  
Db 766 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 825  
Qy 2233 CTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAAAAGAAATCTAGCCTTCTAT 2292  
Db 826 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 885  
Qy 2293 CATAAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTACACGAGTAATAGA 2352  
Db 886 TAATAAATGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 945  
Qy 2353 TTAATAAATACTGAGCGCATTTAAAGTAAATTAATAAATAAAGTCAGTTAAATCTAAAT 2412  
Db 946 TATTAATAATTTAGAAATCTAAATTTAAATAAATAAATAAATAAATAAATAAATAA 1005  
Qy 2413 TGTGAATACATCATTTTGTGATATCATGACAGCTATTCGTTAAATAAGACAGCTATGCT 2472  
Db 1006 AATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1065  
Qy 2473 TATATCAAAAAATATGATGTCGCGCATTTCTCAGCATTAACACATGATTCGATCGAG 2532  
Db 1066 ATATTAATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1125  
Qy 2533 AAAATCAATCGCATCCACCATTTAAAGAGCTCATTTAAAGCTTTTAAATGACATGAC 2592  
Db 1126 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1185  
Qy 2593 TTAATAAAGATGATGATGAAA 2613  
Db 1186 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1206

RESULT 11  
AG340947/c

LOCUS AG340947 1539 bp DNA linear GSS 18-DEC-2004  
DEFINITION Mus musculus molossinus DNA, clone:MSMG01-134C16.T7, genomic survey  
sequence.

ACCESSION AG340947.1 GI:47914257  
VERSION AG340947

KEYWORDS Mus musculus molossinus (Japanese wild mouse)

SOURCE Mus musculus molossinus

ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and  
Shiroishi, T.

## TITLE

Contribution of Asian mouse subspecies Mus musculus molossinus to  
genomic constitution of strain C57BL/6J, as defined by BAC-end  
sequence-SNP analysis  
Genome Res. 14 (12), 2439-2447 (2004)

## JOURNAL

PUBMED 15574823

## REFERENCE

2 (bases 1 to 1539)

## AUTHORS

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

## DIRECT SUBMISSION

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical







Db	553	NANTAAAAATTTTAAATAATATTANAAANATTNNAAATAATNTNAAAAAANTAAANTTTAAAA	612
Qy	2036	TAGATGAAGCTGAGAAAGCTATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATA	2095
Db	613	TNATTTTATTTATATAAATTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	672
Qy	2096	TCCTTAAAAAGATNTTAAAAATCATCCAGATTAAGATGCCAAATTCGCAGTCAGTATTTTTT	2155
Db	673	ATAAAAAATATATTTTAAATTAATAATAAAAAATPAAAAAATATATTTTAAAAAATAAATAA	726
Qy	2156	ATCCCAATACATTAAACGGCTTAGTGAATAAATACTAAACAATATATTTGAAATATAATAAAA	2215
Db	727	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	786
Qy	2216	ATATATTTCGTTATTTGTTCTACATGTTGATTAAGAAATCATCTTACACAGATATCAAAAAAG	2275
Db	787	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	846
Qy	2276	AAATACTAGCCTTCTATCATATAACATCAAGTGAATATTTTACTATAAATAATGATATCTCAT	2335
Db	847	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	906
Qy	2336	ATTACACGAGTAATAGATTAATAAATAAATTCGAGCGCATTTTAAAGTAATATTTAAATAATTA	2395
Db	907	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	966
Qy	2396	GTCAGTTAAATCTTAAATTTGTGAATACATCATTTTTTGATTAATCATGACAGCCTATTCGTTA	2455
Db	967	ATAAAAAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1026
Qy	2456	AAAATGACAGCTATGCTTTATATGAATAAATAATATGATGTCGCGCATGAATTTCTCAGCATTA	2515
Db	1027	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1086
Qy	2516	CACATGATTTGGATCGAGAAATCAATGCGCATCCACCAATTTAAAAAGCTCATTTAAAAACTT	2575
Db	1087	TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1146
Qy	2576	ATTTTAATGACAATGACTTTAAAAAGTATGAATGTGAAA	2613
Db	1147	AAATTAATTTTTTATTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1184

RESULT 14	
CW960936	
LOCUS	
DEFINITION	735 bp DNA linear GSS 21-DEC-2004
	A1AA-aac14d08.b1 Ancylostoma caninum whole genome shotgun library
	(ATAAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.
ACCESSION	CW960936
VERSION	
KEYWORDS	
SOURCE	CW960936.1 GI:56761663
	GSS.
ORGANISM	Ancylostoma caninum (dog hookworm)
	Ancylostoma caninum
	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
REFERENCE	Ancylostomatoidae; Ancylostomatinae; Ancylostoma.
AUTHORS	1 (bases 1 to 735)
	Ronko, I., Martin, J., Wylie, T., Dente, M., Meyer, R., Messina, D.,
	Waterston, R.H., Clifton, S.W. and Wilson, R.
TITLE	Genome Survey sequences from the parasitic nematode Ancylostoma caninum
JOURNAL	Unpublished (2004)
COMMENT	Contact: Mitreva M
	Washington University in St. Louis
	Washington University School of Medicine
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
	Tel: 314 286 1800
	Fax: 314 286 1810
	Email: <a href="mailto:nematode@watson.wustl.edu">nematode@watson.wustl.edu</a>
	Genomic DNA provided by John Hawdon ( <a href="mailto:mtmjmh@gwumc.edu">mtmjmh@gwumc.edu</a> ) DNA
	sequenced by Washington University Genome Sequencing Center
FEATURES	Class: shotgun.
	Location/Qualifiers

```

source
1. .735
/organism="Ancylostoma caninum"
/mol_type="genomic DNA"
/strain="Baltimore"
/db_xref="taxon:29170"
/dev_stage="Adult"
/lab_host="GS10"
/clone_lib="Ancylostoma caninum whole genome shotgun
library (A1AGSS 001)"
/notes=Vector: potw13; Site_1: BstX1; Site_2: BstX1;
Ancylostoma caninum genomic DNA was randomly sheared,
end-repaired and size fractioned to enrich for 2-4 kb
fragments. Genomic DNA was provided by John Hawdon
(mtmjh@wumc.edu) at George Washington University
Sequencing by Washington University Genome Sequencing
Center, St. Louis, MO."

ORIGIN
Query Match 3.0%; Score 87.4; DB 10; Length 735;
Best Local Similarity 47.1%; Pred.No. 2.7e-07;
Matches 268; Conservative 0; Mismatches 301; Indels 0; Gaps 0;

QY 1873 AAATTTAAACATCTTAATAAAATCTGCTATAACCGGTATATACATGGTGATACACATCA 1932
Db 22 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 81

QY 1933 ATTAAGAACTTGGCATTCAAAAGAAAACCATTTTGGTGTAGTCAATCGTCATTAAAT 1992
Db 82 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 141

QY 1993 AGCAAGGCATACTTATTATATATATGACGAATTTGATGATTTAGATGAAAGTAGAAAG 2052
Db 142 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 201

QY 2053 TATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTTAAAGATATTAAA 2112
Db 202 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 261

QY 2113 ATCATCCAGAAATAAGATGCCAAATCGCAGTCAGTATTTTTATCCCAATACATTAAAC 2172
Db 262 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 321

QY 2173 GGCTTAGTGAATAAATCTAACAATATTTTGAATATATAATAATAATAATAATAATAATA 2232
Db 322 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 381

QY 2233 CTACATGTCGATAGATCATCTTTACACCAGATATCAAAAAGAAATACCTAGCCTTCAT 2292
Db 382 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 441

QY 2293 CATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTTACACGAGTAATAGA 2352
Db 442 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 501

QY 2353 TTAATAAACTGAGGGCCATTTAAGTAATATTTAATAAAATTAAGTCAGTTAAATCTAAAT 2412
Db 502 AATAATAATTATCATCAATATCATATAATAATAATAATAATAATAATAATAATAATAA 561

QY 2413 TGTGAATACATCATTTTTTGATTAATCATGA 2441
Db 562 CATCAACAACAACATCATGATAAATAATCA 590

RESULT 15
AG347098/c
LOCUS
DEFINITION
Mus musculus molossinus DNA, clone:MSMg01-142102.T7, genomic survey
sequence.
ACCESSION
AG347098
VERSION
AG347098.1 GI:47920408
KEYWORDS
GSS.
SOURCE
Mus musculus molossinus (Japanese wild mouse)
ORGANISM
Mus musculus molossinus

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

# REFERENCE AUTHORS

1  
Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and  
Shiroishi, T.

**TITLE**  
Contribution of Asian mouse subspecies *Mus musculus molossinus* to  
genomic constitution of strain C57BL/6J, as defined by BAC-end  
sequence-SNP analysis

**JOURNAL**  
Genome Res. 14 (12), 2439-2447 (2004)

15574823

2 (bases 1 to 1268)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

**REFERENCE**  
Direct Submission

**TITLE**  
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
(E-mail: hattori@psc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

**COMMENT**  
Clones are derived from the mouse BAC library MSMg01. For BAC  
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : T7

**LIBRARY**

Vector : pBACE3.6

R.Site 1 : ECoRI

R.Site 2 : EcoRI

**FEATURES**  
Location/Qualifiers

1..1268  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clones="MSMg01-142102.T7"  
/sex="male"  
/tissue type="mixture of kidney and spleen"  
/clone\_lib="MSMg01 Mouse Male BAC Library"

## ORIGIN

Query Match 3.0%; Score 87.4; DB 10; Length 1268;  
Best Local Similarity 45.1%; Pred. No. 2.8e-07;  
Matches 439; Conservative 0; Mismatches 526; Indels 9; Gaps 3;

Qy 1948 ATTCAAAGAAAAACCACTTTTGGTGTAGTCAATCAGTCATTAAATAGACAAGGCATAACT 2007

Db 1246 AATAAAATAANTATAAATTAATTTATAAATAATTTAAATAATNATAAATAAATAATATATAT 1187

Qy 2008 TATTATAATTAATGACGAATTTGATGATTTA-GATGAAAGTAGAAGATATATTTTCAATAA 2066

Db 1186 AAATATAATAATTAATAATATAAAAAATAATAAATAATTAATAAATAAATAAATAAATAA 1127

Qy 2067 AACCGCTGAATATCAAGAAGAGATTGATATCTTAAAGATATTAAATATCAATCCAGAATAA 2126

Db 1126 ATTAATAAATATAAAAAATAAATAATTAATTAATTAATTAATTAATAATAATATATAA 1067

Qy 2127 AGATGCCAAAATCGGAGTCAGTATTTTTTATCCCAATACATTAAACGGCTTAGTGAAAAA 2186

Db 1066 ATATAAAATAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1007

Qy 2187 ACTAAACAATATATTGAATAATAAAAAATATATTCGTTATTTGTTCTACATGTTGATAA 2246

Db 1006 AAATATAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 947

Qy 2247 GAATCATCTTACACCAGATATCAAAAAAGAAATACTAGCCTTCTATCATCAAAACATCAAGT 2306

Db 946 ATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 894

Qy 2307 GAATATTTTACTAAATAATGATATCTCATATATTACAGAGTAATAGATTATAAATAAACTGA 2366

Db 893 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 834

Qy 2367 GGCGCAATTTAAGTAATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2426

Db 833 TTTATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 774

Qy 2427 TTTTGATAATCATGACAGCGCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAATA 2486

Db 773 ATATTTTATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 714

Qy 2487 TGATGCGGCATGAATTTCTCAGCATTTAACACATGATTGGATCGAGAAAAATCAATGCGCA 2546

Db 713 AATAATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 654

Qy 2547 TCACCAATTTTAAAAAGCTCATTAAAACTTTATTTTAAATGACAAATGACTTAAAAAGTATGAA 2606

Db 653 TATATAATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 594

Qy 2607 TGTGAAGGGGCATCAAGGATGTTTATGACGTATGCCCTAGCGCATGAGCTTCTGAC 2666

Db 593 ATAAAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 534

Qy 2667 GATTATTAAAGAAGTCATCACATCTTGCAGTCAATTTGATAGTGTGCCAGAAATATAACAC 2726

Db 533 ATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 474

Qy 2727 TGAGGATATTTGGTTCCCAATTTTGCACCTTTTAAATCTTAGAAAAAGAAACCGGCCCATGTATT 2786

Db 473 TAAATATAATTTTAAATTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 414

Qy 2787 TAATAAAACATCGACCCCTGACTTATATGCCCTTGGGAACGAAATTTACAATGGACAAATGA 2846

Db 413 TAATAAAA-AAAAATAATTTTATTTTNTTTTAAAAAATAAATAAATAAATAAATAAATAAATAA 355

Qy 2847 ACAAAATTGAAAGTGCAAAAAGAGGAGAAATATACCTGTTTAAACAAGTTTCATTATTAAATAG 2906

Db 354 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 295

Qy 2907 TATAAATCTTATAAA 2920

Db 294 TATAAATTTTAAATA 281

Search completed: January 8, 2006, 12:56:35  
Job time : 10323 secs

**THIS PAGE BLANK (USPTO)**







NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 2344  
LENGTH: 2529  
TYPE: DNA  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-2344

Query Match 2.5%; Score 72.6; DB 3; Length 2529;  
Best Local Similarity 52.5%; Pred. No. 5.4e-07;  
Matches 159; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 1332 AGTTCAATTTATATCCAGCTTATTAACGTGCAACCTATATTCACAGTTGGTAGATAG 1382  
DB 33 AGTGTACATCATGTATCCCGTCTATTAACGTAGAAACCTATTTAGAAAGGCAATATATG 92  
QY 1383 TGCACATGATCAGACTGTTGTTGATCTGAGGTTTGTATTTGTAACGATGTTCAACAGA 1442  
DB 93 TTGAAAAACCAACATGGAAGAAATGGAATCTTAATTAATGAATGAGCTCTACTGA 152  
QY 1443 TAATACCTTAGAAGTATCATTAAGCTTATAGTAAATCCTAGGGTAAGCATCATGTC 1502  
DB 153 TATATGTCAAAAATTAATTAAGAAATTCACAAAGATGATCCAGTTTCGGGTTTCAA 212  
QY 1503 TAAACCAATGGCGGATAGCCTCAGCATCAAAATGCAAGCCGTTCTTTGTTAAAGTTA 1562  
DB 213 TGTAAAAATGGGGAAATGGAAAAGCCTTTAACTGGGTTTCAGAAAGCAAAAGTGA 272  
QY 1563 TTACATTGGCAGTTAGATTAGATGATGATTAATCTTGAGCCTGATGAGTGAATGTGTT 1622  
DB 273 GATATATGTCGAATTTGAAAGTGAAGATTAATGATGATTCATGAGCTTATGAGCGTTTATA 332  
QY 1623 AAA 1625  
DB 333 CAA 335

RESULT 12  
US-09-627-122-21/C  
Sequence 21, Application US/09627122  
Patent No. 6472521  
GENERAL INFORMATION:  
APPLICANT: Uhlmann, Eugen  
APPLICANT: Greiner, Beate  
APPLICANT: Unger, Bernhard  
APPLICANT: Gothe, Gislinde  
APPLICANT: Scherdel, Marc  
TITLE OF INVENTION: OLIGONUCLEOTIDES FOR THE INHIBITION OF HUMAN eg5  
TITLE OF INVENTION: EXPRESSION  
FILE REFERENCE: 02481.1678  
CURRENT APPLICATION NUMBER: US/09/627,122  
CURRENT FILING DATE: 2000-07-27  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 5340  
TYPE: DNA  
ORGANISM: Plasmodium falciparum  
US-09-627-122-21

Query Match 2.5%; Score 72.6; DB 3; Length 5340;  
Best Local Similarity 46.4%; Pred. No. 6.9e-07;  
Matches 237; Conservative 0; Mismatches 274; Indels 0; Gaps 0;

QY 1914 ACATGGATTAACATCAATTAAGAACTTGGCATTCAAAAGAAAAACATTTTGTGT 1973  
DB 1101 AAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1042  
QY 1974 AGTCAATCACTCAATTAATTAAGCAAGGCAATTAATTAATTAATTAATTAATTAATTA 2033  
DB 1041 AAATTAATCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 982  
QY 2034 TTTAGATGAAGTAAGTAATTTTCAATTAACCGCTGAATATCAAGAAGATGTA 2093

DB 981 AAATGTACATATATTAATTAATGATGATTAATTAATGATCAAGGTGATCATTAATTA 922  
QY 2094 TATCTTAAGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2153  
DB 921 TTAATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTA 862  
QY 2154 TTAATCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2213  
DB 861 TTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 802  
QY 2214 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2273  
DB 801 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 742  
QY 2274 AGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2333  
DB 741 AGATCAAGGTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 682  
QY 2334 ATATTACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2393  
DB 681 ATACTTGAAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 622  
QY 2394 AATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2424  
DB 621 TATGATTTAAGTAAGTAATTTTGAACAAATC 591

RESULT 13  
US-09-634-238-29/C  
Sequence 29, Application US/09634238  
Patent No. 6544772  
GENERAL INFORMATION:  
APPLICANT: Glenn, Matthew  
APPLICANT: Havukkala, Ilkka J.  
APPLICANT: Bloksberg, Leonard, N.  
APPLICANT: Lubbers, Mark W.  
APPLICANT: Dekker, James  
APPLICANT: Christenson, Anna C.  
APPLICANT: Holland, Rose  
APPLICANT: O'Toole, Paul W.  
APPLICANT: Reid, Julian R.  
APPLICANT: Coolbear, Timothy  
TITLE OF INVENTION: Polynucleotides, materials incorporating  
TITLE OF INVENTION: them and methods for using them.  
FILE REFERENCE: 11000.1043U  
CURRENT APPLICATION NUMBER: US/09/634,238  
CURRENT FILING DATE: 2000-08-08  
NUMBER OF SEQ ID NOS: 422  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 29  
LENGTH: 13825  
TYPE: DNA  
ORGANISM: Lactobacillus rhamnosus  
US-09-634-238-29

Query Match 2.5%; Score 72.4; DB 3; Length 13825;  
Best Local Similarity 52.7%; Pred. No. 1.1e-06;  
Matches 157; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 1316 TACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1375  
DB 11873 TGCCTTAATTTCTAATTAATTCGTTCCATTTATTAATTAATTAATTAATTAATTA 11814  
QY 1376 TAGATAGTCACTGAATCAAGCTGTTGATCTCAAGGTTTGTATTTGTAACGATGTT 1435  
DB 11813 TAGACAGTTTAATTTGGCAAAACATACGTCATTAATGAATAGTCCCTAGTTGACAGAGAT 11754  
QY 1436 CAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1495  
DB 11753 CGGCAACCGTTCACTGATCAATCTGTAATTAATTAATTAATTAATTAATTAATTA 11694  
QY 1496 TCATGTCTAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1555



US-09-900-038A-3

Query Match 2.8%; Score 80.6; DB 3; Length 6865;  
Best Local Similarity 53.3%; Pred. No. 1.1e-08;  
Matches 170; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 1332 TAGTTCAATTATATCCAGCTTAACTGTGCAAACTAATATCAAGTTCCAGAGATA 1381  
DB 3998 TGTGTTCTATCGTATATACCTATATACACTCGAAGCATATTTAAAGAAATCGTGCAAT 4057  
QY 1382 GTGCACTGAATCAGACTGTGTTGATCTCGAGTTGTAATTTGTAACAGTGGTTCAACAG 1441  
DB 4058 CCGTCTTACAAAGACTATTCATTTGATGATGAAAGTTATACCTGATGATATGATGATCCACTG 4117  
QY 1442 ATAATACCTTAGAGATCAATTAAGCTTTATGTAATATCTTGAAGGATGCATCAGT 1501  
DB 4118 ATAATAGTGAGAAATTTGTGATTAATTTATCTCAAAAGACATGCAATATCTGTAATTC 4177  
QY 1502 CTAAACCAAAATGGCGAATAGCTCAGATCAATGACGCGTTCTTTGCTAAAGTT 1561  
DB 4178 AATAAATAAATGAGGAGTATCTTGCGCAAGAACTAGCTCTTGATTAATCCAGAGCG 4237  
QY 1562 ATTACATTTGGCAGTTAGATTCAGATGATTAATCTTGAGCTGATGCAAGTTGAAGTGT 1621  
DB 4238 AATTCATAACGTTTGTAGATGATGATTTTGTAGCAGCAATTAATTAATGAATATATGT 4297  
QY 1622 TAAAGAAATTTTAAAGA 1640  
DB 4298 TAAAAAATTAATCACTGA 4316

## RESULT 8

US-09-134-000C-2987  
; Sequence 2987, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2987  
; LENGTH: 993  
; TYPE: DNA  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-2987

Query Match 2.6%; Score 77; DB 3; Length 993;  
Best Local Similarity 52.3%; Pred. No. 3.7e-08;  
Matches 170; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 1316 TACCTTAGTTCAATTAATATATCCAGCTTAATACGTGCAACTATATTCAAGTTGCG 1375  
DB 20 TGCCCAAAATAGTATATATGTTCCGTGTATACATGAGAAAAATATTTAGAAAAATGTG 79  
QY 1376 TAGATAGTGCACTGATTCAGACTGTGTTGATCTCGAGGTTTATTTTGAAGATGTT 1435  
DB 80 TAGGCTCTATTTTAGCTCAAAACGTTTACGTGACTTTGAATTAATCTGTGAGAGATGCT 139  
QY 1436 CAACAGATATATACCTTAGAGATGATCAATTAAGCTTTATGTAATTAATCTTAGGTTACGA 1495  
DB 1440 CTCGACAGACTTTGAGAGCATGTGTGATCAGTTTGTCTGAACAAGATCAACGGGTAAAG 159  
QY 1496 TCATGCTTAAACCAATGCGGGAATAGCTTCAGATCAAAATGACCGCTTTCTTTGCTA 1555  
DB 200 TTATCATTAAGAAATGTTGGGCTAAGCATGCTGTAAATGCTGAATTAAGAAATAGCAA 259  
QY 1556 AAGGTTATTAATTTGGGCACTTGAATTCAGATGATTAATCTTGAAGCCGTGATGAGTTGAC 1615

DB 260 CAGGTGAGTATTTAGGTTTCGTAGATGATGATTAATTCAGATGATATGATGAAAC 319  
QY 1616 TGTGTTAAAGAAATTTTAAAGA 1640  
DB 320 TATTAATTAACAATATTCGTAAAGA 344

## RESULT 9

US-08-998-416-186/C  
; Sequence 186, Application US/08998416  
; Patent No. 6239264  
; GENERAL INFORMATION:  
; APPLICANT: Philippen, Peter  
; APPLICANT: Pohlmann, Rainer  
; APPLICANT: Steiner, Sabine  
; APPLICANT: Mohr, Christine  
; APPLICANT: Wendland, Jurgen  
; APPLICANT: Knechtle, Philipp  
; APPLICANT: Reibschung, Corinne  
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPHII  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 1152  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: No. 6239264artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: No. 6239264th Carolina  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/998,416  
; FILING DATE: 24-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CH 0016/97  
; FILING DATE: 31-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8689  
; TELEFAX: 919-541-8587  
; INFORMATION FOR SEQ ID NO: 186:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 615 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: PAG1074RP  
US-08-998-416-186

Query Match 2.6%; Score 75.8; DB 3; Length 615;  
Best Local Similarity 46.8%; Pred. No. 6e-08;  
Matches 239; Conservative 0; Mismatches 272; Indels 0; Gaps 0;

QY 1980 TCAGTCATTAATAGCAAGCATTAATTAATTAATTAATGACGAATTTGATGATTTAGA 2039  
DB 551 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 492  
QY 2040 TGAAGTAAAGTATATTTTGAATTAACCGCTGAATATCAAGAAGATGATGATCTT 2099  
DB 491 ATTAAGAAATTAAGTTAAATTAATTAATTAATTAATTAATTTCTTAATTAAGAAATTAAT 432  
QY 2100 AAAAGATTAATTAATCATCATCAGATTAAGATGCCAAATCGCAGTCAATTTTATCC 2159

Db	8068	ATTAATTTAAATTATATTAATTAATAATTAATTAATAATTAAGATTAATATTTTAAAGAT	8127
Oy	2037	AGATGAAAGTAGAAAGTATATTTTCAATTAACCGCTGAATATCAAGAGAGATTGATAT	2096
Db	8128	ATTTTAAATAATATTCATTTATATATAGATGATTATTATATTCATGATTAATTAATCG	8187
Oy	2097	CTTAAAGATATTTAAATCATCCGAATAAAGATGCCAAAATGCCAGTCAGTATTTTAA	2156
Db	8188	AAATTAATAATTTAAATTTATTTATTTTGGAAAAATATATTAATTAATTAATTTATTA	8247
Oy	2157	TCCCATATCATTAACCGCTTAGTGAATAAACTAAACAATTTATGAAATTAATTAATA	2216
Db	8248	T-ATATATATTAATAATGATACCTTACCATCCGAATTTATTTTAAATAATTTATATAT	8306
Oy	2217	TATATTCGTATTTGTTCTACATGTTG-ATAGAATCATCTTACACCGATATCAAAAAAG	2275
Db	8307	TAGATATATGATTATATATATTTGTTAATATGATTTTATACAGATCTAATATATTA	8366
Oy	2276	AAATCTAGCCTTCTATCATTAACAATCAAGGAATTTTCTAAATATGATATTCAT	2335
Db	8367	AAATATATATTAATAAAATATTAATAATGATGAAAAAATTTATCAAAATATATTACTPA	8426
Oy	2336	ATTACAGAGTAATGATTAAATTAATAACCTGAGCGCATTTAGTAATATTAATAATTA	2395
Db	8427	CAGATA-AATTAATATGAAATATTAACCATTAATATAGATTTGTTGATTTATTCATATAT	8485
Oy	2396	GTCAGTAAATCTAAATTTGTGAATCATCTTTTGTGATATCATGA 2441	
Db	8486	TCATCATTAATGAAATATTTTATTTATTAATAATTAATAAAAAATATTA 8531	

```

1  RESULT 6
2  US-09-107-532A-2527
3  ; Sequence 2527, Application US/09107532A
4  ; Patent No. 6583275
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Lynn A Doucetle-Stamm and David Bush
7  ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
8  ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
9  ; NUMBER OF SEQUENCES: 7310
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
12 ; STREET: 100 Beaver Street
13 ; CITY: Waltham
14 ; STATE: Massachusetts
15 ; COUNTRY: USA
16 ; ZIP: 02354
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: CD-ROM ISO9660
19 ;
20 ; COMPUTER: PC
21 ; OPERATING SYSTEM: <Unknown>
22 ; SOFTWARE: ASCII
23 ;
24 ; CURRENT APPLICATION DATA:
25 ; APPLICATION NUMBER: US/09/107,532A
26 ; FILING DATE: 30-Jun-1998
27 ;
28 ; PRIOR APPLICATION DATA:
29 ; APPLICATION NUMBER: 60/085,598
30 ; FILING DATE: 14 May 1998
31 ; APPLICATION NUMBER: 60/051571
32 ; FILING DATE: July 2, 1997
33 ;
34 ; ATTORNEY/AGENT INFORMATION:
35 ; NAME: Arindello, Pamela Denoke
36 ; REGISTRATION NUMBER: 40,489
37 ;
38 ; REFERENCE/DOCKET NUMBER: GTC-012
39 ;
40 ; TELECOMMUNICATION INFORMATION:
41 ; TELEPHONE: (781)893-5007
42 ; TELEFAX: (781)893-8277
43 ;
44 ; INFORMATION FOR SEQ ID NO: 2527:
45 ; SEQUENCE CHARACTERISTICS:
46 ; LENGTH: 984 base pairs
47 ; TYPE: nucleic acid
48 ; STRANDEDNESS: double
49 ; TOPOLOGY: circular
50 ;
51 ;
52 ;

```

```

? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Enterococcus faecium
?
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (8) LOCATION 1...964
? SEQUENCE DESCRIPTION: SEQ ID NO: 2527
US-09-107-552A-2527

```

Query Match	2.8%	Score 80.6;	DB 3;	length 984;
Best Local Similarity	52.5%	Pred. No. 5.5e-09;		
Matches 176; Conservative	0;	Mismatches 159;	Indels 0;	Gaps 0;

Qy	1309	AAATGAGTACCTTAGTTGCAATTTAAATCCACCTATAATCTGCAAACTATTTCAA	1368
Db	13	AAATPAAATGTGTGAGATTAGTATTATTGTTCTGTGTAAAGTTGAAAATATTATTAAGA	72
Qy	1369	CGTTGCGGTAGATAGTGCACTGAATCAGACTGTTTGTGATCTCGAGGTTTGATTGTAAAC	1428
Db	73	AAATGTGTAGATTGGATTGATTTAGCCCAACATTACTGATTTTGAAGTTATATTGTAGAT	132
Qy	1429	GATGGTTTCAACAGATAAATACCTTAGAAATGATCAATAAGCTTTAATGTAAATATCTAGG	1488
Db	133	GATGATGTTCTCTGACAAATAGCGGGAAATCTGTANTGATGTGTAAGAAAAGATAAATGCA	192
Qy	1489	GTACGCATCATGTCTTAAACCAATATGGCGGAATAGCCTTCAGCATCAATGACCGGTTTCT	1548
Db	193	GTACGTGTGATCCATTAAGAAAACGGCGGATTAAGCAGTGTAGAAAATGCGGGGATTGAT	252
Qy	1549	TTTGTCTAAAGTTATTATACATTGGGCACTTAAGATTCAAGTGTATTAATCTTGACCCTGATGCA	1608
Db	253	GTTGGAGACGGCAAAATACTTATGGCTTTGTGTGACAGTGTATTAATTGATGAAGAAATYG	312
Qy	1609	GTTGAACGTGTTTAAAGAATTTTTTTAAAGATAA	1643
Db	313	TATGAAATTTGTATGAGAAATTTGAAAATTCATGA	347

```

RESULT 7
US-09-900-038A--3
/ Sequence 3, Application US/09900038A
/ Patent No. 6828128
/ GENERAL INFORMATION:
/ APPLICANT: Miyake, Katsuhide
/ APPLICANT: Matsube, Masaki
/ APPLICANT: Iijima, Shinji
/ TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
/ FILE REFERENCE: 766.53
/ CURRENT APPLICATION NUMBER: US/09/900.038A
/ CURRENT FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: JP 2001-392
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 6865
/ TYPE: DNA
/ ORGANISM: Streptococcus agalactiae type Ib
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (617)..(1789)
/ NAME/KEY: CDS
/ LOCATION: (1816)..(2262)
/ NAME/KEY: CDS
/ LOCATION: (2265)..(2744)
/ NAME/KEY: CDS
/ LOCATION: (2843)..(3979)
/ NAME/KEY: CDS
/ LOCATION: (3982)..(4953)
/ NAME/KEY: CDS
/ LOCATION: (5009)..(5947)

```

```
Db      1201  GAAATGAAACGATCGTGAAGCGGAAAAATATTAAGCTGATATTATGAGAAAAG 1260
Oy      1261  GTCCCTTATCTATAGAAAACCTTTACCAATAGAAAGTTGGCATATCAATAGACTCT 1320
Db      1261  GTCCCTTATCTATAGAAAACCTTTACCAATAGAAAGTTGGCATATCAATAGACTCT 1320
Oy      1321  TTAGTTTCAATTTATATCCAGCTTATTAAGTGTGCAAACTATATTCAAAGTTGCTAGAT 1380
Db      1321  TTAGTTTCAATTTATATCCAGCTTATTAAGTGTGCAAACTATATTCAAAGTTGCTAGAT 1380
Oy      1381  AGTGCACCTGAATCAGACTGTTGTGATCTCGAGGTTTGTATTTGTAACAGTGTTCACA 1440
Db      1381  AGTGCACCTGAATCAGACTGTTGTGATCTCGAGGTTTGTATTTGTAACAGTGTTCACA 1440
Oy      1441  GATATATCTTATGAAGTATGATTAAGCTTTATGTAATTAATCCAGGTTAGCATCANG 1500
Db      1441  GATATATCTTATGAAGTATGATTAAGCTTTATGTAATTAATCCAGGTTAGCATCANG 1500
Oy      1501  TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGACGCGTTCTTTGCTAAAGGT 1560
Db      1501  TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGACGCGTTCTTTGCTAAAGGT 1560
Oy      1561  TATTACATTTGGCAGTTAGATTCAATGATTAATCTTGAGCTGTGATGCACTGTGT 1620
Db      1561  TATTACATTTGGCAGTTAGATTCAATGATTAATCTTGAGCTGTGATGCACTGTGT 1620
Oy      1621  TTTAAAGAAATTTTAAAGATTAAGTGAAGCTGCTGTTGTTATACCACTTAATGAAGCTG 1680
Db      1621  TTTAAAGAAATTTTAAAGATTAAGTGAAGCTGCTGTTGTTATACCACTTAATGAAGCTG 1680
Oy      1681  AATCGGATGTAGCTTAATGCTTAATGCTTAACATTTGSCAGAAATTTTCAAGAAAAA 1740
Db      1681  AATCGGATGTAGCTTAATGCTTAATGCTTAACATTTGSCAGAAATTTTCAAGAAAAA 1740
Oy      1741  CTCACAACGGCTATGATGCTGCAACACTTGAATGTTTCAATGAGCTTGGCATTTA 1800
Db      1741  CTCACAACGGCTATGATGCTGCAACACTTGAATGTTTCAATGAGCTTGGCATTTA 1800
Oy      1801  ACTGATGATTCATATGAAAAATTTGAAATGCCGTGACATGACATGTTTCTCAAACTG 1860
Db      1801  ACTGATGATTCATATGAAAAATTTGAAATGCCGTGACATGACATGTTTCTCAAACTG 1860
Oy      1861  APTGAAAGTTGGAATTTTAAACCTTAAATGCTGATTAACGCTGATTAATCAATGCT 1920
Db      1861  APTGAAAGTTGGAATTTTAAACCTTAAATGCTGATTAACGCTGATTAATCAATGCT 1920
Oy      1921  GATTAACATCATTAAGAACTTGGCATTCAAAAGAAAAACCAATTTGTGTAGTCAAT 1980
Db      1921  GATTAACATCATTAAGAACTTGGCATTCAAAAGAAAAACCAATTTGTGTAGTCAAT 1980
Oy      1981  CAGTCATTAATTAAGACAGGCTAATCTTATTAATTAATGAAGATTTGATTTAGT 2040
Db      1981  CAGTCATTAATTAAGACAGGCTAATCTTATTAATTAATGAAGATTTGATTTAGT 2040
Oy      2041  GAAAGTGAAGAAATTTTTCATATAAAACCGCTGAATATCAAGAAAGATTGATCTTA 2100
Db      2041  GAAAGTGAAGAAATTTTTCATATAAAACCGCTGAATATCAAGAAAGATTGATCTTA 2100
Oy      2101  AAAAGATTTTAA 2112
Db      2101  AAAAGATTTTAA 2112

RESULT 5
US-09-662-254B-27
; Sequence 27, Application US/09662254B
; Patent No. 6933145
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; TITLE OF INVENTION: Vertebrate Cells
```

```
; FILE REFERENCE: UF-221C1XC1
; CURRENT APPLICATION NUMBER: US/09/662, 254B
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 32392
; TYPE: DNA
; ORGANISM: Ambacta moorei entomopoxvirus
US-09-662-254B-27

Query Match      2.8%; Score 82.4; DB 3; Length 32392;
Bec Local Similarity 44.8%; Pred. No. 6.9e-09;
Matches 558; Conservative 0; Mismatches 681; Indels 7; Gaps 6;

Oy      1197  TAAAGAAATGAACCGATCGTGAACGGGAAAAAATTAAGCTCGATATTATGAGAGA 1256
Db      7292  TAAATTAATTAATCTATATTAAGAAATTTAATAATTAATATATAGTGTGGGA 7351
Oy      1257  AAAGTCCCTATATCTATAGAAAATTTTACCAATAGAAAGTTGCAATTAATGAGT 1316
Db      7352  CGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7411
Oy      1317  ACCTTAGTTCAATTTATATCCAGCTTATTAATAGTGCAAACTATATTCAGCTTGCCT 1376
Db      7412  AATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7471
Oy      1377  AGATAGTCACTGAATCAGACTGTTGTGATCTCGAGGTTGTATTTGTAACGATGTTG 1436
Db      7472  AACTAATTAATTAATTAATTAATTTGTTGATAT--AAATTAATTAATTTTCTACACAATAC 7529
Oy      1437  AACAGATATACCTTAGAAGTGAATCAATAGCTTTATGTAATTAATCTAGGCTACGAT 1496
Db      7530  GAATGTTTGAACATATATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7589
Oy      1497  CATGCTTAACCAATATGGCGGAATAGCCTGACATCAATGACGCGTTCTTTGCTAA 1556
Db      7590  AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7649
Oy      1557  AGTTATTAATCATTTGGCAGTTAGATTCAGATGATTAATCTTGAGCCTGATGAGTGA 1616
Db      7650  AATTATGGAATTAACAAATTAATTAATTTTG-TACTAATATTAATTAATTAATTAAT 7708
Oy      1617  GTGTTTAAAGAAATTTTAAAGATTAACGCTAGCTGTGTTTATACACTAATTAAGAA 1676
Db      7709  ATTTAAAAAATCTGTTAAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 7768
Oy      1677  CGTCAATCCGATGCTAGCTTAATGCTTAATGCTTAATGSCCGAATTTTCAAGAGA 1736
Db      7769  AATAGCTTTGATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7828
Oy      1737  AAAACCTCAACGCGTATGATGCTCAACACTTGAAGTTCAGCATTAAGAGCTTGCA 1796
Db      7829  AATATGCTATAGATTAATTTGAAAAATCAGTAATTTTAATCAATTAAGAGTATTA 7888
Oy      1797  TTTAACTGATGATTCATGAAAAAATGAAAAATGCGGTGAATATGACATGTTCTCA 1856
Db      7889  CTTAATATATTAATGATATGTAATTAATTAATTTTATGAAAAATTAATTTAAATTA 7948
Oy      1857  ACTCAGTGAAGTTGAAAAATTTAAACCTTTAATTAATTAATTAATTAATTAATTA 1916
Db      7949  ATTTAAATTAATTAATTAATTAATTAATTAAT--ATAATTTCTTTAAATGTTTAA 8007
Oy      1917  TGGTATTAACATCAATTAAGAAATCTTGCAATTAAGAAATTAATTTGTTGTAGT 1976
Db      8008  TAAAAAATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8067
Oy      1977  CATCAGTCATTAATTAAGCAAGCATTAATTAATTAATTAATTAATTAATTAATTA 2036
```





Db 181 AATGTAAAGAAAACCTCCGACCAATTC-----TTATGTAGT 219  
Qy 181 AAAGAGAAAAAGTCAATGTTTGGCATAGTCCGTTAGATTTGGCAACCACTGTACTT 240  
Db 220 GAAAGATTAATAAAGACAGTGTGGCGATAGCTCATTAAGATTCGCAACACAGCTGTACTT 279  
Qy 241 TCCACGTTAAAAAATTAGTACTTCTGTGCTCGAAAAAACAAGTTAAAAATTAATG 300  
Db 280 TCCACGTTAAAAAATTAGTACTTCTGTGCTCGAAAAAACAAGTTAAAAATTAATG 339  
Qy 301 AAATGCTCACTGAGAGAAATCTGAAAATGCGAGGTAAAGACGCTGCGCTGTACCA 360  
Db 340 AAATCTATCACTGGGAAAAAATCGAGAACGCAAAATCAGAAAGTGGAACTAGTACC 399  
Qy 361 AAAGATTTTCCCAAAAGATGTGTTTAGCGCTTAACTGATCATGTTAATGATTTTACA 420  
Db 400 AAAGATTTTCCCAAAAGATGTGTTTAGCGCTTAACTGATCATGTTAATGATTTTACA 459  
Qy 421 TGGTCAAAAAGCGAAAGAAAGCTGGCATTAATAACCTGAACATCAATGTGTCTT 480  
Db 460 TGGTCAAAAAGCTGAAAAAAGCTTAGGTAAAGCTGTAAATTAAGAAATTCGCTT 519  
Qy 481 TCTATTATGCTTACAACATTCGATCGACCGCAATTTTATCGATTACATTTAGCTGTTA 540  
Db 520 TCTATTATTTATTCCTACATTTAATGTCGATCGATTTTATGATATAACGTTAGCTGTTG 579  
Qy 541 GTAAACCAAAAAACATTAACCGCTTTGAAGTTATCGTAGCATGATGTGTGTACGAA 600  
Db 580 GTCAATCAGAAAAACAACTACCAATTTGAAGTCGTTGTGCAGATGATGTGTGTAGGAA 639  
Qy 601 GATCTATCCGATCATTTGCGCAATTAAGAAATTAATGGATATTGCTAGCTCAGACA 660  
Db 640 AACTTACCTTACATGTGTGCAAAAAATGCAACAAAACCTTGACATAAGTATTAAGACA 699  
Qy 661 AAAGATTAACGTTTTCAGACCGACGCTCGGAATATGGAATTAACGTTACCAAAATAT 720  
Db 700 AAAGATTAATGATATCAATTTGTGTGATGCAAGAACTTAGGTTTAGTACACAAAGAT 759  
Qy 721 GACTTATTTGCGTAACTCGATGTGATATGCGGCAATTCATTTAGGTTCAATCTTAT 780  
Db 760 GATTTGTCTCGATTTAGATGCGATATGCGACCAACAATTTAGGTTCAATCTTAT 819  
Qy 781 GTTGCAGACTATTAAGATGATGATTAACAATGATGTCCAAAGAAATATACATCAT 840  
Db 820 CTTACGAACTATTAAGACATGATTTGTTTAAATGACATTAAGAAATATGATGAT 879  
Qy 841 ACACACATATTGACCCCAAAAGCTCTTAAATTAACGCGATTTGCTTGATCATTTACA 900  
Db 880 ACTCATATATTAACGAGAACATTCCTTAAGCATCCATTTTATATAGATCACTACCT 939  
Qy 901 GAAAGTAAAAACAATATATAGTGTGCGCAAAAGGGAAAGAACATTTCTCTGATG 960  
Db 940 GAAACGCTACAAATTAACAATCCTTGATTAACATAAAGAAATATATGTTGATG 999  
Qy 961 CGCTTGAACATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCTTCCGTTT 1020  
Db 1000 AGATTATGAACATTTCAAAAAAACAAGTAATCTAGCTATGATTTCTCCGTTCTGAT 1059  
Qy 1021 TTTGCGGCGGATATGTTGCTTCCGTTAAAAAATGCTAAATATCCGTTTCTTTGAT 1080  
Db 1060 TTTGTTGCGGATATGTTGCTTCTTAAAGAAATGCTAAATATATAGTTGTTGAT 1119  
Qy 1081 GAGGAATTAATCACTGGGTGAGAGATGTGAAATTTGATATGCTTATTCGTTAC 1140  
Db 1120 GAAAGATTTTATCATTTGGGGGGGGAAGATGTAGAAATTTGTTACAGATTAATTTGCCAA 1179  
Qy 1141 GGTAGTTTCTTAAACATATGATGCGATTAATGCTTACATCAAGAGCAACAGGTAA 1200  
Db 1180 GCGTGTTTTTCAGAGTAAATGACGCGAGATGCGCATCCATCAAAACCACTGTGTAA 1239  
Qy 1201 GAAAAAGAAACGATGTGAGGCGGAAAAAATATTAACGCTGATTTATGAGAGAAAG 1260

Db 1240 GAAATGAAACAGAACCGGAAGCTGTGTAAGATTTACGCTTAAATTTGAAAAAG 1299  
Qy 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAATTCGATATCAATAGATCCT 1320  
Db 1300 GTACCTTATCATATAGAAAGCTTTTACCAATAGAAATTCGATATCAATAGATCCT 1359  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATATCTGTGCAAACTATTTCAACGTTGCTAGAT 1380  
Db 1360 TTAGTTTCAATTTATATCCCGCTTATATCTGTGCAAACTATTTCAACGTTGCTAGAT 1419  
Qy 1381 AGTGCATGATTCAGCTGTTGATCTCGAGGTTTGTATTTGTAACGATGTTCAACA 1440  
Db 1420 AGTGCATTAATCAAACTGTTGATCTCGAGGTTTGTATTTGTAACGATGTTCAACA 1479  
Qy 1441 GATAATACCTTAGAAGTATCAATAGCTTTATGATTAATCTTAGGTAACGATCAG 1500  
Db 1480 GATAATACCTTAGAAGTATCAATAGCTTTATGATTAATCTTAGGTAACGATCAG 1539  
Qy 1501 TCTAAACCAATGGCGGAATAGCTCAGCATCAAAATGACGCGTTTCTTTGCTTAAAGT 1560  
Db 1540 TCTAAACCAATGGCGGAATAGCTCAGCATCAAAATGACGCGTTTCTTTGCTTAAAGT 1599  
Qy 1561 TATTAATTTGGCGATTAATTCAGATGATTAATCTTAGGCTGATGAGTTGAACTGAT 1620  
Db 1600 TATTAATTTGGCGATTAATTCAGATGATTAATCTTAGGCTGATGAGTTGAACTGAT 1659  
Qy 1621 TTAATAAGATTTTAAAGATTAACGCTAGCTTGTGTTTATACCACTAATAGAACGTC 1680  
Db 1660 TTAATAAGATTTTAAAGATTAACGCTAGCTTGTGTTTATACCACTAATAGAACGTC 1719  
Qy 1681 AATCGGATGCTAGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCT 1740  
Db 1720 AATCGGATGCTAGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCT 1779  
Qy 1741 CTCACAGCGCTATGATGCTCACCATTTGGAATGTTCAAGATTAGAGCTTGGATTTA 1800  
Db 1780 CTCACAGCGCTATGATGCTCACCATTTGGAATGTTGATGATGATGATGATGATGAT 1839  
Qy 1801 ACTGATGATTCATGAAAAAATGAAAAATCCGATGATGATGATGATGATGATGATGAT 1860  
Db 1840 ACGATGATTTTAAGAAAAATTTGAAAAACCGGATGATGATGATGATGATGATGATGAT 1899  
Qy 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATATAAATCTGCTATTAACCGTATTAATGAT 1920  
Db 1900 AGTGAAGTTGAAAAATTTAAACATCTTAATATAAATCTGCTATTAACCGGATTAATGAT 1959  
Qy 1921 GATTAACATCAATTAAGAAATCTGCAATTTGGAATGTTGATGATGATGATGATGAT 1980  
Db 1960 GATTAACATCAATTAAGAAATCTGCAATTTGGAATGTTGATGATGATGATGATGAT 2019  
Qy 1981 CAGTATTAATTAAGCAAGGCTAATCTTAATTAATTAATTAATTAATTAATTAATTAAT 2040  
Db 2020 CAGTATTAATTAAGCAAGGCTAATCTTAATTAATTAATTAATTAATTAATTAATTAAT 2079  
Qy 2041 GAAAGTAAAGTATTTTCAATTAACCGCTGAATATCAAGAGATGATGATGAT 2100  
Db 2080 GAAAGTAAAGTATTTTCAATTAACCGCTGAATATCAAGAGATGATGATGAT 2139  
Qy 2101 AAAGATTAATTAATCAATCAATTAAGTGAATGCAAAATGCAATGATGATGAT 2160  
Db 2140 AAAGATTAATTAATCAATCAATTAAGTGAATGCAAAATGCAATGATGATGAT 2199  
Qy 2161 AATACATTAAGGCTTATGTAAGAAAGCTTAACCAATTAATTAATTAATTAATTAAT 2220  
Db 2200 AATACATTAAGGCTTATGTAAGAAAGCTTAACCAATTAATTAATTAATTAATTAAT 2259  
Qy 2221 TTGCTTATGTTCTATCATGTTGATTAAGATCATCTTACACGATATCAAAAGAAATA 2280  
Db 2260 TTGCTTATGTTCTATCATGTTGATTAAGATCATCTTACACGATATCAAAAGAAATA 2319  
Qy 2281 CTAGCCTTCTATCATTAACATCAAGTGAATATTTTACTAATTAATGATATCTCATTTAC 2340  
Db 2320 TTGCTTCTATCATTAAGCAAGTGAATATTTTACTAATTAATGATATCTCATTTAC 2379

```
Db 1219 GAAATGAAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGACGAGAAAG 1278
Qy 1261 GTCCCTTATCTATAGAAACCTTTTACCAATAGACATTCGCATATCAATAGAGTACCT 1320
Db 1279 GTCCCTTATCTATAGAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1338
Qy 1321 TTAGTTTCAATTTATATCCAGCTTTATAACCTGTGCAAACTATATTCAACGTTGCGTAGAT 1380
Db 1339 TTAGTTTCAATTTATATCCAGCTTTATAACCTGTGCAAACTATATTCAACGTTGCGTAGAT 1398
Qy 1381 AGTCACATGAATCAGACTGTTGTTGATCTCGAGTTTGTATTTGTATACGATGTTTCAACA 1440
Db 1399 AGTCACATGAATCAGACTGTTGTTGATCTCGAGTTTGTATTTGTATACGATGTTTCAACA 1458
Qy 1441 GATAATACCTTTAGAGTGATCAATAAGCTTTATCGTAAATATCTAGGGTACGCATCATG 1500
Db 1459 GATAATACCTTTAGAGTGATCAATAAGCTTTATCGTAAATATCTAGGGTACGCATCATG 1518
Qy 1501 TCTAAACCAATGCGGAATAGCCTCAGCATCAATGACGCGTTTCTTTTGTCTAAAGGT 1560
Db 1519 TCTAAACCAATGCGGAATAGCCTCAGCATCAATGACGCGTTTCTTTTGTCTAAAGGT 1578
Qy 1561 TATTACATTTGGCGAGTTAGATTGATGATGATTTATCTTGAGCGCTGATGAGTTGAACCTGTG 1620
Db 1579 TATTACATTTGGCGAGTTAGATTGATGATGATTTATCTTGAGCGCTGATGAGTTGAACCTGTG 1638
Qy 1621 TTTAAAGAAATTTTAAAGATATAAAGCTAGCTTGTGTTTATACCACTTAATAGAAACGTC 1680
Db 1639 TTTAAAGAAATTTTAAAGATATAAAGCTAGCTTGTGTTTATACCACTTAATAGAAACGTC 1698
Qy 1681 AATCCGATGTTAGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATG 1740
Db 1699 AATCCGATGTTAGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATG 1758
Qy 1741 CTCAACACGGCTATGATGCTCACCACTTTAGAAATGTTACGATGATGATGATGATGATGATG 1800
Db 1759 CTCAACACGGCTATGATGCTCACCACTTTAGAAATGTTACGATGATGATGATGATGATGATG 1818
Qy 1801 ACTGATGATTTCAATGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTT 1860
Db 1819 ACTGATGATTTCAATGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTT 1878
Qy 1861 AGTGAAGTTGGAAATTTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1920
Db 1879 AGTGAAGTTGGAAATTTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1938
Qy 1921 GATAACACATCAATTAAGAAACCTTGGCATCAAAAGAAACCAATTTTGTGTTAGTCAAT 1980
Db 1939 GATAACACATCAATTAAGAAACCTTGGCATCAAAAGAAACCAATTTTGTGTTAGTCAAT 1998
Qy 1981 CAGTCATTAATAGACAGGATCACTTTATTAATTTATGACGAAATTTGATGATTTAGAT 2040
Db 1999 CAGTCATTTAATAGACAGGATCACTTTATTAATTTATGACGAAATTTGATGATTTAGAT 2058
Qy 2041 GAAAGTGAAGATGATATTTTCAATAAACCCTGATATCAAGAAAGAGATTTGATCTTA 2100
Db 2059 GAAAGTGAAGATGATATTTTCAATAAACCCTGATATCAAGAAAGAGATTTGATCTTA 2118
Qy 2101 AAAGATATTAATAATCAATCCAGAAATTAAGATGCGCAAAATCGCAGTCAGTATTTTATCCC 2160
Db 2119 AAAGATATTAATAATCAATCCAGAAATTAAGATGCGCAAAATCGCAGTCAGTATTTTATCCC 2178
Qy 2161 AATACATTAACGGCTTAGTGAAATTAACCAATATTTATGAAATTAATTAATAAATA 2220
Db 2179 AATACATTAACGGCTTAGTGAAATTAACCAATATTTATGAAATTAATTAATAAATA 2238
Qy 2221 TTCGTTATGTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAGAAATA 2280
Db 2239 TTCGTTATGTTCTACATGTTGATAAGAAATCATCTTACACAGATATCAAAAGAAATA 2298
Qy 2281 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTTAAATATGATATCTCATATTAC 2340
Db 2299 CTAGCCTTCTATCAATAACATCAAGTGAATATTTTACTTAAATATGATATCTCATATTAC 2358
```

```
Qy 2341 ACCAGTAATAGATTAAATAAATACTGAGGCGCATTTAAGTAATATTAAATAATTAAGTCAG 2400
Db 2359 ACCAGTAATAGATTAAATAAATACTGAGGCGCATTTAAGTAATATTAAATAATTAAGTCAG 2418
Qy 2401 TTTAAATCTAAATTTGTAATACATCATTTTGTGATTAATCATGACAGCCTATTTCGTTAAAT 2460
Db 2419 TTTAAATCTAAATTTGTAATACATCATTTTGTGATTAATCATGACAGCCTATTTCGTTAAAT 2478
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGGGATGAATTTCTCAGCATTAACACAT 2520
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGGGATGAATTTCTCAGCATTAACACAT 2538
Qy 2521 GATTGATCCAGAAAAATCAATGCGCATCCACCACTTTAAAAAGCTCATTTAAAACTTATTTT 2580
Db 2539 GATTGATCCAGAAAAATCAATGCGCATCCACCACTTTAAAAAGCTCATTTAAAACTTATTTT 2598
Qy 2581 AATGACAAATGATTAATAAAGATGATGAAAAAGGGGCATCAAGGATGTTTATGACG 2640
Db 2599 AATGACAAATGATTAATAAAGATGATGAAAAAGGGGCATCAAGGATGTTTATGACG 2658
Qy 2641 TATGCCCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCAATCATCTTGCAGTCA 2700
Db 2659 TATGCCCTAGCGCATGAGCTTCTGACGATTTATTAAGAAGTCAATCATCTTGCAGTCA 2718
Qy 2701 ATTGATAGTGTGCGCAGATATAACACTGAGGATTTTGGTTCCAAATTTGCACITTTAATC 2760
Db 2719 ATTGATAGTGTGCGCAGATATAACACTGAGGATTTTGGTTCCAAATTTGCACITTTAATC 2778
Qy 2761 TTAGAAAAAGAAAAACCGCCCATGTTTATTAATAAACAATCGACCTGACTTATATGCTTGG 2820
Db 2779 TTAGAAAAAGAAAAACCGCCCATGTTTATTAATAAACAATCGACCTGACTTATATGCTTGG 2838
Qy 2821 GAACGAAATTTACAAATGCGCAATGAACAAATTTGAAAGTGCAGAAAGAGAGAGAAATATA 2880
Db 2839 GAACGAAATTTACAAATGCGCAATGAACAAATTTGAAAGTGCAGAAAGAGAGAGAAATATA 2898
Qy 2881 CCTGTTAAACAAGTTCTATTATTAATAGTATAACTCTATAA 2919
Db 2899 CCTGTTAAACAAGTTCTATTATTAATAGTATAACTCTATAA 2937
```

## RESULT 3

```
US-09-437-277-4
; Sequence 4: Application US/09437277
; Patent No. 644447
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCE: 5820.551
; CURRENT APPLICATION NUMBER: US/09/437,277
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 4
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; US-09-437-277-4
```

```
Query Match 77.8%; Score 2271.2; DB 3; Length 2979;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;

Qy 1 ATGAATACATTTATCAGCAATTAAGCAATATAAAGCAATATAACGCAATGACTATCAATTAGCACTC 60
Db 61 ATGAATACATTTATCAGCAATTAAGCAATATAAAGCAATATAAAGCAATGACTATGAATTAGCACTC 120
Qy 61 AAATTTTGAAGTCCGCGGAAATCTATGGACGGAATTTGTTGAATTTTCAAAATACC 120
Db 121 AAATTTTGAAGTCTGCTGAACCTACGGCGGAAATTCGTTGAATTTTCAAAATATC 180
Qy 121 AAATGCAAGAAAAAATCTCTCAGCAGCATCTCTCTGTTAAATTCAGCAGCATCTTCTCTGTAAT 180
```



QY 301 AATTTGCTCACTGAGAGAAATCTGAAAATCGGAGGTAAAGAGCGGTGCGCTTGTACCA 360  
Db 319 AATTTGCTCACTGAGAGAAATCTGAAAATCGGAGGTAAAGAGCGGTGCGCTTGTACCA 378  
QY 361 AAAGATTTCCTCAAGAGATCTGGTTTAAAGCGCTTTTACCTGATCAATGTTAAATGATTTTACA 420  
Db 379 AAAGATTTCCTCAAGATCTGGTTTAAAGCGCTTTTACCTGATCAATGTTAAATGATTTTACA 438  
QY 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAACATCAACATGTTGGTCTT 480  
Db 439 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTGAACATCAACATGTTGGTCTT 498  
QY 481 TCTATTATCGTTTACCAATCAATCGACCGCAATTTTATCGATTACATTAGCGCTGTTTAA 540  
Db 499 TCTATTATCGTTTACCAATCAATCGACCGCAATTTTATCGATTACATTAGCGCTGTTTAA 558  
QY 541 GTAAACCAAAAACACACATTTACCGCTTTGAAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db 559 GTAAACCAAAAACACATTTACCGCTTTGAAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618  
QY 601 GATCTATCACCGATCATTCGCAATATGAAATATAAATTTGATATTCGCTAGCTCAGACAA 660  
Db 619 GATCTATCACCGATCATTCGCAATATGAAATATAAATTTGATATTCGCTAGCTCAGACAA 678  
QY 661 AAAGATAACGGTTTTCAGCCAGTCCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT 720  
Db 679 AAAGATAACGGTTTTCAGCCAGTCCGCTCGGAATATGGGATTAACGCTTAGCAAAATAT 738  
QY 721 GACTTTATTTGGCTTACTCGATGATGATGCGGCAAAATCCATTTATGGGTTTCACTTTAT 780  
Db 739 GACTTTATTTGGCTTACTCGATGATGATGCGGCAAAATCCATTTATGGGTTTCACTTTAT 798  
QY 781 GTTCGAGAGCTATTAGAGATGATGATTTAAATCAATCATTTGTCAGAGAAATACATCGAT 840  
Db 799 GTTCGAGAGCTATTAGAGATGATGATTTAAATCAATCATTTGTCAGAGAAATACATCGAT 858  
QY 841 ACACAACATATTGACCCAAAAGACTTCTTAATTAACCGAGTTTGTCTGAATCATTTACCA 900  
Db 859 ACACAACATATTGACCCAAAAGACTTCTTAATTAACCGAGTTTGTCTGAATCATTTACCA 918  
QY 901 GAAGTGAACCAATTAATAGTGTGTCGCAAAAGGGAGGAACAGTTTCTCTGGATTGG 960  
Db 919 GAAGTGAACCAATTAATAGTGTGTCGCAAAAGGGAGGAACAGTTTCTCTGGATTGG 978  
QY 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTT 1020  
Db 979 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTT 1038  
QY 1021 TTTGCGGGGTAAATGTTGCTTTTCGCTAAAAATGGCTTAAATAATCCGGTTTCTTTGAT 1080  
Db 1039 TTTGCGGGGTAAATGTTGCTTTTCGCTAAAAATGGCTTAAATAATCCGGTTTCTTTGAT 1098  
QY 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC 1140  
Db 1099 GAGGAATTTAATCACTGGGGTGGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTAC 1158  
QY 1141 GGTAGTTTCTTTAAAACTATTGATGGCAATTTATGGCTTACCAATCAAGAGCCACAGGTAAA 1200  
Db 1159 GGTAGTTTCTTTAAAACTATTGATGGCAATTTATGGCTTACCAATCAAGAGCCACAGGTAAA 1218  
QY 1201 GAAATGAACCGATCGTGAAGCGGAAAAATATTAGCTTCGATTTATTCAGAGAGAAAG 1260  
Db 1219 GAAATGAACCGATCGTGAAGCGGAAAAATATTAGCTTCGATTTATTCAGAGAGAAAG 1278  
QY 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCTATCAATAGAGTACCT 1320  
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCTATCAATAGAGTACCT 1338  
QY 1321 TTAGTTTCAATTTTATATCCAGCTTATTAATCTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
Db 1339 TTAGTTTCAATTTTATATCCAGCTTATTAATCTGTGCAAACTATATTCAACGTTGCGTAGAT 1398

QY 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAACGATGGTTCAACA 1440  
Db 1399 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAACGATGGTTCAACA 1458  
QY 1441 GATAATACCTTTAGAAGTGAATCAATAGCTTTTATGGTAATAATCTTAGGGTACGCAATCATG 1500  
Db 1459 GATAATACCTTTAGAAGTGAATCAATAGCTTTTATGGTAATAATCTTAGGGTACGCAATCATG 1518  
QY 1501 TCTAAACCAAAATCGGCAATAGCTCAGCATCAATTCAGAGCGGTTTCTTTTGTCTAAAGGT 1560  
Db 1519 TCTAAACCAAAATCGGCAATAGCTCAGCATCAATTCAGAGCGGTTTCTTTTGTCTAAAGGT 1578  
QY 1561 TATTACATTTGGCGAGTTAGATTAGATTGATTCTTTAGAGCTGATGAGCTTGAACCTGTGT 1620  
Db 1579 TATTACATTTGGCGAGTTAGATTAGATTGATTCTTTAGAGCTGATGAGCTTGAACCTGTGT 1638  
QY 1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
Db 1639 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1698  
QY 1681 AATCCGATGCTAGCTTAATCGCTTAATGGTTTACAATTTGGCCAGAAATTTTTCACGAGAAAA 1740  
Db 1699 AATCCGATGCTAGCTTAATCGCTTAATGGTTTACAATTTGGCCAGAAATTTTTCACGAGAAAA 1758  
QY 1741 CTCAACACGCTATGATGCTCAACCTTTTGAATGTTTACGATTAGAGCTTGGCATTTA 1800  
Db 1759 CTCAACACGCTATGATGCTCAACCTTTTGAATGTTTACGATTAGAGCTTGGCATTTA 1818  
QY 1801 ACTGATGATTCAATGAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1819 ACTGATGATTCAATGAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1878  
QY 1861 AGTGAAAGTTGGAATAATTTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1920  
Db 1879 AGTGAAAGTTGGAATAATTTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1938  
QY 1921 GATAACAACATTAAGAAACCTTGGCAATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Db 1939 GATAACAACATTAAGAAACCTTGGCAATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1998  
QY 1981 CAGTCATTAATAGACAAGGCATTAATTTATTAATTTATGACGAAATTTTGTATTTAGAT 2040  
Db 1999 CAGTCATTAATAGACAAGGCATTAATTTATTAATTTATGACGAAATTTTGTATTTAGAT 2058  
QY 2041 GAAAGTGAAGATGATATTTTCAATTAATAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
Db 2059 GAAAGTGAAGATGATATTTTCAATTAATAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2118  
QY 2101 AAAGATATTAAATTCATCCAGAAATAAGATGCCAAAAATCGCAGTCAGTATTTTTTATCCC 2160  
Db 2119 AAAGATATTAAATTCATCCAGAAATAAGATGCCAAAAATCGCAGTCAGTATTTTTTATCCC 2178  
QY 2161 AATACATTAACCGCTTTAGTGAATAAACTAAACATATTATTGAAATATAATAAAATATA 2220  
Db 2179 AATACATTAACCGCTTTAGTGAATAAACTAAACATATTATTGAAATATAATAAAATATA 2238  
QY 2221 TTGGTTATTTCTTACATGTTGTAAGAATCTCTTACACAGATATCAAAAAAGAAATA 2280  
Db 2239 TTGGTTATTTCTTACATGTTGTAAGAATCTCTTACACAGATATCAAAAAAGAAATA 2298  
QY 2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358  
QY 2341 ACGAGTAAATAGATTAAATAAACTGAGCGGATTTTAAAGTAAATATTAAATTAAGTCAG 2400  
Db 2359 ACGAGTAAATAGATTAAATAAACTGAGCGGATTTTAAAGTAAATATTAAATAAATTAAGTCAG 2418  
QY 2401 TTTAAATCTAAATTTGTTGAATACATCATTTTGTGAATCAATGACAGCCTTATTCGTTAAAAAT 2460  
Db 2419 TTTAAATCTAAATTTGTTGAATACATCATTTTGTGAATCAATGACAGCCTTATTCGTTAAAAAT 2478  
QY 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTTCTCAGCATTTAACACAT 2520

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 05:35:37 ; Search time 527 Seconds  
(without alignment)

9849.108 Million cell updates/sec

Title: US-10-642-248-1

Perfect score: 2920

Sequence: 1 atgaatcattatcacagc.....taatagataactctataaa 2920

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/6H COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq:\*

7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*

8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*

9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2919	100.0	2937	3	US-09-469-200E-8
2	2917.4	99.9	2937	3	US-10-172-527A-9
3	2271.2	77.8	2979	3	US-09-437-277-4
4	2108.8	72.2	2112	3	US-09-437-277-2
5	82.4	2.8	32392	3	US-09-662-254B-27
6	80.6	2.8	984	3	US-09-107-532A-2527
7	80.6	2.8	6865	3	US-09-900-038A-3
8	77	2.6	993	3	US-09-134-000C-2987
9	75.8	2.6	615	3	US-08-998-416-186
10	74.4	2.5	1141	3	US-09-806-708B-22
11	72.6	2.5	2329	3	US-09-134-000C-2344
12	72.6	2.5	5340	3	US-09-627-122-21
13	72.4	2.5	5340	3	US-09-634-238-29
14	71.8	2.5	636	3	US-08-998-416-1137
15	71	2.4	50000	3	US-09-662-254B-23
16	70.6	2.4	837	3	US-08-998-416-288
17	70.6	2.4	14602	2	US-08-597-236-1
18	70.6	2.4	14602	2	US-08-746-682A-1
19	70.2	2.4	1002	3	US-09-107-532A-1469
20	70	2.4	891	3	US-09-816-028A-30
21	70	2.4	891	3	US-10-303-162-30
22	70	2.4	891	3	US-10-303-134-30
23	70	2.4	891	3	US-10-303-118-30
24	70	2.4	891	3	US-10-303-128-30

25	69.8	2.4	205044	3	US-09-949-016-15851	Sequence 15851, A
26	69.8	2.4	205044	3	US-09-949-016-15852	Sequence 15852, A
27	69.8	2.4	205044	3	US-09-949-016-15853	Sequence 15853, A
28	69.8	2.4	223471	3	US-09-949-016-12387	Sequence 12387, A
29	69.8	2.4	223471	3	US-09-949-016-12724	Sequence 12724, A
30	69.8	2.4	223471	3	US-09-949-016-12725	Sequence 12725, A
c 31	69.6	2.4	11474	3	US-09-495-406-1	Sequence 1, Appl
c 32	69.6	2.4	11474	3	US-09-816-028A-1	Sequence 1, Appl
c 33	69.6	2.4	11474	3	US-10-303-162-1	Sequence 1, Appl
c 34	69.6	2.4	11474	3	US-10-303-134-1	Sequence 1, Appl
c 35	69.6	2.4	11474	3	US-10-303-118-1	Sequence 1, Appl
c 36	69.6	2.4	11474	3	US-10-303-128-1	Sequence 1, Appl
c 37	68.8	2.4	1785	3	US-09-601-198-156	Sequence 156, App
38	68.4	2.3	906	3	US-09-495-406-14	Sequence 14, Appl
39	68.4	2.3	906	3	US-09-816-028A-26	Sequence 26, Appl
40	68.4	2.3	906	3	US-10-303-162-26	Sequence 26, Appl
41	68.4	2.3	906	3	US-10-303-134-26	Sequence 26, Appl
42	68.4	2.3	906	3	US-10-303-118-26	Sequence 26, Appl
43	68.4	2.3	906	3	US-10-303-128-26	Sequence 26, Appl
44	67.6	2.3	612	3	US-09-902-540-1357	Sequence 1357, Ap
45	67.4	2.3	1039	3	US-09-902-540-1280	Sequence 1280, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-469-200E-8  
; Sequence 8, Application US/09469200E  
; Patent No. 6833264  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kehama  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/09/469,200E  
; CURRENT FILING DATE: 1999-12-21  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pastuerella Multocida  
US-09-469-200E-8

Query Match	100.0%	Score	2919;	DB	3;	Length	2937;
Best Local Similarity	100.0%	Pred. No.	0;				
Matches	2919;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	ATGATACATATATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC	60				
DB	19	ATGAATACATATATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC	78				
QY	61	AAATTTATTTGAAAGTCGCGGAAATCTATGGACGAAATTTGTTGAATTTCAAAATACC	120				
DB	79	AAATTTATTTGAAAGTCGCGGAAATCTATGGACGAAATTTGTTGAATTTCAAAATACC	138				
QY	121	AAATGCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTAAT	180				
DB	139	AAATGCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAATTCAGCACATCTTTCTGTAAT	198				
QY	181	AAAGAGAAAAAGTCAATGTTTGCATAGTCGTTAGATATTGCAACACAACTGTTACTTT	240				
DB	199	AAAGAGAAAAAGTCAATGTTTGCATAGTCGTTAGATATTGCAACACAACTGTTACTTT	258				
QY	241	TCCACGTTAAAAAATTTAGTACTTTTCTGACTCGAAAAAACAACGTTAAAAAATAATGG	300				
DB	259	TCCACGTTAAAAAATTTAGTACTTTTCTGACTCGAAAAAACAACGTTAAAAAATAATGG	318				



Query Match 88.1%; Score 4502.5; DB 5; Length 965;  
Best Local Similarity 86.9%; Pred. No. 0;  
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

Search completed: January 6, 2006, 16:16:11  
Job time : 123 secs

```
Qy 1 MNTLSQAIKAYNSNDYOLATLKFESAEIYGRKIVEFOITRCKEKLAAHPSVNSAHLVSN 60
Db 1 MNTLSQAIKAYNSNDYOLATLKFESAEIYGRKIVEFOITRCKEKLAAHPSVNSAHLVSN 60
Qy 61 KEEKVNVCDSPDLIATQLLSNVKKLVLSDEKNTLKNKKVLTTEKSENAEVAVALVP 120
Db 54 EDKKNSVCDSSLDIATQLLSNVKKLVLSSEKNSLKNKKVSTGKSENAEIRKVELVP 113
Qy 121 KDFPKDLVLAFLPDHVNDFPTWYKRRKRLGKPEHGVGSLIYVTFPRPALISITLACL 180
Db 114 KDFPKDLVLAFLPDHVNDFPTWYKRRKRLGKPEHGVGSLIYVTFPRPALISITLACL 173
Qy 181 VNOKTHYFPEVITYDDSGOEDLSPIRQYENKLDIRVYRQKNGFOASAAHNGRLAKY 240
Db 174 VNOKTHYFPEVITYDDSGOEDLSPIRQYENKLDIRVYRQKNGFOASAAHNGRLAKY 233
Qy 241 DFIGLLDCDAPNPLWVSYVAELLEDDBLTIIGPRKYIDTOHIDPKDFLNNASLLESLP 300
Db 234 DFIGLLDCDAPNPLWVSYVAELLEDDBLTIIGPRKYIDTOHIDPKDFLNNASLLESLP 293
Qy 301 EVKTNNSVAAKGEQTSVLDHRLQEFKTEMLRLSDSPFPFAAGNVAFPAKMLNKGSPFD 360
Db 294 EVKTNNSVAAKGEQTSVLDHRLQEFKTEMLRLSDSPFPFAAGNVAFPAKMLNKGSPFD 353
Qy 361 BEFNHNGGEVEFGYRLEFRYSGSPFKTIDGIMAYHOEPPGKENETDREAGKNITLDIRREK 420
Db 354 BEFNHNGGEVEFGYRLEFRYSGSPFKTIDGIMAYHOEPPGKENETDREAGKNITLDIRREK 413
Qy 421 VPYIYRKLPIEDSHINRVLVSIYIPAVNCANYIQRCVDSALNQTVDVLEVCICNDGST 480
Db 414 VPYIYRKLPIEDSHINRVLVSIYIPAVNCANYIQRCVDSALNQTVDVLEVCICNDGST 473
Qy 481 DNTLEVINKLKYGNNPRYIRMSKPNGGIAASNAVSPAKGYTIGQLDSDYLEPDAVELC 540
Db 474 DNTLEVINKLKYGNNPRYIRMSKPNGGIAASNAVSPAKGYTIGQLDSDYLEPDAVELC 533
Qy 541 LKEFLDKDTLACYTTNRANVPDGSILANGYNWPEFSREKLTAMTAAHFRMFTIRAMHL 600
Db 534 LKEFLDKDTLACYTTNRANVPDGSILANGYNWPEFSREKLTAMTAAHFRMFTIRAMHL 593
Qy 601 TDGFNEKIENAVVDYDMEFLKLSVEGKFKHLNKICYNRVLHGDNSTSIKKLGIOKKNHFFVYN 660
Db 594 TDGFNEKIENAVVDYDMEFLKLSVEGKFKHLNKICYNRVLHGDNSTSIKKLGIOKKNHFFVYN 653
Qy 661 QSLNRQGITYYNDEPDLDSEKRYIFNKTAEYQOEIDILKDIKIIIONKDAKIAVSIFFP 720
Db 654 QSLNRQGITYYNDEPDLDSEKRYIFNKTAEYQOEIDILKDIKIIIONKDAKIAVSIFFP 713
Qy 721 NTLNGLVKKLNNIIEYVKNIFVIVLHVDKHLTPDIKKEILAFYHGVNIIILNNDISYY 780
Db 714 NTLNGLVKKLNNIIEYVKNIFVIVLHVDKHLTPDIKKEILAFYHGVNIIILNNDISYY 773
Qy 781 TSNRLIKTEBAHLSNINKLSQNLNCEYIIPDNHDSL FVKNDSYAYMKKYDVGNMFSALTH 840
Db 774 TSNRLIKTEBAHLSNINKLSQNLNCEYIIPDNHDSL FVKNDSYAYMKKYDVGNMFSALTH 833
Qy 841 DWTEKINAHPPFKLLIKTYFNDDLSKSNYKASQGMFTYALAHLELLTIKEVITSCQS 900
Db 834 DWTEKINAHPPFKLLIKTYFNDDLSKSNYKASQGMFTYALAHLELLTIKEVITSCQS 893
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGVFNKTSSTLTYPWERKLOMTNEOISAKKGENI 960
Db 894 IDSVPEYNTEDIWFQFALLILEKKTGVFNKTSSTLTYPWERKLOMTNEOISAKKGENI 953
Qy 961 PVNKFIIINSITL 972
Db 954 PVNKFIIINSITL 965
```

```
QY 841 DWIEKINAHPPFKLITKYFENDNDLKSNNVKGASQGMFTYALAHLLITIIKEVITSQOS 900
|||
DB 834 DWIEKINAHPPFKLITKYFENDNDLKSNNVKGASQGMFTYALAHLLITIIKEVITSQOS 893
QY 901 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWPKLQWNTBOQIESAKGENI 960
DB 894 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWPKLQWNTBOQIESAKGENI 953
QY 961 PUNKFIINSITL 972
DB 954 PUNKFIINSITL 965

RESULT 14
US-10-642-248-4
; Sequence 4, Application US/10642248
; Publication No. US20040132143A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; APPLICANT: Jing, Wei
; TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METHO
; FILE REFERENCE: 3554.097
; CURRENT APPLICATION NUMBER: US/10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 09/842,484
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 965
; TYPE: PR
; ORGANISM: Pasteurella multocida
US-10-642-248-4

Query Match 88.1%; Score 4502.5; DB 4; Length 965;
Best Local Similarity 86.9%; Pred. No. 0;
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;
```

```
QY 241 DFIGLDDCDMAPNPLMWSYVAEILBEDDDLTIGPRKYIDTOHIDPROFLNNALESLELP 300
|||
DB 234 DFIGLDDCDMAPNPLMWSYVAEILBEDDDLTIGPRKYIDTOHIDPROFLNNALESLELP 293
QY 301 EVKTNNSVAAKGEQTVSLDNRLEQFEKTENLRISDSFFRPPAAGNVAFAKKMLNKSQFED 360
DB 294 ETATNNNPSTSKSNISLDMRLBHFKKTDLRLCDSFFRYFSCGNAVAFSKMLNKNVGF 353
QY 361 EEFNHWGGEDEVEFGYRLFRYGSPEKTIIDGIMAYHOEPPGKENETDREGAKNITLDIMREK 420
DB 354 EEFNHWGGEDEVEFGYRLFRYGSPEKTIIDGIMAYHOEPPGKENETDREGAKNITLDIMREK 413
QY 421 VPIYRKLPIEDSHINRVPVLSIYIPAYNCANYTORCVDSALNQTVDVLEVCICNDGST 480
DB 414 VPIYRKLPIEDSHIRIPVLSIYIPAYNCANYTORCVDSALNQTVDVLEVCICNDGST 473
QY 481 DNTLEVINKLYGNPNRVRIRMSKPNGGIASASNAAVSPAKGYITQOLDSDDYLEPDAVELC 540
DB 474 DNTLEVINKLYGNPNRVRIRMSKPNGGIASASNAAVSPAKGYITQOLDSDDYLEPDAVELC 533
QY 541 LKEFLKOKTLACVYTTNRNVPDSSLTANGYNWPEPSREKLTMTAMIAHFMFTIRAWHL 600
DB 534 LKEFLKOKTLACVYTTNRNVPDSSLTANGYNWPEPSREKLTMTAMIAHFMFTIRAWHL 593
QY 601 TDGFNEKIEANAVDYDMFKLSEVGKFKHLNKICYNRVLHGDNSTIKKLGIQKQNFVVVN 660
DB 594 TDGFNEKIEANAVDYDMFKLSEVGKFKHLNKICYNRVLHGDNSTIKKLGIQKQNFVVVN 653
QY 661 QSLNRQGITYYNYNDEPDLDDESRYIIFNKIAEYOEEDILDKDIKIQKDAKIAVSTYRP 720
DB 654 QSLNRQGITYYNYNDEPDLDDESRYIIFNKIAEYOEEDILDKDIKIQKDAKIAVSTYRP 713
QY 721 NTNLGLVYKLANIIEYNNKIFVIYVLHVDKHLTDPIKKEILAFHKGQVNLILNNDISY 780
DB 714 NTNLGLVYKLANIIEYNNKIFVIYVLHVDKHLTDPIKKEILAFHKGQVNLILNNDISY 773
QY 781 TSNRLIKTEAHLNINIKLSQNLNCEYIIFPNHDSLFFVKNDSYAMKRYDYGMNFSALTH 840
DB 774 TSNRLIKTEAHLNINIKLSQNLNCEYIIFPNHDSLFFVKNDSYAMKRYDYGMNFSALTH 833
QY 841 DWIEKINAHPPFKLITKYFENDNDLKSNNVKGASQGMFTYALAHLLITIIKEVITSQOS 900
DB 834 DWIEKINAHPPFKLITKYFENDNDLKSNNVKGASQGMFTYALAHLLITIIKEVITSQOS 893
QY 901 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWPKLQWNTBOQIESAKGENI 960
DB 894 IDSVPEYNTEDIWFOFALLILEKKTGHVFNKSTLTLYMPWPKLQWNTBOQIESAKGENI 953
QY 961 PUNKFIINSITL 972
DB 954 PUNKFIINSITL 965

RESULT 15
US-10-197-153-3
; Sequence 3, Application US/10197153
; Publication No. US20050124046A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCE: 3554.080
; CURRENT APPLICATION NUMBER: US/10/197,153
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 965
; TYPE: PR
; ORGANISM: Pasteurella multocida
US-10-197-153-3
```

121 KDPKDLVLAPLDPHNDFTWYKRRKRLGKPEHGHVGLSIIIVTTFNRPAILSLTACL 180  
114 KDPKDLVLAPLDPHNDFTWYKRRKSLGKPVNKNIGLSIIPTFNRSRIIDITLACL 173  
181 VNOKTHYPEVIVTDGSOEDLSPIIROYENKLDIRYVQKONGFOQASABRNGLAKY 240  
174 VNOKTHYPEVIVTDGSOEDLSPIIROYENKLDIRYVQKONGFOQASABRNGLAKY 233  
241 DFIGLDDCMAPNPLVHSHVYVAELLEDLTIIGPRKYIDTOHIDPKDFLNASLESPL 300  
234 DFVSIILDDCMAPNPLVHSHVYVAELLEDLTIIGPRKYIDTOHIDPKDFLNASLESPL 293  
301 EVKTNNSVAAKGEGTVSLDWRLEQFTEKTNRLSDSPFRFAAGNVAFAKKNLNGSGFPD 360  
294 ETATNNPSITSGNISLDRLEHFKKTDNLRLCDSPPFRYFCGNAFSEKWLNVGWGFD 353  
361 EBFNHGGEDVEFGYRLFAKGCFFRVIDGGMAYHQBPCKENETDREAGNITLDMREK 420  
354 EBFNHGGEDVEFGYRLFAKGCFFRVIDGGMAYHQBPCKENETDREAGNITLDMREK 413  
421 VPIYIRKLLPIEDSHINRPLVSIYIPAYNCANYIQCVDSDALNQTVVLEVCICNDGST 480  
414 VPIYIRKLLPIEDSHINRPLVSIYIPAYNCANYIQCVDSDALNQTVVLEVCICNDGST 473  
481 DNTLEVINKLYGNPNRVRIMSKPNKGASIAASNAVSAFAGYIIGQLSDDDYLEPDAVELC 540  
474 DNTLEVINKLYGNPNRVRIMSKPNKGASIAASNAVSAFAGYIIGQLSDDDYLEPDAVELC 533  
541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYWPESREKLTTAMTAHFRMFTIRAWHL 600  
534 LKEFLKDKTLACVYTTNRNVPDGLSIANGYWPESREKLTTAMTAHFRMFTIRAWHL 593  
601 TDGFNEKIENAVDYDMFLKSLSEVGKFKHLNKI CYNRVLHGDNTSIKKLGIQKKNHFWVNV 660  
594 TDGFNEKIENAVDYDMFLKSLSEVGKFKHLNKI CYNRVLHGDNTSIKKLGIQKKNHFWVNV 653  
661 QSLNRQGITVYNYDEPDDLSERKTYFNKTAEQBEIDILKDIKIQNDKAKIAVSIFYP 720  
654 QSLNRQGITVYNYDEPDDLSERKTYFNKTAEQBEIDILKDIKIQNDKAKIAVSIFYP 713  
721 NTNLGLVKLNNIIEYNNKIFVILHVDKNHLPDIKKELTAFYKHQVNNILNNDISYY 780  
714 NTNLGLVKLNNIIEYNNKIFVILHVDKNHLPDIKKELTAFYKHQVNNILNNDISYY 773  
781 TSRLIKTEAHLNINKLSQLNLNCEYIIFDNHDSLFVNKDSYAYMKKYDVGNFSAETH 840  
774 TSRLIKTEAHLNINKLSQLNLNCEYIIFDNHDSLFVNKDSYAYMKKYDVGNFSAETH 833  
841 DWTEKINAHPPFKKLIKTYFNDNDLSMNVKGSQGMFMYALAHELLTIIKEVITSQCS 900  
834 DWTEKINAHPPFKKLIKTYFNDNDLSMNVKGSQGMFMYALAHELLTIIKEVITSQCS 893  
901 IDSVPENTEDINWFQALLILEKKTGHVFNKTSITLTYMPWERKQWNTNQSIAKGENI 960  
894 IDSVPENTEDINWFQALLILEKKTGHVFNKTSITLTYMPWERKQWNTNQSIAKGENI 953  
961 PVNKFIIINSITL 972  
954 PVNKFIIINSITL 965

RESULT 13  
US-10-217-613-8  
; Publication 8, Application US/10217613  
; Publication No. US20030113845A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL  
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND US  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 35541.081  
; CURRENT APPLICATION NUMBER: US/10/217, 613  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER 09/283,402

PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/080,414  
PRIOR FILING DATE: 1998-04-02  
PRIOR APPLICATION NUMBER: 09/178,851  
PRIOR FILING DATE: 1998-10-26  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 8  
LENGTH: 965  
TYPE: PRT  
ORGANISM: Paasteurella multocida  
US-10-217-613-8

Query Match 88.1%; Score 4502.5; DB 4; Length 965;  
Best Local Similarity 86.9%; Pred. No. 0;  
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

1 MNTLSQAIKAYNSNDYQALALKEKSAIYGRKIVFEFOITCKEKLKLSAHPNSAHLNVN 60  
1 MNTLSQAIKAYNSNDYQALALKEKSAIYGRKIVFEFOITCKEKLKLSAHPNSAHLNVN 53  
61 KEEKVNVCDSPDLIATQALLSNVKKLVLSDEKNTLNKWKLLTEKKSENAEVAVALVP 120  
54 EKKNSVCDSSLDIATQALLSNVKKLVLSDEKNTLNKWKLLTEKKSENAEVAVALVP 113  
121 KDFPKDLVLAPLDPHNDFTWYKRRKRLGKPEHGHVGLSIIIVTTFNRPAILSLTACL 180  
114 KDFPKDLVLAPLDPHNDFTWYKRRKSLGKPVNKNIGLSIIPTFNRSRIIDITLACL 173  
181 VNOKTHYPEVIVTDGSOEDLSPIIROYENKLDIRYVQKONGFOQASABRNGLAKY 240  
174 VNOKTHYPEVIVTDGSOEDLSPIIROYENKLDIRYVQKONGFOQASABRNGLAKY 233  
241 DFIGLDDCMAPNPLVHSHVYVAELLEDLTIIGPRKYIDTOHIDPKDFLNASLESPL 300  
234 DFVSIILDDCMAPNPLVHSHVYVAELLEDLTIIGPRKYIDTOHIDPKDFLNASLESPL 293  
301 EVKTNNSVAAKGEGTVSLDWRLEQFTEKTNRLSDSPFRFAAGNVAFAKKNLNGSGFPD 360  
294 ETATNNPSITSGNISLDRLEHFKKTDNLRLCDSPPFRYFCGNAFSEKWLNVGWGFD 353  
361 EBFNHGGEDVEFGYRLFAKGCFFRVIDGGMAYHQBPCKENETDREAGNITLDMREK 420  
354 EBFNHGGEDVEFGYRLFAKGCFFRVIDGGMAYHQBPCKENETDREAGNITLDMREK 413  
421 VPIYIRKLLPIEDSHINRPLVSIYIPAYNCANYIQCVDSDALNQTVVLEVCICNDGST 480  
414 VPIYIRKLLPIEDSHINRPLVSIYIPAYNCANYIQCVDSDALNQTVVLEVCICNDGST 473  
481 DNTLEVINKLYGNPNRVRIMSKPNKGASIAASNAVSAFAGYIIGQLSDDDYLEPDAVELC 540  
474 DNTLEVINKLYGNPNRVRIMSKPNKGASIAASNAVSAFAGYIIGQLSDDDYLEPDAVELC 533  
541 LKEFLKDKTLACVYTTNRNVPDGLSIANGYWPESREKLTTAMTAHFRMFTIRAWHL 600  
534 LKEFLKDKTLACVYTTNRNVPDGLSIANGYWPESREKLTTAMTAHFRMFTIRAWHL 593  
601 TDGFNEKIENAVDYDMFLKSLSEVGKFKHLNKI CYNRVLHGDNTSIKKLGIQKKNHFWVNV 660  
594 TDGFNEKIENAVDYDMFLKSLSEVGKFKHLNKI CYNRVLHGDNTSIKKLGIQKKNHFWVNV 653  
661 QSLNRQGITVYNYDEPDDLSERKTYFNKTAEQBEIDILKDIKIQNDKAKIAVSIFYP 720  
654 QSLNRQGITVYNYDEPDDLSERKTYFNKTAEQBEIDILKDIKIQNDKAKIAVSIFYP 713  
721 NTNLGLVKLNNIIEYNNKIFVILHVDKNHLPDIKKELTAFYKHQVNNILNNDISYY 780  
714 NTNLGLVKLNNIIEYNNKIFVILHVDKNHLPDIKKELTAFYKHQVNNILNNDISYY 773

Db 781 TSNRLIITEAHLNINKLSQNLNCEYIIIDNHDLSLFVNDSDYAYMKKYDVGMMFSALTH 840  
Qy 841 DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSQS 900  
Db 841 DWIEKINAHPPFKKLIITYFNDNDLRSNNVKGASQGMFTYALAHALLTIIKEVITSQS 900  
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNTKSTLTITMPWERKLOWTNEQIESAKRGNI 960  
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNTKSTLTITMPWERKLOWTNEQIXSARGNI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972  
RESULT 11  
US-09-842-484A-4  
; Sequence 4, Application US/09842484A  
; Publication No. US20030104601A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL L.  
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 4605.003  
; CURRENT APPLICATION NUMBER: US/09/842,484A  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 965  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-09-842-484A-4  
Query Match 88.1%; Score 4502.5; DB 3; Length 965;  
Best Local Similarity 86.9%; Pred. No. 0;  
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

Qy 1 MNTLSQAIKAYNSNDYQALALFKESAETIYGRKIVFQITCKEKL SAHPSVNSAHLNVN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFKESAETIYGRKIVFQITCKEKL SAHPSVNSAHLNVN 60  
Qy 61 KEEKVNVCDSPDIATQTLNLSNVKLLVLSDESKNTLKNWKLLTEKKSSENAEVRALVLP 120  
Db 54 EDKNSVCDSSLDIATQTLNLSNVKLLVLSDESKNTLKNWKLLTEKKSSENAEVRALVLP 113  
Qy 121 KDFPKDLVLPDPHNDFTWYKRRKRLGKIPKHOHVGSLSIITVFNRPAILSLITLACL 180  
Db 114 KDFPKDLVLPDPHNDFTWYKRRKRLGKIPKHOHVGSLSIITVFNRPAILSLITLACL 173  
Qy 181 VNQKTHYFEVITDDGQESDLSPIRQYENKLDIRYVRQKDNQFGQASARNMGLAKY 240  
Db 174 VNQKTHYFEVITDDGQESDLSPIRQYENKLDIRYVRQKDNQFGQASARNMGLAKY 233  
Qy 241 DFIGLDCDMPNPLVHVSVAELLEDLDTIIGRPKIDTQHDIDPKDPLNNALESILP 300  
Db 234 DFIGLDCDMPNPLVHVSVAELLEDLDTIIGRPKIDTQHDIDPKDPLNNALESILP 293  
Qy 301 EYKTNNSVAAKGEGTVSLDWRLEQFTEKNTENLSDSPFRFFAAGNVAFKWLNVKSGFFD 360  
Db 294 ETATNNFISITSGNISLDWRLEHFKKTDNLRLCSDPPFRYFCGNGVAFSEKWLNVKSGFFD 353  
Qy 361 EEFNHWGGEDEVFGYRLFRYGFYKTIIDGIMAYHQBPPGKENETDREAGKNTLIMREK 420  
Db 354 EEFNHWGGEDEVFGYRLFRYGFYKTIIDGIMAYHQBPPGKENETDREAGKNTLIMREK 413  
Qy 421 VPYIYRKLLPIEDSHNRVPLSVIYIPAYNCANYIQRQVDSALNOTVVDLEVCINDGST 480  
Db 414 VPYIYRKLLPIEDSHNRVPLSVIYIPAYNCANYIQRQVDSALNOTVVDLEVCINDGST 473  
Qy 481 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSAFAGYYIQLDSDDDYLEPDAVELC 540

Db 474 DNTLEVINKLYGNPRVIMSKPNGGIASASNAVSAFAGYYIQLDSDDDYLEPDAVELC 533  
Qy 541 LKPEFLKDKTTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTITAMIAHHPMFRTIRAWHL 600  
Db 534 LKPEFLKDKTTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTITAMIAHHPMFRTIRAWHL 593  
Qy 601 TDGFNEKIEVADYDMFLKLSVGVKFKHLANKI CYNRVLHGDNTSIKKGIGQKKNHFVVVN 660  
Db 594 TDGFNEKIEVADYDMFLKLSVGVKFKHLANKI CYNRVLHGDNTSIKKGIGQKKNHFVVVN 653  
Qy 661 QSLNRQGIITYNYDEDFDLDDESRYIFNKTAEQEEIDILDKIKI IQNKDAKIAVSIFYP 720  
Db 654 QSLNRQGIITYNYDYDKFDDLDDESRYIFNKTAEQEEMDILKDLKIQNKDAKIAVSIFYP 713  
Qy 721 NTNLGVKLNIIIEYNNKIFVIVLHVDKHLDPDIKEILAFYHKKHQNILLNNDISYY 780  
Db 714 NTNLGVKLNIIIEYNNKIFVIVLHVDKHLDPDIKEILAFYHKKHQNILLNNDISYY 773  
Qy 781 TSNRLIITEAHLNINKLSQNLNCEYIIIDNHDLSLFVNDSDYAYMKKYDVGMMFSALTH 840  
Db 774 TSNRLIITEAHLNINKLSQNLNCEYIIIDNHDLSLFVNDSDYAYMKKYDVGMMFSALTH 833  
Qy 841 DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSQS 900  
Db 834 DWIEKINAHPPFKKLIITYFNDNDLRSNNVKGASQGMFTYALAHELLTIIKEVITSQS 893  
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNTKSTLTITMPWERKLOWTNEQIESAKRGNI 960  
Db 894 IDSVPEYNTEDIWFQFALLILEKKTGHVFNTKSTLTITMPWERKLOWTNEQIQSAKRGNI 953  
Qy 961 PVNKFIIINSITL 972  
Db 954 PVNKFIIINSITL 965

## RESULT 12

US-10-217-613-3  
; Sequence 3, Application US/10217613  
; Publication No. US20030113845A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL  
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND US  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 35541.081  
; CURRENT APPLICATION NUMBER: US/10/217,613  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; LENGTH: 965  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-10-217-613-3

Query Match 88.1%; Score 4502.5; DB 4; Length 965;  
Best Local Similarity 86.9%; Pred. No. 0;  
Matches 845; Conservative 61; Mismatches 59; Indels 7; Gaps 2;

Qy 1 MNTLSQAIKAYNSNDYQALALFKESAETIYGRKIVFQITCKEKL SAHPSVNSAHLNVN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFKESAETIYGRKIVFQITCKEKL SAHPSVNSAHLNVN 53  
Qy 61 KEEKVNVCDSPDIATQTLNLSNVKLLVLSDESKNTLKNWKLLTEKKSSENAEVRALVLP 120  
Db 54 EDKNSVCDSSLDIATQTLNLSNVKLLVLSDESKNTLKNWKLLTEKKSSENAEVRALVLP 113

/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (90)..(90)  
/ OTHER INFORMATION: either Asn, Asp, Glu or Gln  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (113)..(113)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (158)..(158)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (164)..(164)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (192)..(192)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (201)..(201)  
/ OTHER INFORMATION: either Asn, Asp, Glu or Gln  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (206)..(206)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (211)..(211)  
/ OTHER INFORMATION: either Asn, Asp, Glu or Gln  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (225)..(225)  
/ OTHER INFORMATION: either Phe or Tyr  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (233)..(233)  
/ OTHER INFORMATION: either Met or Leu  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (243)..(243)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (253)..(253)  
/ OTHER INFORMATION: either Asn, Asp, Glu or Gln  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (279)..(279)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (288)..(288)  
/ OTHER INFORMATION: either Asn, Asp, Glu or Gln  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (292)..(292)  
/ OTHER INFORMATION: either Asn, Asp, Glu or Gln  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (316)..(316)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (329)..(329)  
/ OTHER INFORMATION: either Phe or Tyr  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (340)..(340)  
/ OTHER INFORMATION: either Phe or Tyr  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE

/ LOCATION: (405)..(405)  
/ OTHER INFORMATION: either Asn, Asp, Glu or Gln  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (439)..(439)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (744)..(744)  
/ OTHER INFORMATION: either Ile or Val  
/ FEATURE:  
/ NAME/KEY: MISC\_FEATURE  
/ LOCATION: (952)..(952)  
/ OTHER INFORMATION: either Asn, Asp, Glu or Gln  
/ US-10-217-613-9

Query Match 92.7%; Score 4733; DB 4; Length 972;  
Best Local Similarity 92.7%; Pred. NO. 0;  
Matches 901; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

Qy	1	MNTLSQAIKAYNSNDYQALALKLFPEKSAEYGRKI VEFQITKCKEKL SAHPSVNSAHL SVN	60
Db	1	MNTLSQAIKAYNCNDYXALALKLFPEKSAEYGRKI VEFQIIKCEKLSANPSVNEANL SVN	60
Qy	61	KXEKVNVCDSPLDIATQLLLSNVKLVLSDSSEKNTLKNKWKLLTEKKSENAEYRAVALVP	120
Db	61	EKEKNVVCDSPLDIATQLLISNVKLTLSKSEKNSLKNKWKLLTEKKSENAEYRAVALVP	120
Qy	121	KOPPKDLVLPDPHVNDFTWYKRRKGRIGIKPEHQHVGLSIIVTFNRPAILSLTACL	180
Db	121	KOPPKDLVLPDPHVNDFTWYKRRKGRIGIKPENQXGLSIIXPTFNRPAILDITLACL	180
Qy	181	VNQKTHYPEEVIITDDGSQEDLSPIROYENKLDIRYVRQKONGFOASAARNMGLRLAKY	240
Db	181	VNQKTHYPEVXVADDSQEXLLPIXRQYEXKLDIRYVRQKONGXQACARNRGLRLAKY	240
Qy	241	DFIGLLDCDMPNPLMVHSYVAELLEDLTTIGPRKYITDQHI DPKDFLNNASLESPL	300
Db	241	DFXGILDCDMPXQLMVHSYLAELLEDLTTIGPRKYDTQNI DAEXFLNXASLESPL	300
Qy	301	EYKTNNSVAAKGEVTSLDMRLEQEKTEENLRSLSDSPFPAAGNVAFKAKWLNKSGFFD	360
Db	301	ETATNNPAKGEKNXSLDMRLEQFEKTXNRLCDSPPFXFAAGNVAFKAKWLNKSGFFD	360
Qy	361	EEFNHWGGEDVFGYRLFRYGSFFFTIDGIMAYHQBPCKENETDREAGNITLDMREK	420
Db	361	EEFNHWGGEDVFGYRLFRKGCFFRTIDGMAYHQBPCKENETXREAGKNITLDMREK	420
Qy	421	VPIYVRKLLPIEDSHINRVPLSVIYIPAYNCANYIQRVDSALNQTVVLEVCICNDGST	480
Db	421	VPIYVRKLLPIEDSHINRPLSVIYIPAYNCANYIQRVDSALNQTVVLEVCICNDGST	480
Qy	481	DNTLEVINKLYGNPRVIRMSKPNGGIASANAUSFAKGYITGOLDSDDYLEPDAVELC	540
Db	481	DNTIEVINKLYGNPRVIRMSKPNGGIASANAUSFAKGYITGOLDSDDYLEPDAVELC	540
Qy	541	LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL	600
Db	541	LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL	600
Qy	601	TDFNEKIEAVDYDMFLKLSVGFKPKHLNKI CYNRVLHGDNTSIKKLGIQKQHFPVNV	660
Db	601	TDFNENIENAVDYDMFLKLSVGFKPKHLNKI CYNRVLHGDNTSIKKLGIQKQHFPVNV	660
Qy	661	QSLNRQGITVYNYDEPDDLDESRYIFNKTAEQBEIDILKDIKTONKDAKTAVSIFYP	720
Db	661	QSLNRQGINVYNYDEPDDLDESRYIFNKTAEQBEIDILKDIKTONKDAKTAVSIFYP	720
Qy	721	NTLGLVKKLNNII EYKNKIFVILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY	780
Db	721	NTLGLVKKLNNII EYKNKIFVILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY	780
Qy	781	TSNRLIKTEAHL SNINKLSQLNCEYIIFDNHDSL FVKND SYAYMKKYVDVGNMFSALTH	840

Db781TSNRLIKTEAHLNINKLSQNLNCEYIIIDFNHDSLFVNKDSYAYMKKYDVGMMFSAUTH840

Qy841DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCQS900

Db841DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCQS900

Qy901IDSVPYNTEDIWFOFALLILEKKTGHVFNKTSITLTYMPWERKLOWNEQIESAKRGENI960

Db901IDSVPYNTEDIWFOFALLILEKKTGHVFNKTSITLTYMPWERKLOWNEQIESAKRGENI960

Qy961PVNKFIIINSITL972

Db961PVNKFIIINSITL972

RESULT 9

US-11-096-190-9

; Sequence 9, Application US/11096190

; Publication No. US20050221446A1

; GENERAL INFORMATION:

; APPLICANT: Widner, William

; APPLICANT: Sloma, Alan

; APPLICANT: Thomas, Michael D.

; APPLICANT: Tang, Maria

; TITLE OF INVENTION: Methods For Producing A Hyaluronic Acid In A Bacillus Cell

; FILE REFERENCE: 10596.200-US

; CURRENT APPLICATION NUMBER: US/11/096,190

; CURRENT FILING DATE: 2005-03-31

; PRIOR APPLICATION NUMBER: 60/558,507

; PRIOR FILING DATE: 2004-03-31

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 9

; LENGTH: 972

; TYPE: PRT

; ORGANISM: Pasteurella multocida

US-11-096-190-9

Query Match99.9%; Score 5104; DB 6; Length 972;

Best Local Similarity99.9%; Pred. No. 0;

Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy1MNTLSQAIKAYNSNDYQLALKLFEKSABIIYGRKIYEFQITKCEKLSAHPNSVNSAHLN60

Db1MNTLSQAIKAYNSNDYQLALKLFEKSABIIYGRKIYEFQITKCEKLSAHPNSVNSAHLN60

Qy61KEEKVNVCDSPDIATQALLSNVKKLVLSDSSEKNTLKNKWKLLTEKKSENAEVRVALVP120

Db61KEEKVNVCDSPDIATQALLSNVKKLVLSDSSEKNTLKNKWKLLTEKKSENAEVRVALVP120

Qy121KDFPKDLVLAPLDHVNDFWTYKKRKRGLIPEHQHVGSLSIIVTTFNRPALISITLACL180

Db121KDFPKDLVLAPLDHVNDFWTYKKRKRGLIPEHQHVGSLSIIVTTFNRPALISITLACL180

Qy181VNQKTHYPFEVITVDGSGQEDLSPIIROYENKLDIRYVRQKDNFGQASARNMGLRLAKY240

Db181VNQKTHYPFEVITVDGSGQEDLSPIIROYENKLDIRYVRQKDNFGQASARNMGLRLAKY240

Qy241DFIGLLDCDMPANPLVWHSYVAELLEDLDTIIGRPKYIDTQHDIDPKDFLNNASLESIP300

Db241DFIGLLDCDMPANPLVWHSYVAELLEDLDTIIGRPKYIDTQHDIDPKDFLNNASLESIP300

Qy301EYKVTNNSVAAKGGTGVSLDWRLEQFEKTEKNTLSDSPRRFFAAGNVAFPAKKWLNKSGFFD360

Db301EYKVTNNSVAAKGGTGVSLDWRLEQFEKTEKNTLSDSPRRFFAAGNVAFPAKKWLNKSGFFD360

Qy361EEFNHWGGSDVBFYGLRFLRYGSFFKTIIDGIMAYHQBPPGKENETDREAGKNITLDMIREK420

Db361EEFNHWGGSDVBFYGLRFLRYGSFFKTIIDGIMAYHQBPPGKENETDREAGKNITLDMIREK420

Qy421VPYIYRKLLPIEDSHINRVLPSIYIPAYNCANYIORCVDSALNQTVDVLEVCINDGST480

Db421VPYIYRKLLPIEDSHINRVLPSIYIPAYNCANYIORCVDSALNQTVDVLEVCINDGST480

Qy481DNTLEVINKLYGNPRVRINSKONGGIASASNAVSPAKCVYIGQLSDDDYLBPDVAVELC540

Db481DNTLEVINKLYGNPRVRINSKONGGIASASNAVSPAKCVYIGQLSDDDYLBPDVAVELC540

Qy541LK6FLPKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTITAMIAHFRMFTIRAWHL600

Db541LK6FLPKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTITAMIAHFRMFTIRAWHL600

Qy601TDGFNEKIENAVYDMFLKLSSEVGFKHLNKCYNRVLHGDNTSIKKLGIOKQKHFFVVVN660

Db601TDGFNEKIENAVYDMFLKLSSEVGFKHLNKCYNRVLHGDNTSIKKLGIOKQKHFFVVVN660

Qy661QSLNRQGITTYNYDEPDLDSESKYIIFNKTAEQEEIDILKDKIIONKODAKIAVSIFYP720

Db661QSLNRQGITTYNYDEPDLDSESKYIIFNKTAEQEEIDILKDKIIONKODAKIAVSIFYP720

Qy721NTLNLGLVKLNIIIEYNKNIFVIVLHVDKNHLPDIKKEILAFYHKHQVNILLNNDISYY780

Db721NTLNLGLVKLNIIIEYNKNIFVIVLHVDKNHLPDIKKEILAFYHKHQVNILLNNDISYY780

Qy781TSNRLIKTEAHLNINKLSQNLNCEYIIIDFNHDSLFVNKDSYAYMKKYDVGMMFSAUTH840

Db781TSNRLIKTEAHLNINKLSQNLNCEYIIIDFNHDSLFVNKDSYAYMKKYDVGMMFSAUTH840

Qy841DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCQS900

Db841DWIEKINAHPPFKKLIITYFNDNDLKSNNVKGASQGMFTYALAHELLTIIKEVITSCQS900

Qy901IDSVPYNTEDIWFOFALLILEKKTGHVFNKTSITLTYMPWERKLOWNEQIESAKRGENI960

Db901IDSVPYNTEDIWFOFALLILEKKTGHVFNKTSITLTYMPWERKLOWNEQIESAKRGENI960

Qy961PVNKFIIINSITL972

Db961PVNKFIIINSITL972

RESULT 10

US-10-217-613-9

; Sequence 9, Application US/10217613

; Publication No. US20030113845A1

; GENERAL INFORMATION:

; APPLICANT: DEANGELIS, PAUL

; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND US

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 35541.081

; CURRENT APPLICATION NUMBER: US/10/217,613

; PRIOR FILING DATE: 2002-08-12

; PRIOR APPLICATION NUMBER: 09/283,402

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/080,414

; PRIOR FILING DATE: 1998-04-02

; PRIOR APPLICATION NUMBER: 09/178,851

; PRIOR FILING DATE: 1998-10-26

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 972

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: consensus sequence

; NAME/KEY: MISC FEATURE

; LOCATION: (17)-(17)

; OTHER INFORMATION: either Asn, Asp, Glu or Gln

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (62)-(62)

; OTHER INFORMATION: either Asn, Asp, Glu or Gln

; FEATURE:

US-10-217-613-9



```
Db 1 MNTLSQAIKAYNSNDYQALALKEKSAEYGRKIVFQITKCKEKLSAHPSVNSAHLVN 60
Qy 61 KEEKVNVCDSPLDIATQALLSNVKKLVLSDEKNTLNKWKLLTEKKSENAEYRAVALVP 120
Db 61 KEEKVNVCDSPLDIATQALLSNVKKLVLSDEKNTLNKWKLLTEKKSENAEYRAVALVP 120
Qy 121 KDFPKDLVLAPLDHVDFTWYKKRKRGLGKPEHQHVGLSIIVTTFNRPAILSLTACL 180
Db 121 KDFPKDLVLAPLDHVDFTWYKKRKRGLGKPEHQHVGLSIIVTTFNRPAILSLTACL 180
Qy 181 VNQKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVRQKONGFOASAARNMGLRLAKY 240
Db 181 VNQKTHYPEVIVTDDGSQEDLSPIIROYENKLDIRYVRQKONGFOASAARNMGLRLAKY 240
Qy 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTQHIDPKDFLNNASLLESPL 300
Db 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTQHIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGGTIVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFAKKWLNKSGFPD 360
Db 301 EVKTNNSVAAKGGTIVSLDWRLEQFEKTENLRSLSDSPFRFAAGNVAFAKKWLNKSGFPD 360
Qy 361 EEPNHWGGEDVEFGYRLFYRGSFFKTIIDGIMAYHQBPPEGKNETDREAGNITLDMREK 420
Db 361 EEPNHWGGEDVEFGYRLFYRGSFFKTIIDGIMAYHQBPPEGKNETDREAGNITLDMREK 420
Qy 421 VPIYIRKLLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Db 421 VPIYIRKLLPIEDSHINRVLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480
Qy 481 DNTLEVINKLYGNPRVIRMSKNGGIIASASNAVSAFAGYIIGOLDSDDYLPDPAVELC 540
Db 481 DNTLEVINKLYGNPRVIRMSKNGGIIASASNAVSAFAGYIIGOLDSDDYLPDPAVELC 540
Qy 541 LKEFLKDKTLCACVYTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLCACVYTNRNVPDGLSIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIEANVDYDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIOKQKHFFVNVN 660
Db 601 TDGFNEKIEANVDYDMFLKSEVGKPKHLNKICYNRVLHGDNTSIKKLGIOKQKHFFVNVN 660
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
```

RESULT 8

US-10-309-560-8

; Sequence 8, Application US/10309560

; Publication No. US20030235893A1

; GENERAL INFORMATION:

Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGHNFSALTH 840  
Qy 841 DWIEKINAHPPFKKLIKTYFNNDNLDKSMNVKGSQGMFTYALAHALLTIIKEVITSCQS 900  
Db 841 DWIEKINAHPPFKKLIKTYFNNDNLDKSMNVKGSQGMFTYALAHALLTIIKEVITSCQS 900  
Qy 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPWVERKLOWTNEQIESAKRGENI 960  
Db 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPWVERKLOWTNEQIESAKRGENI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972  
RESULT 6  
US-10-172-527-10  
; Sequence 10, Application US/10172527  
; Publication No. US20030092118A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Kahama  
; APPLICANT: Deangelis, Paul  
; TITLE OF INVENTION: HYALURONAN SYNTHASE GENES AND EXPRESSION THEREOF IN BACILLUS SUBTILIS  
; FILE REFERENCE: 3554.048  
; CURRENT APPLICATION NUMBER: US/10/172.527  
; CURRENT FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: 60/297,788  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 60/297,744  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 09/469,200  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 10  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: pasteurella multocida  
US-10-172-527-10  
Query Match 99.9%; Score 5104; DB 4; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNTLSQAIKAYNSNDYQALALFESAKIYGRKIVEFOITKCKEKLSAHPSVNSAHLNVN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFESAKIYGRKIVEFOITKCKEKLSAHPSVNSAHLNVN 60  
Qy 61 KEEKNVNCDSPUDATQALLSNVKKLVLSDESKNTLKNKKLLTEKKSENAEVRAVALVP 120  
Db 61 KEEKNVNCDSPUDATQALLSNVKKLVLSDESKNTLKNKKLLTEKKSENAEVRAVALVP 120  
Qy 121 KDFPKDLVLAPLDHVNDFWTKYKRRKRLGKPEHQHVGSLSIIVTFNRPAILSTLACL 180  
Db 121 KDFPKDLVLAPLDHVNDFWTKYKRRKRLGKPEHQHVGSLSIIVTFNRPAILSTLACL 180  
Qy 181 VNQKTHYPFEVITVDGQEDLSPIIRQYENKLDIYVRQKNGFQASARNMGLRLAKY 240  
Db 181 VNQKTHYPFEVITVDGQEDLSPIIRQYENKLDIYVRQKNGFQASARNMGLRLAKY 240  
Qy 241 DFIGLLDCDMANPLWVHSYVAELLEDLDTIIGPRKVIDTOHIDPKDFLNNASLESIP 300  
Db 241 DFIGLLDCDMANPLWVHSYVAELLEDLDTIIGPRKVIDTOHIDPKDFLNNASLESIP 300  
Qy 301 EVKTTNSVAAKGEVTSLDWRLEQFEKTENLRLSDSPFRFFAAGNVAFPAKWLKNSGFPD 360  
Db 301 EVKTTNSVAAKGEVTSLDWRLEQFEKTENLRLSDSPFRFFAAGNVAFPAKWLKNSGFPD 360  
Qy 361 EEFNHWGGEDVDFGRLFRYGSFFKTIIDGIMAYHQBPCKENETDREAGKNTILIMREK 420

Db 361 EEFNHWGGEDVDFGRLFRYGSFFKTIIDGIMAYHQBPCKENETDREAGKNTILIMREK 420  
Qy 421 VPIYIRKLLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480  
Db 421 VPIYIRKLLPIEDSHINRPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCICNDGST 480  
Qy 481 DNTLEVINLKLYGNPRVRJMSKPNKGGLASASNAVSAFAGKYIIGOLDSDDDYLEDPAVELC 540  
Db 481 DNTLEVINLKLYGNPRVRJMSKPNKGGLASASNAVSAFAGKYIIGOLDSDDDYLEDPAVELC 540  
Qy 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNNWPEPSREKLTTAMIAHFRMFTIRAWHL 600  
Db 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNNWPEPSREKLTTAMIAHFRMFTIRAWHL 600  
Qy 601 TDGFNEKIEANAVDYDMFLKLSYGVGKFKHLNKCYNRVLHGDNTSIKKLGIOKKNHFFVVVN 660  
Db 601 TDGFNEKIEANAVDYDMFLKLSYGVGKFKHLNKCYNRVLHGDNTSIKKLGIOKKNHFFVVVN 660  
Qy 661 QSLNRQGITYYNDEPDLDDESRYIFNKTAEOEEDIDILDKIIONKDAKIAVSIFYP 720  
Db 661 QSLNRQGITYYNDEPDLDDESRYIFNKTAEOEEDIDILDKIIONKDAKIAVSIFYP 720  
Qy 721 NTNLGLVKLNNIIEYNKNIIFVIVLHVDKNHLPDIKKEILAFYHGHQVNNILLNNDISYY 780  
Db 721 NTNLGLVKLNNIIEYNKNIIFVIVLHVDKNHLPDIKKEILAFYHGHQVNNILLNNDISYY 780  
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGHNFSALTH 840  
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGHNFSALTH 840  
Qy 841 DWIEKINAHPPFKKLIKTYFNNDNLDKSMNVKGSQGMFTYALAHALLTIIKEVITSCQS 900  
Db 841 DWIEKINAHPPFKKLIKTYFNNDNLDKSMNVKGSQGMFTYALAHALLTIIKEVITSCQS 900  
Qy 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPWVERKLOWTNEQIESAKRGENI 960  
Db 901 IDSVPEYNTEDIWQFALLILEKKTGHVFNKTSITLTYPWVERKLOWTNEQIESAKRGENI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972  
RESULT 7  
US-10-326-185-95  
; Sequence 95, Application US/10326185  
; Publication No. US20030175902A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloma, Alan  
; APPLICANT: Behr, Regine  
; APPLICANT: Widner, William  
; APPLICANT: Tang, Maria  
; APPLICANT: Sternberg, David  
; APPLICANT: Brown, Stephen  
; TITLE OF INVENTION: Methods for Producing Hyaluronan In a Recombinant Host Cell  
; FILE REFERENCE: 10241.200-US  
; CURRENT APPLICATION NUMBER: US/10/326.185  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/342,644  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 95  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-10-326-185-95  
Query Match 99.9%; Score 5104; DB 4; Length 972;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNTLSQAIKAYNSNDYQALALFESAKIYGRKIVEFOITKCKEKLSAHPSVNSAHLNVN 60

```
Db 61 KBEKVNVCDSPLDIATQALLSNVKKVLSDSEKNTLKNKWLKTEKKSNAEVRVALVP 120
Qy 121 KDPKDLVLAPLDPHNDFTWYKRRKRLGKPEHQHVGLSIIIVTFNRPAILSIITLACL 180
Db 121 KDPKDLVLAPLDPHNDFTWYKRRKRLGKPEHQHVGLSIIIVTFNRPAILSIITLACL 180
Qy 181 VNQKTHYPEVIVTDDGSQEDLSPIIRQYENKLDIRYVQKONGFQASARNMGLRLAKY 240
Db 181 VNQKTHYPEVIVTDDGSQEDLSPIIRQYENKLDIRYVQKONGFQASARNMGLRLAKY 240
Qy 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTOHIDPKDFLNASLESPL 300
Db 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTOHIDPKDFLNASLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFECTENLRSDSPFRFFAAGNVAFAKKNWLNKSGFFD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFECTENLRSDSPFRFFAAGNVAFAKKNWLNKSGFFD 360
Qy 361 EEFNHWGGEDVEFGYRLFYSGSFKTIIDGIMAYHQBPFGKENETDREAGKNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFYSGSFKTIIDGIMAYHQBPFGKENETDREAGKNITLDMREK 420
Qy 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQRVCVDSALNQTVDLVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQRVCVDSALNQTVDLVCICNDGST 480
Qy 481 DNTLEVINKLYGNPNRVRIMSKPENGSIASASNAVSFAKGYIIGOLDSDDDYLPDAVELC 540
Db 481 DNTLEVINKLYGNPNRVRIMSKPENGSIASASNAVSFAKGYIIGOLDSDDDYLPDAVELC 540
Qy 541 LKEFLKDKTLACVYTTNRNPNVPGSLIANGYNWPFESREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLACVYTTNRNPNVPGSLIANGYNWPFESREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIEANVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKQNFVAVN 660
Db 601 TDGFNEKIEANVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKQNFVAVN 660
Qy 661 QSLNRQGITVYNDDEFDLDESRYIFNKTAEQEIEIDILKDIIONKDAKIAVSIYFP 720
Db 661 QSLNRQGITVYNDDEFDLDESRYIFNKTAEQEIEIDILKDIIONKDAKIAVSIYFP 720
Qy 721 NTNLGLVKLLNIIIEYNKNI FVILVHVDKNHLTPDIKKEILAFYKHQVNIILNNDISYY 780
Db 721 NTNLGLVKLLNIIIEYNKNI FVILVHVDKNHLTPDIKKEILAFYKHQVNIILNNDISYY 780
Qy 781 TSRLIKTEAHLNINKLQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH 840
Db 781 TSRLIKTEAHLNINKLQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH 840
Qy 841 DWTKEKINAHPFPKLLIKTYFNDNDLKSMMVKGASQGMEMTYALAHELLTIIKEVITSCOS 900
Db 841 DWTKEKINAHPFPKLLIKTYFNDNDLKSMMVKGASQGMEMTYALAHELLTIIKEVITSCOS 900
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKGENI 960
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKSTLTLYMPWERKLOWTNEQIESAKGENI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
```

## RESULT 5

```
US-09-879-959-10
; Sequence 10, Application US/0987959
; Patent No. US20020160489A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kshama
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION
; TITLE OF INVENTION: IN BACILLUS SUBTILIS
```

```
; FILE REFERENCE: 3554.049
; CURRENT APPLICATION NUMBER: US/09/879,959
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 972
; TYPE: PRT
; ORGANISM: pasteurella multocida
US-09-879-959-10
```

```
Query Match 99.9%; Score 5104; DB 3; Length 972;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 971; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALALKLFESAEIYGRKIVEFOITKCKEKLSAHPSVNSAHLNVN 60
Db 1 MNTLSQAIKAYNSNDYQALALKLFESAEIYGRKIVEFOITKCKEKLSAHPSVNSAHLNVN 60
Qy 61 KBEKVNVCDSPLDIATQALLSNVKKVLSDSEKNTLKNKWLKTEKKSNAEVRVALVP 120
Db 61 KBEKVNVCDSPLDIATQALLSNVKKVLSDSEKNTLKNKWLKTEKKSNAEVRVALVP 120
Qy 121 KDPKDLVLAPLDPHNDFTWYKRRKRLGKPEHQHVGLSIIIVTFNRPAILSIITLACL 180
Db 121 KDPKDLVLAPLDPHNDFTWYKRRKRLGKPEHQHVGLSIIIVTFNRPAILSIITLACL 180
Qy 181 VNQKTHYPEVIVTDDGSQEDLSPIIRQYENKLDIRYVQKONGFQASARNMGLRLAKY 240
Db 181 VNQKTHYPEVIVTDDGSQEDLSPIIRQYENKLDIRYVQKONGFQASARNMGLRLAKY 240
Qy 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTOHIDPKDFLNASLESPL 300
Db 241 DFIGLLDCDMPNPLVHVSVAELLEDLTIIGPRKYIDTOHIDPKDFLNASLESPL 300
Qy 301 EVKTNNSVAAKGEGTVSLDWRLEQFECTENLRSDSPFRFFAAGNVAFAKKNWLNKSGFFD 360
Db 301 EVKTNNSVAAKGEGTVSLDWRLEQFECTENLRSDSPFRFFAAGNVAFAKKNWLNKSGFFD 360
Qy 361 EEFNHWGGEDVEFGYRLFYSGSFKTIIDGIMAYHQBPFGKENETDREAGKNITLDMREK 420
Db 361 EEFNHWGGEDVEFGYRLFYSGSFKTIIDGIMAYHQBPFGKENETDREAGKNITLDMREK 420
Qy 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQRVCVDSALNQTVDLVCICNDGST 480
Db 421 VPYIYRKLLPIEDSHINRVLVSIYIPAYNCANYIQRVCVDSALNQTVDLVCICNDGST 480
Qy 481 DNTLEVINKLYGNPNRVRIMSKPENGSIASASNAVSFAKGYIIGOLDSDDDYLPDAVELC 540
Db 481 DNTLEVINKLYGNPNRVRIMSKPENGSIASASNAVSFAKGYIIGOLDSDDDYLPDAVELC 540
Qy 541 LKEFLKDKTLACVYTTNRNPNVPGSLIANGYNWPFESREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLACVYTTNRNPNVPGSLIANGYNWPFESREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIEANVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKQNFVAVN 660
Db 601 TDGFNEKIEANVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKQNFVAVN 660
Qy 661 QSLNRQGITVYNDDEFDLDESRYIFNKTAEQEIEIDILKDIIONKDAKIAVSIYFP 720
Db 661 QSLNRQGITVYNDDEFDLDESRYIFNKTAEQEIEIDILKDIIONKDAKIAVSIYFP 720
Qy 721 NTNLGLVKLLNIIIEYNKNI FVILVHVDKNHLTPDIKKEILAFYKHQVNIILNNDISYY 780
Db 721 NTNLGLVKLLNIIIEYNKNI FVILVHVDKNHLTPDIKKEILAFYKHQVNIILNNDISYY 780
Qy 781 TSRLIKTEAHLNINKLQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH 840
Db 781 TSRLIKTEAHLNINKLQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH 840
```

; Sequence 2, Application US/10642248  
; Publication No. US20040132143A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Jing, Wei  
; TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METHO  
; FILE REFERENCE: 3554.097  
; CURRENT APPLICATION NUMBER: US/10/642,248  
; CURRENT FILING DATE: 2003-08-15  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR FILING DATE: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR FILING DATE: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR FILING DATE: 09/842,484  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR FILING DATE: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-10-642-248-2

Query Match 100.0%; Score 5108; DB 4; Length 972;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALALFKESABEYGRKIVEFOITCKEKLSAHPSVNSAHLVSN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFKESABEYGRKIVEFOITCKEKLSAHPSVNSAHLVSN 60

Qy 61 KEEKNVNCDSPLDIATQALLSNVKKVLVSDSEKNTLKNKWKLTTEKKSNAEVRVALVP 120  
Db 61 KEEKNVNCDSPLDIATQALLSNVKKVLVSDSEKNTLKNKWKLTTEKKSNAEVRVALVP 120

Qy 121 KDPKDLVLAPLDHVNDFWTKKRRKRLGIKPEHQHVGSLSIIVTFNRPALLSITLACL 180  
Db 121 KDPKDLVLAPLDHVNDFWTKKRRKRLGIKPEHQHVGSLSIIVTFNRPALLSITLACL 180

Qy 181 VNQKTHYFPEVITVDDGSOEDLSPIIROVENKLDIRYRQKNGFQSAARNMGLRLAKY 240  
Db 181 VNQKTHYFPEVITVDDGSOEDLSPIIROVENKLDIRYRQKNGFQSAARNMGLRLAKY 240

Qy 241 DFIGLLDCDMPNPLWHSYVAELLEDLTTIGPRKVIDTQHIIDPKPLNNASLESIP 300  
Db 241 DFIGLLDCDMPNPLWHSYVAELLEDLTTIGPRKVIDTQHIIDPKPLNNASLESIP 300

Qy 301 EVKTNNSVAAKGEVTVSLDWRLEQEKTEKNTLRLSDSPRFFPAAGNVAPAKWLKNSGFPD 360  
Db 301 EVKTNNSVAAKGEVTVSLDWRLEQEKTEKNTLRLSDSPRFFPAAGNVAPAKWLKNSGFPD 360

Qy 361 EBFNHWGGBDVEFGYRLFRYGSFFKTIIDGIMAYHQEPKNETDREAGKNTITLDMREK 420  
Db 361 EBFNHWGGBDVEFGYRLFRYGSFFKTIIDGIMAYHQEPKNETDREAGKNTITLDMREK 420

Qy 421 VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCINDGST 480

Db 421 VPYIYRKLPIEDSHINRVPLVSIYIPAYNCANYIQRCDVSALNQTVDLEVCINDGST 480  
Qy 481 DNTLEVINKLYGNPNVRIMSKPENGIGASASNAAVSFAGYIYGQDSDDDYLPDVAVELC 540  
Db 481 DNTLEVINKLYGNPNVRIMSKPENGIGASASNAAVSFAGYIYGQDSDDDYLPDVAVELC 540  
Qy 541 LK6FLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHHPMTTIRAWHL 600  
Db 541 LK6FLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHHPMTTIRAWHL 600  
Qy 601 TDGFNEKIENAVYDMFLKLSEVGKPKHLNKICYNRVLHGDNTSIKKGIGQKKNHFVYVN 660  
Db 601 TDGFNEKIENAVYDMFLKLSEVGKPKHLNKICYNRVLHGDNTSIKKGIGQKKNHFVYVN 660  
Qy 661 QSLNRQGITVYNYDEFDLDESRYIFNKTAEOEEDILDKIKIQNKDAKIAVSIFYP 720  
Db 661 QSLNRQGITVYNYDEFDLDESRYIFNKTAEOEEDILDKIKIQNKDAKIAVSIFYP 720  
Qy 721 NTLNGVLVKLNNIIEYNKNI FVIVLHVDKNHLTPDIKKEILAFYHKGQVNLNNDISYY 780  
Db 721 NTLNGVLVKLNNIIEYNKNI FVIVLHVDKNHLTPDIKKEILAFYHKGQVNLNNDISYY 780  
Qy 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAHLTH 840  
Db 781 TSNRLIKTEAHLNINKLSQNLNCEYIIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAHLTH 840  
Qy 841 DWIEKINAHPPFKKLIKTYFNDNDLSKMNKYGASQGMFMTYALAHELLTTIIKEVITSQOS 900  
Db 841 DWIEKINAHPPFKKLIKTYFNDNDLSKMNKYGASQGMFMTYALAHELLTTIIKEVITSQOS 900  
Qy 901 IDSVPENTEDINWQFALLILEKKTGHVFNKTSITLYMPWERKLOWTNEQIESAKRGNI 960  
Db 901 IDSVPENTEDINWQFALLILEKKTGHVFNKTSITLYMPWERKLOWTNEQIESAKRGNI 960  
Qy 961 PVNKFIIINSITL 972  
Db 961 PVNKFIIINSITL 972

RESULT 4  
US-11-109-855-9  
; Sequence 9, Application US/11109855  
; Publication No. US20050202540A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kehama  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/11/109,855  
; CURRENT FILING DATE: 2005-04-20  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pasteurella Multocida  
US-11-109-855-9

Query Match 100.0%; Score 5108; DB 6; Length 972;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTLSQAIKAYNSNDYQALALFKESABEYGRKIVEFOITCKEKLSAHPSVNSAHLVSN 60  
Db 1 MNTLSQAIKAYNSNDYQALALFKESABEYGRKIVEFOITCKEKLSAHPSVNSAHLVSN 60

Qy 61 KEEKNVNCDSPLDIATQALLSNVKKVLVSDSEKNTLKNKWKLTTEKKSNAEVRVALVP 120

```
Db 301 EVKTNNSVAAKGEGTVDLWRLEQPEKTEENLRSLSDSPFRFAAGNVAFAKWLKSGFFD 360
Qy 361 EEFNHWGGEDVEFYRLFRYGSPFKTIDGIMAYHQBPQKGENETDREAGNITLDMREK 420
Db 361 EEFNHWGGEDVEFYRLFRYGSPFKTIDGIMAYHQBPQKGENETDREAGNITLDMREK 420
Qy 421 VPYIYRKLPIEDSHINRVLPSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Db 421 VPYIYRKLPIEDSHINRVLPSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Qy 481 DNTLEVINKLKYNPRVRIMSKPNGGASASNAASVPAKGYIIGOLDSDDDYLPDPAVELC 540
Db 481 DNTLEVINKLKYNPRVRIMSKPNGGASASNAASVPAKGYIIGOLDSDDDYLPDPAVELC 540
Qy 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIEANVDYDMFLKLSVKGPKHLNKI CYNRVLHGDNTSIKKLGIQKQNHFFVNVN 660
Db 601 TDGFNEKIEANVDYDMFLKLSVKGPKHLNKI CYNRVLHGDNTSIKKLGIQKQNHFFVNVN 660
Qy 661 QSLNRQGITYYNYDEPDLDDESRKYIFNKTAEQEEDILDKIIONKDAKIAVSIFYP 720
Db 661 QSLNRQGITYYNYDEPDLDDESRKYIFNKTAEQEEDILDKIIONKDAKIAVSIFYP 720
Qy 721 NTNLGLVKLNNIIEYNKNI FVIVLHVDKNHLPDIIKKEILAFYHKHQVNILLNNDISYY 780
Db 721 NTNLGLVKLNNIIEYNKNI FVIVLHVDKNHLPDIIKKEILAFYHKHQVNILLNNDISYY 780
Qy 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAALTH 840
Db 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAALTH 840
Qy 841 DWIEKINAHPPFKLKITFYFNDNDLKSMMVKGASQGMFTYALAHELLITIIKEVITSCQS 900
Db 841 DWIEKINAHPPFKLKITFYFNDNDLKSMMVKGASQGMFTYALAHELLITIIKEVITSCQS 900
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKQWNTNEQIESAKRGENI 960
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKQWNTNEQIESAKRGENI 960
```

## RESULT 2

```
US-10-011-771B-9
; Sequence 9, Application US/10011771B
; Publication No. US20030082780A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H.
; APPLICANT: DeAngelis, Paul
; APPLICANT: Kumari, Kshama
; TITLE OF INVENTION: Hvaluronan Synthase Gene and Uses Thereof
; FILE REFERENCE: 3554.011
; CURRENT APPLICATION NUMBER: US/10/011, 771B
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 09/178,851
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: US 60/064,435
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Pastuerella Multocida
US-10-011-771B-9
```

Query Match 100.0%; Score 5108; DB 4; Length 972;  
Best Local Similarity 100.0%; Pred. No. 0;

```
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNTLSQAIKAYNSNDYQALAKLPEKSAEYIGRKIVFQITTKCKEKLSAHPSVNSAHLNVN 60
Db 1 MNTLSQAIKAYNSNDYQALAKLPEKSAEYIGRKIVFQITTKCKEKLSAHPSVNSAHLNVN 60
Qy 61 KEEKVNVCDSPLDIATQLLLSNVKLVLSDESKNTLKNKWLKTEKKSNAEYRAVALVP 120
Db 61 KEEKVNVCDSPLDIATQLLLSNVKLVLSDESKNTLKNKWLKTEKKSNAEYRAVALVP 120
Qy 121 KPPPKDLVLAPLDDHNDFTWYKKRKLGIKPEHQHVGLSIIVTTFNRPAILSIITLACL 180
Db 121 KPPPKDLVLAPLDDHNDFTWYKKRKLGIKPEHQHVGLSIIVTTFNRPAILSIITLACL 180
Qy 181 VNOKTHYPEVIVTDDGSOEDLSPIIRQYENKLDIRYVRQKONGFOASAAARNMGLRLAKY 240
Db 181 VNOKTHYPEVIVTDDGSOEDLSPIIRQYENKLDIRYVRQKONGFOASAAARNMGLRLAKY 240
Qy 241 DFIGLLDCDMPNPLWVHSYVAELLEDDDLTIIGPRKYIDTQHIDPKDFLNNASLLESPL 300
Db 241 DFIGLLDCDMPNPLWVHSYVAELLEDDDLTIIGPRKYIDTQHIDPKDFLNNASLLESPL 300
Qy 301 EVKTNNSVAAKGEGTVDLWRLEQPEKTEENLRSLSDSPFRFAAGNVAFAKWLKSGFFD 360
Db 301 EVKTNNSVAAKGEGTVDLWRLEQPEKTEENLRSLSDSPFRFAAGNVAFAKWLKSGFFD 360
Qy 361 EEFNHWGGEDVEFYRLFRYGSPFKTIDGIMAYHQBPQKGENETDREAGNITLDMREK 420
Db 361 EEFNHWGGEDVEFYRLFRYGSPFKTIDGIMAYHQBPQKGENETDREAGNITLDMREK 420
Qy 421 VPYIYRKLPIEDSHINRVLPSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Db 421 VPYIYRKLPIEDSHINRVLPSIYIPAYNCANYIQRCDVSALNQTVVDLEVCICNDGST 480
Qy 481 DNTLEVINKLKYNPRVRIMSKPNGGASASNAASVPAKGYIIGOLDSDDDYLPDPAVELC 540
Db 481 DNTLEVINKLKYNPRVRIMSKPNGGASASNAASVPAKGYIIGOLDSDDDYLPDPAVELC 540
Qy 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Db 541 LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTAMIAHFRMFTIRAWHL 600
Qy 601 TDGFNEKIEANVDYDMFLKLSVKGPKHLNKI CYNRVLHGDNTSIKKLGIQKQNHFFVNVN 660
Db 601 TDGFNEKIEANVDYDMFLKLSVKGPKHLNKI CYNRVLHGDNTSIKKLGIQKQNHFFVNVN 660
Qy 661 QSLNRQGITYYNYDEPDLDDESRKYIFNKTAEQEEDILDKIIONKDAKIAVSIFYP 720
Db 661 QSLNRQGITYYNYDEPDLDDESRKYIFNKTAEQEEDILDKIIONKDAKIAVSIFYP 720
Qy 721 NTNLGLVKLNNIIEYNKNI FVIVLHVDKNHLPDIIKKEILAFYHKHQVNILLNNDISYY 780
Db 721 NTNLGLVKLNNIIEYNKNI FVIVLHVDKNHLPDIIKKEILAFYHKHQVNILLNNDISYY 780
Qy 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAALTH 840
Db 781 TSRLIKTEAHLNINKLSQNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGWNFSAALTH 840
Qy 841 DWIEKINAHPPFKLKITFYFNDNDLKSMMVKGASQGMFTYALAHELLITIIKEVITSCQS 900
Db 841 DWIEKINAHPPFKLKITFYFNDNDLKSMMVKGASQGMFTYALAHELLITIIKEVITSCQS 900
Qy 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKQWNTNEQIESAKRGENI 960
Db 901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSITLTYPMPWERKQWNTNEQIESAKRGENI 960
Qy 961 PVNKFIIINSITL 972
Db 961 PVNKFIIINSITL 972
```

RESULT 3  
US-10-642-248-2

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:04:42 ; Search time 119 Seconds  
(without alignments)  
3412.858 Million cell updates/sec

Title: US-10-642-248-2  
Perfect score: 5108  
Sequence: 1 MNTLSQAIKAYNSDYQAL.....SAKGENIPVKNKFIINSITL 972

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_Main\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5108	100.0	972	4	US-10-011-768B-9
2	5108	100.0	972	4	US-10-011-771B-9
3	5108	100.0	972	4	US-10-642-248-2
4	5108	100.0	972	6	US-11-109-855-9
5	5104	99.9	972	3	US-09-879-959-10
6	5104	99.9	972	4	US-10-172-527-10
7	5104	99.9	972	4	US-10-326-185-95
8	5104	99.9	972	4	US-10-309-560-8
9	5104	99.9	972	6	US-11-096-190-9
10	4733	92.7	972	4	US-10-217-613-9
11	4502.5	88.1	965	3	US-09-842-484A-4
12	4502.5	88.1	965	4	US-10-217-613-3
13	4502.5	88.1	965	4	US-10-217-613-8
14	4502.5	88.1	965	4	US-10-642-248-4
15	4502.5	88.1	965	5	US-10-197-153-3
16	4502.5	88.1	965	6	US-11-042-530-4
17	4490.5	87.9	965	3	US-09-842-484A-2
18	4490.5	87.9	965	4	US-10-184-485-3
19	4490.5	87.9	965	6	US-11-042-530-2
20	3697	72.4	703	4	US-10-217-613-1
21	3697	72.4	703	4	US-10-217-613-7
22	3697	72.4	703	4	US-10-642-248-9
23	3697	72.4	703	5	US-10-197-153-1
24	3673.5	71.9	702	4	US-10-184-485-1
25	2209	43.2	686	4	US-10-216-289-2
26	2209	43.2	686	4	US-10-216-289-4
27	332.5	6.5	648	4	US-10-282-122A-47924

ALIGNMENTS

RESULT 1

US-10-011-768B-9  
; Sequence 9, Application US/10011768B  
; Publication No. US20030073221A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Kumari, Kahama  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/10/011.768B  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 972  
; TYPE: PRT  
; ORGANISM: Pastuerella Multocida  
US-10-011-768B-9

Query Match	100.0%;	Score 5108;	DB 4;	Length 972;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 972;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MNTLSQAIKAYNSDYQAL	KLFKPSAIEYGRKIVEFOITCKEKL	SAHPSVNSAHL	SVN 60
Db	1	MNTLSQAIKAYNSDYQAL	KLFKPSAIEYGRKIVEFOITCKEKL	SAHPSVNSAHL	SVN 60
QY	61	KEEKVNCDSPLDIATQ	LLSNVKKLVLSDESKNTLKNKWKLLTEKSENAEVR	VALVP 120	
Db	61	KEEKVNCDSPLDIATQ	LLSNVKKLVLSDESKNTLKNKWKLLTEKSENAEVR	VALVP 120	
QY	121	KDFPKDLVLAPLPHVNDFTWYKKR	KRLGIKPEHQHVGLSIIIVTTFNRP	AILSTLACL 180	
Db	121	KDFPKDLVLAPLPHVNDFTWYKKR	KRLGIKPEHQHVGLSIIIVTTFNRP	AILSTLACL 180	
QY	181	VNQKTHYPFEVIVTDDGSQEDLSPIIRQYENKLDI	RYRQKNGFQA	SAARNMGLR	LAKY 240
Db	181	VNQKTHYPFEVIVTDDGSQEDLSPIIRQYENKLDI	RYRQKNGFQA	SAARNMGLR	LAKY 240
QY	241	DFIGLLDCDMPNPLWVHSYVAE	LLED	DDLTIIIGPRKYIDTQHDIDPKDFLNNASLES	UP 300
Db	241	DFIGLLDCDMPNPLWVHSYVAE	LLED	DDLTIIIGPRKYIDTQHDIDPKDFLNNASLES	UP 300
QY	301	EYKTNNSVAAKGEQTVSLDWRLEQPEKTENLR	LSDSPRFFAAGNVFAF	AKWLNKSG	FFD 360



Db	1480	GATATACCTTAGAGTGATCAATAGCTTTATGGTAAATCTTAGGGTACGCATCATG	1539
Qy	1501	TTAAACCAAAATGGCGGAATAGCTCAGCATCAAAATGACGCCGTTCCTTTGCTAAAGGT	1560
Db	1540	TCTAAACCAAAATGGCGGAATAGCTCAGCATCAAAATGACGCCGTTCCTTTGCTAAAGGT	1599
Qy	1561	TATTACATTCGGGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCGATTTGAACGTGTG	1620
Db	1600	TATTACATTCGGGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCGATTTGAACGTGTG	1659
Qy	1621	TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC	1680
Db	1660	TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC	1719
Qy	1681	AATCCGATTCGGTACCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCACGAGAAAA	1740
Db	1720	AATCCGATTCGGTACCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCACGAGAAAA	1779
Qy	1741	CTCACACGGCTATGATTGCTCACCATTCTAGAAATGTTTACGATTTAGAGCTTCGCATTTA	1800
Db	1780	CTCACACGGCTATGATTGCTCACCATTCTAGAAATGTTTACGATTTAGAGCTTCGCATTTA	1839
Qy	1801	ACTGATCGATTCAATGAAAAAATGAAAAATGCCGTAGCATATGACATGTTCTCTCAAACTC	1860
Db	1840	ACGATCGATTCAATGAAAAAATGAAAAATGCCGTAGCATATGACATGTTCTCTCAAACTC	1899
Qy	1861	AGTGAAGTTGGAAATTTAAACATCTTAAATAAATCTGCTATTAACCGTGATTTACATGGT	1920
Db	1900	AGTGAAGTTGGAAATTTAAACATCTTAAATAAATCTGCTATTAACCGTGATTTACATGGT	1959
Qy	1921	GATAACACATCAATTAGAAACTTGGCATTCGAAGAAAAACCAATTTTGTGTAGTCAAT	1980
Db	1960	GATAACACATCAATTAGAAACTTGGCATTCGAAGAAAAACCAATTTTGTGTAGTCAAT	2019
Qy	1981	CAGTCATTAAATAGACAAGGCATACTTATTAATTAATGACCAATTTGATGATTTAGAT	2040
Db	2020	CAGTCATTAAATAGACAAGGCATACTTATTAATTAATGACCAATTTGATGATTTAGAT	2079
Qy	2041	GAAGTAGAAGTATATTTTCAATAAACCCTGGAATATCAAGAAGAGATTGATATCTTA	2100
Db	2080	GAAGTAGAAGTATATTTTCAATAAACCCTGGAATATCAAGAAGAGATTGATATCTTA	2139
Qy	2101	AAAGATATTAATATCCAGNAATAAGATGCCAAATCCGAGTCAGTATTTTATATCCC	2160
Db	2140	AAAGATCTTAACTCATTTCAAAATAAAGATGCCAAATCCGAGTCAGTATTTTATATCCC	2199
Qy	2161	AATACATTAAACGGCTTAGTGAAAAAATCAAAATATTTATGAAATATAATAAAATATA	2220
Db	2200	AATACATTAAACGGCTTAGTGAAAAAATCAAAATATTTATGAAATATAATAAAATATA	2259
Qy	2221	TTGGTTATTGTTCTACATGTTGATGAAGTATCTTAACAGATATCAAAAAAGAAATA	2280
Db	2260	TTGGTTATTGTTCTACATGTTGATGAAGTATCTTAACAGATATCAAAAAAGAAATA	2319
Qy	2281	CTAGCCTTCTATCAATAACATCAAGTGAATTTTACTAATAATGATATCTCATATTAC	2340
Db	2320	TTGGCTTTCTATCAATAACATCAAGTGAATTTTACTAATAATGATATCTCATATTAC	2379
Qy	2341	ACGAGTAATAGATTAAATAAAACCTGAGCGCATTTTAAGTAATATAATAAATTAAGTCAG	2400
Db	2380	ACGAGTAATAGATTAAATAAAACCTGAGCGCATTTTAAGTAATATAATAAATTAAGTCAG	2439
Qy	2401	TTAAATCTAAATTTGTAATACATCATTTTGTGATTAATCATGACGCTTATCGTTAAAAAT	2460
Db	2440	TTAAATCTAAATTTGTAATACATCATTTTGTGATTAATCATGACGCTTATCGTTAAAAAT	2499
Qy	2461	GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTTAACACAT	2520
Db	2500	GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTTAACACAT	2559
Qy	2521	GATTGGATCGAGAAAAATCAATGCCCATCCACATTTTAAAAAGCTCATTTAAAACTTATTTT	2580

Db	2560	GATTGGATCGAGAAAAATCAATCGCATCCACCATTTTAAAAAGCTGATTTAAACCTATTTT	2619
Qy	2581	AATGACAATCAGCTTTAAAGAGTATGAATGTGAAGGGGCATCAAGGTATGTTTATGACG	2640
Db	2620	AATGACAATCAGCTTTAAAGAGTATGAATGTGAAGGGGCATCAAGGTATGTTTATGACG	2679
Qy	2641	TATGCCCTAGCGCATGAGCTTCTGACGATTTATTTAAAGAAAGTCAATCATCTTCCAGTCA	2700
Db	2680	TATGCCCTAGCGCATGAGCTTCTGACGATTTATTTAAAGAAAGTCAATCATCTTCCAGTCA	2739
Qy	2701	ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGACACTTTTAATC	2760
Db	2740	ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGACACTTTTAATC	2799
Qy	2761	TTAGAAAAAGAAACCGGCCATGTTATTTAATAAAACATCGACCTGACTTATATGCGCTTGG	2820
Db	2800	TTAGAAAAAGAAACCGGCCATGTTATTTAATAAAACATCGACCTGACTTATATGCGCTTGG	2859
Qy	2821	GAACGAAAAATTACAATGGACAAATGAACAAATTTGAAAGTGCAAAAAAGAGGAGAAAAATATA	2880
Db	2860	GAACGAAAAATTACAATGGACAAATGAACAAATTTGAAAGTGCAAAAAAGAGGAGAAAAATATA	2919
Qy	2881	CCTGTTAAACAAAGTTTCATTTATTAATAGTATTAACCTCTATAAA	2920
Db	2920	CCGTTTAAACAAAGTTTCATTTATTAATAGTATTAACCGCTATAAA	2959

Search completed: January 8, 2006, 17:27:54  
Job time : 2080 secs

QY 1921 GATAACACATCAATTTAGAACTTGGCAATTCAAAGAAACCAATTTTGTGTAGTCAAT 1980  
DB 1921 GATAACACATCAATTTAGAACTTGGCAATTCAAAGAAACCAATTTTGTGTAGTCAAT 1980  
QY 1981 CAGTCATTTAAATAGACAAGGCATTAACCTTATTAATATGACGAATTTGATGATTTAGAT 2040  
DB 1981 CAGTCATTTAAATAGACAAGGCATTAACCTTATTAATATGACGAATTTGATGATTTAGAT 2040  
QY 2041 GAAAGTAGAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
DB 2041 GAAAGTAGAAGTATATTTTCAATAAAAACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
QY 2101 AAAGATATTAATCAATCCAGATTAAGATGCCAAATCGCAGTCAAGTATTTTATCCC 2160  
DB 2101 AAAGATATTAATCAATCCAGATTAAGATGCCAAATCGCAGTCAAGTATTTTATCCC 2160  
QY 2161 AATACATTTAAACGGCTTAGTGAATAAATCTAAACAATATTTATGAATATAATAAAAAATATA 2220  
DB 2161 AATACATTTAAACGGCTTAGTGAATAAATCTAAACAATATTTATGAATATAATAAAAAATATA 2220  
QY 2221 TTCGTTATTTGTTCTACATGTTGATGAAGATCATCTTACACAGATATCAAA 2271  
DB 2221 TTCGTTATTTGTTCTACATGTTGATGAAGATCATCTTACACAGATATCTAA 2271

RESULT 15  
US-09-842-484A-3  
; Sequence 3, Application US/09842484A  
; Publication No. US20030104601A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL L.  
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 4605.003  
; CURRENT APPLICATION NUMBER: US/09/842,484A  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2979  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-09-842-484A-3

Query Match 77.6%; Score 2266.4; DB 3; Length 2979;  
Best Local Similarity 86.4%; Pred. No. 0;  
Matches 2523; Conservative 0; Mismatches 376; Indels 21; Gaps 1;

QY 1 ATGAATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
DB 61 ATGAATACATTTATCAAGCAATAAAGCATATAACAGCAATGACTATGAATTAGCACTC 120  
QY 61 AAATATTGTAAGTTCGGCGGAATCTATGACGGAATTTGTAATTTCAATATACC 120  
DB 121 AAATATTGTAAGTTCGCTGAAACCTACGGCGGAATTCGTTGAATTTCAATATATC 180  
QY 121 AAATGTAAGAAATCTCTCAGCACATCTCTCTGTTAAATTCAGCACATCTTTCTGTAAAT 180  
DB 181 AAATGTAAGAAATCTCTCAGCAAATTC-----TTATGTAACT 219  
QY 181 AAAGAGAAAAAGTCAATGTTTGGCATGTTCGGTAGTTCGGTAGATATTGCAACACAACTGTTACTT 240  
DB 220 GAAGATAAAAAAACAAGTGTTCGGTAGCTCATTTAGATATCGCAACACAGCTCTTACTT 279  
QY 241 TCCACGTAATAAATATTAGTACTTTCTGACTCGGAAAAAACAACGTTTAAAAAATAATCG 300  
DB 280 TCCACGTAATAAATATTAGTCTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAATCG 339  
QY 301 AAATGCTCACTGAGAGAAATCTGAAAAATCGCGAGTGAAGCGGTTCGCGCTTGTATCCA 360  
DB 340 AAATCTATCACTGGGAAAAAATCGGAGAACGCAAGAAATCAGAAAGTGGAACTAGTACCC 399

QY 361 AAAGATTTTCCCAAGATCTGGTTTATAGCCCTTTACCTGATCATGTTAAATGATTTTACA 420  
DB 400 AAAGATTTTCTTAAGATCTGTTCTTGTCTCCATTTGCCAGATCATGTTAAATGATTTTACA 459  
QY 421 TGGTACAAAAAGCGAAAGAAAGACTTTGGCATATAAAGCTGAAACATCAACATGTTGGTCTT 480  
DB 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATTAAGGCTGTAAATTAAGAATATCGGTCTT 519  
QY 481 TCTATTTATCGTTACAAACATTTCAATCGACCAGCAATTTTATCGATTTACATTTAGCCCTGTTT 540  
DB 520 TCTATTTATTTTCTTACATTTAATCGTAGCCGTTATTTTAGATATAAAGCTTAGCCCTGTTT 579  
QY 541 GTAAACCAAAAAACACATTTACCCCTTTTCAAGTTTATCGTGACAGATGATGGTAGTCAGGAA 600  
DB 580 GTCAATTCAGAAAAACAACTACCCATTTTGAAGTTCGTTGTGACAGATGATGGTAGTAAGGAA 639  
QY 601 GATCTATCACCGATCATTTCCGCAATATGAATAAATTAATTTGGATATTCGTACGTCAGACAA 660  
DB 640 AACTTACTTACCATTTGTGCAAAAAATACGAAACAAAACTTGACATAAAGATATGTAAGACAA 699  
QY 661 AAAGATTAACGGTTTTCAGCCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAAAAT 720  
DB 700 AAAGATTTATGGATATCAATTTGTGTGACGTCAGAACTTAGGTTTACGTCAGCAAAAGTAT 759  
QY 721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGGTTTCAATCTTTAT 780  
DB 760 GATTTTGTCTCGATTTCTAGACTGCGATATGSCACCAACAATTTATGGGTTTCAATCTTTAT 819  
QY 781 GTTGCAGAGCTTTATGAAAGATGATTTAAACAATCATTTGTTCCAGAAAAATACATTCGAT 840  
DB 820 CTTACAGAACTATTAGAAAGACAATGATTTGTTTAAATTTGGACCTAGAAAAATATGTGGAT 879  
QY 841 ACACAACATATTGACCCAAAAAGACTTCTTAATTAACCGAGTTTTCGTTGAATCATTTACCA 900  
DB 880 ACTCATATATTACCGCAGAACTTCTTAAACGATCCATTAACGATCCATTAATAGAATCACTACT 939  
QY 901 GAAGTGAACCAATTAATAGTTGTTCCGCAAAAGGGAAAGAAACAGTTTCTCTGGATTGG 960  
DB 940 GAAACCGCTACAAATTAACATCTTCGATTACATCAAAAGGAATATATATCGTTGGATTGG 999  
QY 961 CGCTTAGAACAAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCGCTTTT 1020  
DB 1000 AGATTAGAACATTTCAAAAAACCGATAATCTACGCTATGTGATTTCTCCGTTTCCGTTAT 1059  
QY 1021 TTTGCGGCGGTAATGTTGCTTTCGTAATAAATGGCTAAATTAATTCGTTTCTTTCGAT 1080  
DB 1060 TTTAGTTTCGCGTAATGTTGCAATTTTCTAAAGAAATGGCTTAAATAAGTAGTTGGTTCGAT 1119  
QY 1081 GAGGAATTTAATCACTCGGCGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGCTTAC 1140  
DB 1120 GAAGAAATTTAATCATTTGGGGGGCGAAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA 1179  
QY 1141 GGTAGTTTCTTTTAAACCTATTGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200  
DB 1180 GGTCTGTTTTTCAGAGTAATTTGACGGCGAAATGGCATACCATCAAGAAACCACTGGTAAA 1239  
QY 1201 GAAATGAAACCGATCGTGAAGCGGAAAAAATATTTAGCTCGATTTATGAGAGAAAG 1260  
DB 1240 GAAATGAAACAGACCGGAAAGCTGGTAAAAAGTATTTCGCTTTAAAAATTTGTGAAGAAAAAG 1299  
QY 1261 GTCCCTTATATCTATAGAAAACTTTTACAAATAGAAAGATTCGCATATCAATAGAGTACCT 1320  
DB 1300 GTACCTTTACATCTATAGAAAGCTTTTCCATATGAAGATTCACATATTCATAGATACCT 1359  
QY 1321 TTAGTTTCAATTTTATATCCAGCTTTAATCTGTGCAAACTATTTCAACGTTGCGTAGAT 1380  
DB 1360 TTAGTTTCTATTTTATCTCCCGCTTTAATCTGTGCAAAATTAATTTCAAAGATGTGTAGAT 1419  
QY 1381 AGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTCAACA 1440  
DB 1420 AGTGTCTTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAAACGATGGTCAACA 1479  
QY 1441 GATAATACCTTAGAAGTATCAATAAGCTTTTATGTTAAATTAATCTTAGGGTAGCGATCATG 1500

;  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/842,484  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 2271  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-10-642-248-20

Query Match 77.78; Score 2269.4; DB 7; Length 2271;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGAATACATTTATCACAAGCAATAAAGACATATAACAGCAATGACATATCAATTAGCACTC	60
Db	1	ATGATACATTTATCACAAGCAATAAAGACATATAACAGCAATGACATATCAATTAGCACTC	60
Qy	61	AAATTTATTTGAAAGTCGGCGGAAATCTATGACGCGAAATTTGTTGAATTTCAAATPACC	120
Db	61	AAATTTATTTGAAAGTCGGCGGAAATCTATGACGCGAAATTTGTTGAATTTCAAATPACC	120
Qy	121	AAATGCAAGAAAGAACTCTCAGCACATCTCTGTTAAATTCAGCACATCTTCTGTAAAT	180
Db	121	AAATGCAAGAAAGAACTCTCAGCACATCTCTGTTAAATTCAGCACATCTTCTGTAAAT	180
Qy	181	AAAGAAAGAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACAACTGTTACTT	240
Db	181	AAAGAAAGAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACAACTGTTACTT	240
Qy	241	TCCAACTGAAAGAAATTTAGTACTTTCTGACTCGCGAAAGAAACACGTTTAAAGAAATGG	300
Db	241	TCCAACTGAAAGAAATTTAGTACTTTCTGACTCGCGAAAGAAACACGTTTAAAGAAATGG	300
Qy	301	AAATGCTCTAGAGAGAAATCTGAAATTCGGAGGTAGAGCGGTGCGCCCTTGTACCA	360
Db	301	AAATGCTCTAGAGAGAAATCTGAAATTCGGAGGTAGAGCGGTGCGCCCTTGTACCA	360
Qy	361	AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTACTGATCATGTTAATGATTTTACA	420
Db	361	AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTACTGATCATGTTAATGATTTTACA	420
Qy	421	TGGTACAAAAGCGAAAGAAAGACTTGGCATATAAAGCTGAAACATCAACATGTTGGTCTT	480
Db	421	TGGTACAAAAGCGAAAGAAAGACTTGGCATATAAAGCTGAAACATCAACATGTTGGTCTT	480
Qy	481	TCTATTATCGTTACAAACATTCATCGACCGACGCAATTTTATCGATTACATTAGCCTGTTA	540
Db	481	TCTATTATCGTTACAAACATTCATCGACCGACGCAATTTTATCGATTACATTAGCCTGTTA	540
Qy	541	GTAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Db	541	GTAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Qy	601	GATCTATCACCGATCATTTGCGCAATATGAAATATAATTTGGATATTCGCTACGTCAGACAA	660
Db	601	GATCTATCACCGATCATTTGCGCAATATGAAATATAATTTGGATATTCGCTACGTCAGACAA	660
Qy	661	AAAGATACGGTTTTCAGCCAGTGGCGCTCGGAATATGGATTACCGCTTAGCAAAATAT	720
Db	661	AAAGATACGGTTTTCAGCCAGTGGCGCTCGGAATATGGATTACCGCTTAGCAAAATAT	720
Qy	721	GACTTTTATGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGTTTCAATTTAT	780
Db	721	GACTTTTATGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGTTTCAATTTAT	780
Qy	781	GTTGCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGTTCCAGAAATAATCATCGAT	840
Db	781	GTTGCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGTTCCAGAAATAATCATCGAT	840

Qy	841	ACACAACATATTGACCCAAAAGACTTCTTAAATAAACGCGAGTTTGTCTGTAATCATTACCA	900
Db	841	ACACAACATATTGACCCAAAAGACTTCTTAAATAAACGCGAGTTTGTCTGTAATCATTACCA	900
Qy	901	GAAGTGAAGAACCAATTAATAGTGTGGCGGAAAGGGAAGGAACAGTTTCTCTGGATTGG	960
Db	901	GAAGTGAAGAACCAATTAATAGTGTGGCGGAAAGGGAAGGAACAGTTTCTCTGGATTGG	960
Qy	961	CGCTTAGAACCAATTCGAAAAAAGACAGAAAAATCTCCGCTTATCCGATTCCGCTTCCGTTT	1020
Db	961	CGCTTAGAACCAATTCGAAAAAAGACAGAAAAATCTCCGCTTATCCGATTCCGCTTCCGTTT	1020
Qy	1021	TTTTCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATCCCGTTTCTTTGAT	1080
Db	1021	TTTTCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATCCCGTTTCTTTGAT	1080
Qy	1081	GAGGAATTTAATCACTCGGGGTGAGAAAGATGCGAATTTGGATATCGCTTATTTCCGTTAC	1140
Db	1081	GAGGAATTTAATCACTCGGGGTGAGAAAGATGCGAATTTGGATATCGCTTATTTCCGTTAC	1140
Qy	1141	GGTAGTTTCTTTTAAAACTATTGATGCTTATGCGCTTACCATCAAGAGCCACCAAGTAAA	1200
Db	1141	GGTAGTTTCTTTTAAAACTATTGATGCGATTTATGCGCTTACCATCAAGAGCCACCAAGTAAA	1200
Qy	1201	GAAAAATGAAGCCGATCGTGAAGCGGGAAGAAATATTAACGCTCGATATTATGAGAGAAAAA	1260
Db	1201	GAAAAATGAAGCCGATCGTGAAGCGGGAAGAAATATTAACGCTCGATATTATGAGAGAAAAA	1260
Qy	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAATTCGATATCAATAGAGTACCT	1320
Db	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAATTCGATATCAATAGAGTACCT	1320
Qy	1321	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTAACGTTGCGTAGAT	1380
Db	1321	TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTAACGTTGCGTAGAT	1380
Qy	1381	AGTGCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA	1440
Db	1381	AGTGCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA	1440
Qy	1441	GATAATACCTTTAGAAAGTCAATAGCTTTTATGGTAAATAATCCTAGGTTACGATCATG	1500
Db	1441	GATAATACCTTTAGAAAGTCAATAGCTTTTATGGTAAATAATCCTAGGTTACGATCATG	1500
Qy	1501	TCTAAACCAAAATGCGGAATAGCTCAGCATCAAAATGCGAGCTTCTTTTGTCTAAAGGT	1560
Db	1501	TCTAAACCAAAATGCGGAATAGCTCAGCATCAAAATGCGAGCTTCTTTTGTCTAAAGGT	1560
Qy	1561	TATTACATTTGGGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCACTGAACTGTGT	1620
Db	1561	TATTACATTTGGGAGTTAGATTTCAGATGATTATCTTGAGCCTGATGCACTGAACTGTGT	1620
Qy	1621	TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCATTAATAGAAAAAGTC	1680
Db	1621	TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCATTAATAGAAAAAGTC	1680
Qy	1681	AATCCGATGCTAGCTTAATCGCTAATGTTTACAAATTTGGCAGAAATTTTCCAGAGAAAAA	1740
Db	1681	AATCCGATGCTAGCTTAATCGCTAATGTTTACAAATTTGGCAGAAATTTTCCAGAGAAAAA	1740
Qy	1741	CTCAACACGCTATGATTGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA	1800
Db	1741	CTCAACACGCTATGATTGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA	1800
Qy	1801	ACTGATGGATTTCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCAAACTC	1860
Db	1801	ACTGATGGATTTCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCAAACTC	1860
Qy	1861	AGTGAAGTTGGAATAATTTTAAACATCTTAATAAATCTGCTATACCGTGTATTACATGGT	1920
Db	1861	AGTGAAGTTGGAATAATTTTAAACATCTTAATAAATCTGCTATACCGTGTATTACATGGT	1920

Db 1180 GGCTGTTTTTCAGAGTAATTTGACGGCGGAATGGCCATCCATCAAGAACCCACCTGGTAAA 1239  
Qy 1201 GAAATGAAACCGATCGTGAAGCGGGAATAATATACGCTCGATATATATGAGAGAAAAG 1260  
Db 1240 GAAATGAAACGAGAACGCGAGCTGGTAAAAGTATTACGCTTAAAAATTTGTGAAAGAAAAG 1299  
Qy 1261 GTCCCTTATATCTATAGAAAATCTTTACCAATAGAGATTGCGCATATCAATAGAGTACCT 1320  
Db 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGAAATTCACATATTCATAGAAATACCT 1359  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATAAATGTCGCAAACTATATTCAAAGCTTGGCTAGAT 1380  
Db 1360 TTAGTTTCTATTTATATCCCGCTTATAAATGTCGCAAAATTTATTCAAAGATGTGTAGAT 1419  
Qy 1381 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1440  
Db 1420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1479  
Qy 1441 GATAATACCTTAGAAGTATCAATTAAGCTTTATGTAATATATCCTAGGGTACGCATCATG 1500  
Db 1480 GATAATACCTTAGAAGTATCAATTAAGCTTTATGTAATATATCCTAGGGTACGCATCATG 1539  
Qy 1501 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCGTTCCTTTGCTAAAGGT 1560  
Db 1540 TCTAAACCAATGGCGGAATAGCCTCAGCATCAAAATGCAGCGTTCCTTTGCTAAAGGT 1599  
Qy 1561 TATTACATTTGGCAGCTTAGATTAGATTAGATTATCTTGAGCCTGATGCGAGTTGAACCTGTT 1620  
Db 1600 TATTACATTTGGCAGCTTAGATTAGATTAGATTATCTTGAGCCTGATGCGAGTTGAACCTGTT 1659  
Qy 1621 TTAAGAAATTTTAAAGATATAAAGCTAGCTAGCTGTTGTTATACCAATTAAGAACCTC 1680  
Db 1660 TTAAGAAATTTTAAAGATATAAAGCTAGCTAGCTGTTGTTATACCAATTAAGAACCTC 1719  
Qy 1681 AATCCGGATGGTAGCTTAATGCTAATGTTTAAATGTCGCAAGATTTTCAAGAGAAAA 1740  
Db 1720 AATCCGGATGGTAGCTTAATGCTAATGTTTAAATGTCGCAAGATTTTCAAGAGAAAA 1779  
Qy 1741 CTCACACGGCTATGATTGCTCACCACCTTTAGAAATGTTTCAAGATTAGAGCTTGGCATTTA 1800  
Db 1780 CTCACACGGCTATGATTGCTCACCACCTTTAGAAATGTTTACGATTAGAGCTTGGCATTTA 1839  
Qy 1801 ACTGATGAATCAATGAAAGAAATTTGAAATGCGGTAGACTATGACATGTTCTCAAACTC 1860  
Db 1840 ACGGATGGATTTAAGCGAAATATTGAAACGCGGTGATATGACATGTTCTCTAAACTC 1899  
Qy 1861 AGTGAAGTGGAAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGTT 1920  
Db 1900 AGTGAAGTGGAAATTTAAACATCTTAATAAATCTGCTATAACCGGTATTACATGTT 1959  
Qy 1921 GATAACACATCAATTAAGAAATCTTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 1980  
Db 1960 GATAACACATCAATTAAGAAATCTGGCATTTCAAAAGAAAAACCATTTTGTGTAGTCAAT 2019  
Qy 1981 CAGTCATTAATAGACAGGCATCAATTTATTAATATGACGAATTTGATGATTTAGAT 2040  
Db 2020 CAGTCATTAATAGACAGGCATCAATTTATTAATATGACGAATTTGATGATTTAGAT 2079  
Qy 2041 GAACTAGAAAGTATATTTTCAATAAACCGCTGATATCAAGAGAGAGATTGATATCTTA 2100  
Db 2080 GAAAGTAGAAAGTATATCTTCAATAAACCGCTGATATCAAGAGAAATGATATGTTA 2139  
Qy 2101 AAAGATATTAATATCATCAGAAATAAGATGTCGCAAAATCGCAGTCAGTATTTTTTATCCC 2160  
Db 2140 AAAGATCTTAATCTCAATCAAAATAAGATGCCAAATCGCAGTCAGTATTTTTCTATCCC 2199  
Qy 2161 AATACTAAACCGCTTAGTGAAGAAATCAAACTAAACAATTTATTGAAATATAAATAATA 2220  
Db 2200 AATACTAAACCGCTTAGTGAAGAAATCTAAACAATTTATTGAAATATAAATAATA 2259  
Qy 2221 TTGCGTATTGTTCTACATGTTGATAGAAATCATCTTTACACCGAGATATCAAAAAAGAAATA 2280  
Db 2260 TTGCGTATTATTCTACATGTTGATAGAAATCATCTTTACACCGAGATATCAAAAAAGAAATA 2319

Qy 2281 CTAGCCTTTATCATATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340  
Db 2320 TTGCTTTCTATCATAGCACCAGTAGAATATTTTACTAAATATGACATCTCATATTAC 2379  
Qy 2341 ACAGAGTAATAGATTAAATAAAAAAGCTGAGCGCATTTAAAGTAAATATAATAAATTAAAGTCAG 2400  
Db 2380 ACAGAGTAATAGACTAAATAAAAAAGCTGAGGCACATTTAAAGTAAATATAATAAATTAAAGTCAG 2439  
Qy 2401 TTAATCTAAATTTGTGAATACATCAATTTTGTGAATATCATGACAGCCTATTTCGTTAAABAAT 2460  
Db 2440 TTAATCTAAATTTGTGAATACATCAATTTTGTGAATATCATGACAGCCTATTTCGTTAAABAAT 2499  
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATCTCGGCATGAATTTTCTCAGCATTTAACACAT 2520  
Db 2500 GACAGCTATGCTTATATGAAAAAATATGATCTCGGCATGAATTTTCTCAGCATTTAACACAT 2559  
Qy 2521 GATTGGATCGAGAAAAATCAATGCGCATCCACATTTTAAAAAGCTGATTTAAAAACCTATTATT 2580  
Db 2560 GATTGGATCGAGAAAAATCAATGCGCATCCACATTTTAAAAAGCTGATTTAAAAACCTATTATT 2619  
Qy 2581 AATGACATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGAGC 2640  
Db 2620 AATGACATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGAGC 2679  
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCATCACATCTTGCCAGTCA 2700  
Db 2680 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCATCACATCTTGCCAGTCA 2739  
Qy 2701 ATTGATAGTGTGCAGAAATATAACACTGAGGATATTTGGTTTCCAAATTTGCACCTTTTAATC 2760  
Db 2740 ATTGATAGTGTGCAGAAATATAACACTGAGGATATTTGGTTTCCAAATTTGCACCTTTTAATC 2799  
Qy 2761 TTAGAAAAAGAAAAACCGGCATGTATTTTAAATAACATCGACCCCTGACTTATATGCTTTGG 2820  
Db 2800 TTAGAAAAAGAAAAACCGGCATGTATTTTAAATAACATCGACCCCTGACTTATATGCTTTGG 2859  
Qy 2821 GAAAGAAATTTACATGAGCAAAATGAAACAAATTTGAAAGTCAAAAAAGAGGAGAAATATA 2880  
Db 2860 GAAAGAAATTTACATGAGCAAAATGAAACAAATTTGAAAGTCAAAAAAGAGGAGAAATATA 2919  
Qy 2881 CCTGTTAAACAAGTTTCATTTTAAATAGTATAACTCTATAAA 2920  
Db 2920 CCGTTAAACAAGTTTCATTTTAAATAGTATAACGCTATAAA 2959

## RESULT 14

US-10-642-248-20  
; Sequence 20, Application US/10642248  
; Publication No. US20040132143A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Jing, Wei  
; TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METH  
; TITLE OF INVENTION: MAKING AND USING SAME  
; FILE REFERENCE: 3554.097  
; CURRENT APPLICATION NUMBER: US/10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414

```
Qy 2341 ACAGTAATAGATTAAATAAAAACTGAGCGCAATTTAAGTAATATTAATAAATTAAGTCAG 2400
Db |||||||
Qy 2380 ACAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAATATTAATAAATTAAGTCAG 2439
Db |||||||
Qy 2401 TTAATCTAAATTGTGTAATCATCATTTTGTGTAATCATGACAGCCTATTTCGTTAAAAAT 2460
Db |||||||
Qy 2440 TTAATCTAAATTGTGTAATCATCATTTTGTGTAATCATGACAGCCTATTTCGTTAAAAAT 2499
Db |||||||
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGCGCATGAATTTCTGAGCAATTAACACAT 2520
Db |||||||
Qy 2500 GACAGCTATGCTTATATGAAAAAATATGATGCGCATGAATTTCTGAGCAATTAACACAT 2559
Db |||||||
Qy 2521 GATTGGAATCGAGAAATCAATGCGCATCCACCAATTTAAAAAGGCTCAATTAACCAATTTT 2580
Db |||||||
Qy 2560 GATTGGAATCGAGAAATCAATGCGCATCCACCAATTTAAAAAGGCTCAATTAACCAATTTT 2619
Db |||||||
Qy 2581 AATGACAATGACTTTAAAAAGTAAGATGTGAAGGGGCATCAAGGTATGTTTATGACG 2640
Db |||||||
Qy 2620 AATGACAATGACTTTAAAAAGTAAGATGTGAAGGGGCATCAAGGTATGTTTATGACG 2679
Db |||||||
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTAAAGAGTCATCACATCTGCGCAGTCA 2700
Db |||||||
Qy 2680 TATGCGCTAGCGCATGAGCTTCTGACGATTTAAAGAGTCATCACATCTGCGCAGTCA 2739
Db |||||||
Qy 2701 ATTGATAGTGTGCGAGAAATATAACATGAGGATATTTGGTTCCAAATTTGCACTTTTAATC 2760
Db |||||||
Qy 2740 ATTGATAGTGTGCGAGAAATATAACATGAGGATATTTGGTTCCAAATTTGCACTTTAATC 2799
Db |||||||
Qy 2761 TTAGAAAAGAAAAACCGGCCATGATTTTAAATAAACATCGACCCCTGACTTATATGCTTGG 2820
Db |||||||
Qy 2800 TTAGAAAAGAAAAACCGGCCATGATTTTAAATAAACATCGACCCCTGACTTATATGCTTGG 2859
Db |||||||
Qy 2821 GAACGAAATTTACATCGACAAATGACAAATTCGAAAGTCGAAAGGAGGAGGAAATATA 2880
Db |||||||
Qy 2860 GAACGAAATTTACATCGACAAATGACAAATTCGAAAGTCGAAAGGAGGAGGAAATATA 2919
Db |||||||
Qy 2881 CCTGTTAAAGTTTCATTTAATTAATAGTATTAATCTATAA 2920
Db |||||||
Qy 2920 CCCGTTAAAGTTTCATTTAATTAATAGTATTAACGCTATAA 2959
Db |||||||
```

RESULT 13  
US-11-042-530-1  
; Sequence 1, Application US/11042530  
; Publication No. US20050164984A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL L.  
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME  
; FILE REFERENCE: 4605.007  
; CURRENT APPLICATION NUMBER: US/11/042,530  
; CURRENT FILING DATE: 2005-01-24  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/842,484  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2979  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-042-530-1

Query Match 77.8%; Score 2271.2; DB 10; Length 2979;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;  
  
Qy 1 ATGTAATCATTTATCAGCAATTAAGCAATATTAACAGCAATGACTATCAATTTAGCACTC 60  
Db 61 ATGAATCATTTATCAGCAATTAAGCAATATTAACAGCAATGACTATGAATTTAGCACTC 120  
Qy 61 AAATTTATTTGAAAGTCGGCGAAATCTATGAGCGGAAATTTGTTGAATTTCAAAATTACC 120

```
Db |||||||
Qy 121 AAATTTATTTGAGAGTCTGCTGAAACCTACGGCGGAAAAATCGTTGAATTTCCAAATTTATC 180
Qy |||||||
Db 121 AAATGCAAGAAAAAATCTCTCAGCACATCTCTCTGTTAAATTCAGCACATCTCTCTGTTAAAT 180
Db |||||||
Qy 181 AAATGTAAGAAAAAATCTCTGACCAATTC-----TTATGTAAGT 219
Qy |||||||
Db 181 AAAGAAAGAAAAAGTCAATGTTTCGATAGTTCGTTAGATATTTGCAACACAACTGTTTACTT 240
Qy |||||||
Db 220 GAAGATAAAAAAACAAGTGTTCGATAGTCTATAGATATTCGCAACACACAGCTCTTACTT 279
Qy |||||||
Qy 241 TCCAAAGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300
Db |||||||
Qy 280 TCCAAAGTAAAAAATTTAACTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 339
Db |||||||
Qy 301 AAATTTGCTCACTCAGAGAAATCTGAAAAATCGGAGGTAAAGAGCGCTCGCCCTTTGTACCA 360
Db |||||||
Qy 340 AAATCTATCACTCGGAAAAAATCGAGNACGAGAAATCAGAAAGGTGGAACCTAGTACCC 399
Qy |||||||
Db 361 AAAGATTTTCCCAAAGATCTGTTTATAGCCCTTTTACCTGATCATGTTAATGATTTTACA 420
Qy |||||||
Db 400 AAAGATTTTCTTAAAGATCTGTTTCTGCTCCATTCGAGATCATGTTAATGATTTTACA 459
Qy |||||||
Qy 421 TGGTACAAAAAGGAAAAAAGACCTTGGCATTAACCTGAAACATCAACATGTTGTCCTT 480
Db |||||||
Qy 460 TGGTACAAAAATCGAAAAAAGCTTAGGTATAAAGCCTGTAATAAGAAATATCGGTCTT 519
Qy |||||||
Qy 481 TCTATTATCGTTACAAACATTCATCGACACGCAATTTATCGATTACATTAGCCTGTTTA 540
Db |||||||
Qy 520 TCTATTATTAATCTCACTAATTAATCGTAGCGGTATTTAGATATTAAGCTTAGCCTGTTG 579
Qy |||||||
Qy 541 GTAAACCAAAAAACACATTAACCGTTTGAAGTTATCGTGAAGATGTTAGTGTAGTACGAA 600
Db |||||||
Qy 580 GTCAATCAGAAAAAACAACCTACCATTTGAAGTCGTTGTCAGATGATGTTAGTAAAGAA 639
Qy |||||||
Qy 601 GATCTATCAAGGATCATTCGCCAATATGAATAAATTTGGATATTCGCTACGTCAGACAA 660
Db |||||||
Qy 640 AACTTACTTACCATTTGTCAAAAAATACGAAACAAACCTTGACATAAAGTATGTAAAGAA 699
Qy |||||||
Qy 661 AAAGATAACGGTTTCAAGCCAGTGCCTCGGAATATGGGATTTACGCTTAGCAAAAAATAT 720
Db |||||||
Qy 700 AAAGATTAAGATATCAATTTGTGTGAGTACGAAACCTTAGGTTACGTACAGCAAGTAT 759
Qy |||||||
Qy 721 GACTTTATGCGCTTATCTGATATCGGCGCAAAATCAATATGGGTTTCACTTTAT 780
Db |||||||
Qy 760 GATTTGCTCGATTTCTAGACTGCGATATGGCACCAACAAATTTATGGGTTCACTTTAT 819
Qy |||||||
Qy 781 GTTCAGAGCTATTAAGATGATGATTTAAACATCATTTGGTCCAAGAAATATACGAT 840
Db |||||||
Qy 820 CTTCAGAACTATTTAGAAACAATGATTTGTTTAAATTTGACCTAGAAAAATATGTTGAT 879
Qy |||||||
Qy 841 ACACAACATATTGACCCCAAAAGACTCTTAAATAACCGAGTTTGTCTTGAATCATTTACCA 900
Db |||||||
Qy 880 ACTCATTAATTTACCGCAGAAACAAATCTTAAAGTCCATATTTAAAGAACTACTACT 939
Qy |||||||
Qy 901 GAAGTGAAGAAACCAATTAATAGTGTTCGCGCAAAAGGGGAAAGCAAGTTCCTCGATGG 960
Db |||||||
Qy 940 GAACCCGCTACAAATAACAATCTCTCGATTACATCAAAAGGAAATATATCGTTGATGG 999
Qy |||||||
Qy 961 CGCTTAGAACAAATTCGAAAAAACAAGAAATCTCGCTTATCCGATTTCCGCTTTT 1020
Db |||||||
Qy 1000 AGATTAGAACATTTCAAAAAAACCAGTAATCTACGCTCTATGTGATTTCCGCTTTT 1059
Qy |||||||
Qy 1021 TTTGCGGCGGTATGTTGCTTTTCGCTAAAAAATGGCTTAAATAATCGGTTTCTTTGAT 1080
Db |||||||
Qy 1060 TTTGTCGGGTATGTTGATTTTCTAAAGAAATGGCTTAAATAAGTAGTGGTGGTTCGAT 1119
Qy |||||||
Qy 1081 GAGGAATTTAATCACTGGGTGGAAGAGATGTGGAATTTGGAATATCGCTTATTCGTTAC 1140
Db |||||||
Qy 1120 GAAGAAATTTAATCACTGGGGGGGAGAGATGAGAAATTTGGTTACAGATTTATTTGCCAAA 1179
Qy |||||||
Qy 1141 GGTAGTTTCTTTAAACACTATTGATGGCATTTATGCGCTTACCATCAAGAGCCACAGGTAAA 1200
Db |||||||
```

181 AAAAGTAAAGAAAACCTCGACCAATTC-----TTATGTAGT 219  
181 AAAGAAAGAAAAGTCAATGTTTGGCATAGTCGGTTAGATATATGCAACAACAACTGTACTT 240  
220 GAAGATAAAAANAACAGTGTGTGGATAGCTCATTTAGATATCGCAACACAGCTCTACTT 279  
241 TCCAACGTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAACGTTTAAAAAATAAATGG 300  
280 TCCAACGTAAAAAATTTAACTCTATCCGAATCAGAAAAAACAAGTTTAAAAAATAAATGG 339  
301 AAATGTCTCACTGAGAGAAATCTGAABAATCGGAGGTAAAGCGSTCGCCCTCTGTACCA 360  
340 AAACTCTATCACTGGGAAAAAATCGGAGAACGAGAAATCAGAAAGTGGAACTAGTACCC 399  
361 AAAGATTTTCCAAAGATCTGTTTTAGCGCTTTACCTGATCATGTTAAATGATTTTACA 420  
400 AAAGATTTTCTTAAGATCTTGTCTCTGCTCCATTTGCCAGATCATGTTAAATGATTTACA 459  
421 TGGTACAAAAGCGAAAAAGAACTTGGCATAAAAACCTGAAACATCAACATGTTGGTCTT 480  
460 TGGTACAAAATCGAAAAAAGCTTAGGTATAAAGCCCTGTAAATAAGAAATATCGGTCTT 519  
481 TCTATTATGTTTACAACATTCATCGAACCGCAATTTTATCGATTACATTTAGCCCTGTTTA 540  
520 TCTATTATTTATTCCTACATTTAATCGTAGCCGATTTTATAGATATAACGTTAGCCCTGTTG 579  
541 GTAAACCAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
580 GTCAATCAGAAAAAACAACCTACCCATTTGNAAGTCGTTGTTGCAAGATGATGTAAGGAA 639  
601 GATCTATCACCGATCATTTGCCAATATAGAAAAATAATTGGATATTTGCTACGTGAGACAA 660  
640 AACTTACTTACCATTTGTCABAAAAATACGAAACAAAACCTTGACATAAAGTATGTAAGACAA 699  
661 AAAGATACCGTTTTCAAGCCAGTCGCGCTCGAATATGGGATTTAGCTTAGCAAAATAT 720  
700 AAAGATTTAGGATATCAATTTGTGTGCGAGTCAGAAAACCTTAGGTTTACGTACAGCAAGTAT 759  
721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCCAATTTAGGTTTCATTTAT 780  
760 GATTTTGTCTCAATTTAGACTGCGATATGGCACCAACAATTTATGGTTCAATCTTAT 819  
781 GTTCAGAGCTATTAGAAGATGATATTTAAACAATCATTTGGTCCAAAGAAAATACATCGAT 840  
820 CTTCAGAGAACTATTAGAGACAATGATATGTTTTAAATTGGACCTAGAAAAATATGGAT 879  
841 ACACAACATATTGACCCAAAAGACTTCTTAATACGCGAGTTTGGTTGAATCATTTACCA 900  
880 ACTCATAATATTACCGCAGAACAAATTCCTTAAAGATCCCATATTTAATAGAAATCACATCCT 939  
901 GAAGTGAAAAACCAATAATAGTGTGGCGCAAAAGGGGAAGGAACAGTTTCTCTGGATTGG 960  
940 GAAACGGCTACAATAAACAATCTTCGATTAATCAAAAGGAAATATATCGTTGGATTGG 999  
961 CGCTTAGAAACAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCTTTCGCTTTT 1020  
1000 AGATTAGAACATTTCAAAAAAACCAGATAATCTAGCTATGTGATTTCTCCGTTTCGTTAT 1059  
1021 TTTGGCGGGTAATGTTGCTTTCGCTAAAAAATGSCATAAATAAATCCGGTTTCTTTGAT 1080  
1060 TTTGTTGCGGGTAATGTTGCAATTTCTAAAGAAATGSCATAAATAAAGTAGTTGGTTTCGAT 1119  
1081 GAGGAATTTAATCACTGGGGTGAGAGATGTGGAATTTGGATATCGCTTATTTCCGTTAC 1140  
1120 GAAGAAATTTAATCATTTGGGGGGCGGAAGATGTAGAAATTTGGTTACAGATTTATTTGCCAAA 1179  
1141 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCCCTACCATCAAGAGCCACCGGTAAA 1200  
1180 GGTGTTTCTTTCAGAGTAATTTGACGCGGAAATGGCCATCCATCAAGAAACCACTGGTAAA 1239  
1201 GAAATGAAACCGATCGTAGAGCGGGAAAAAATATTTACGCTCGATATTATGAGAGAAAG 1260

1240 GAAATGAAACAGAAACGGAAGCTGGTAAAAAGTATTACGCTTAAAAATTTGTGAAAGAAAAG 1299  
1261 GTCCCTTATATCTATAGAAAACCTTTTACCATAGAAATTCGCATATCAATAGAGTACCT 1320  
1300 GTACCTTACATCTATAGAAAGCTTTTACCATAGAAATTCACATATTCATAGAAATACCT 1359  
1321 TTAGTTTCAAAATTTATATCCAGCTTATAAATCTGTGCAAAATCTATATTCACAGTTTGCCTAGAT 1380  
1360 TTAGTTTCTATTTATATCCCGCTTATAAATCTGTGCNAATTTATATTCAAAGATGTGTAGAT 1419  
1381 AGTCACCTGAATCAGACTGTTTGTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1440  
1420 AGTCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1479  
1441 GATTAATACCTTTAGAGTGATCAATAAGCTTTTATGGTAAATATCTTAGGGTAGCATCATG 1500  
1480 GATAATACCTTTAGAGTGATCAATAAGCTTTTATGGTAAATATCTTAGGGTAGCATCATG 1539  
1501 TCTAAACCAAAATGCGGAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGGT 1560  
1540 TCTAAACCAAAATGCGGAAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGGT 1599  
1561 TATTACATTTGGCGAGTTTAGATTTAGATTTAGATTTATCTTGAGCCTGATGCAAGTTGAACTGTGT 1620  
1600 TATTACATTTGGCGAGTTTAGATTTAGATTTAGATTTATCTTGAGCCTGATGCAAGTTGAACTGTGT 1659  
1621 TTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTAAATAGAAACGTC 1680  
1660 TTAAAGAAATTTTAAAGATAAAAACGCTAGCTTGTGTTTATACCACTAAATAGAAACGTC 1719  
1681 AATCGGATGTGAGCTTAATCGCTAAATGCTTACAAATGCGCCAGAAATTTTACAGAGAAAAA 1740  
1720 AATCGGATGTGAGCTTAATCGCTAAATGCTTACAAATGCGCCAGAAATTTTACAGAGAAAAA 1779  
1741 CTCACAAACGCTATGATTTGCTCACCACCTTTAGAAATGTTTACAGATTTAGAGCTTTGGCATTTA 1800  
1780 CTCACAAACGCTATGATTTGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTTGGCATTTA 1839  
1801 ACTGATGATTTCAATGAAAAAATTTGAAATGCGCGTAGACTATGACATGTTCTCTCAACCTC 1860  
1840 ACGGATGATTTTAAACGAAAAATTTGAAACCGCGTGAATTTAGACATGTTCTCTTAAACCTC 1899  
1861 AGTGAAGTTGGAAAAATTTAAACATCTTAAATCTGCTATAACCGTGTATTACATGCT 1920  
1900 AGTGAAGTTGGAAAAATTTAAACATCTTAAATCTGCTATAACCGGATTTACATGCT 1959  
1921 GATAACACATCAATTTAAGAAACCTTGGCATTTCAAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
1960 GATAACACATCAATTTAAGAAACCTTGGCATTTCAAAAAGAAAAACCAATTTTGTGTAGTCAAT 2019  
1981 CAGTCATTTAAATAGACAAGGCATTAATTTATTAATTTATGAGCAATTTGATGATTTAGAT 2040  
2020 CAGTCATTTAAATAGACAAGGCATTAATTTATTAATTTATGACAAATTTGATGATTTAGAT 2079  
2041 GAAAGTGAAGATATTTTCAATAAAAACCGCTGAATATCAAGAGAGAGATTTGATATCTTTA 2100  
2080 GAAAGTGAAGATATTTTCAATAAAAACCGCTGAATATCAAGAGAGAAATTTGATATGTTA 2139  
2101 AAAGATATTTAAATCATCCAGAAATAAGATGCAAAAATGCGCAGTCAGTATTTTTTATCCC 2160  
2140 AAAGATCTTAACTCATTTCAAAATAAGATGCAAAAATGCGCAGTCAGTATTTTTTATCCC 2199  
2161 AATAATTTAAACCGCTTAGTGAATAAATACTAAACATATTTTGAATATTAATAAATAATA 2220  
2200 AATAATTTAAACCGCTTAGTGAATAAATACTAAACATATTTTGAATATTAATAAATAATA 2259  
2221 TTTGCTTATTTGTTCTACATGTTGATGAATCATCTTTACACAGATATCAAAAAGAAAAATA 2280  
2260 TTTGCTTATTTTCTACATGTTGATGAATCATCTTTACACAGATATCAAAAAGAAAAATA 2319  
2281 CTAGCCTTCTATCATATAAACATCAAGTGAATTTTTTCTAAATAATGATATCTCATATTAC 2340  
2320 TTGGCTTCTTATCATATAAGCACCAGTGAATATTTTACTATAATAATGACATCTCATATTAC 2379



Qy	1321	GTCCCTTATATCTATAGAAAAC	TTTACCAATAGAGANTTCCGATATCAATAGAGTACCT	1322
Db	1300	GTACCTTTACATCTATAGAAAGCT	TTTTACCAATAGAGANTTCAATATTCATAGAATAACCT	1359
Qy	1321	TTAGTGTTCAAATTTATATATCCCGCTT	TAACTGTGCAAACTATATTCCAACGTCGCGTAGAT	1380
Db	1360	TTAGTGTTCATTTATATATCCCGCTT	TAACTGTGCAAAATTTATATTCAAAGATGTGTAGAT	1419
Qy	1381	AGTGCACCTGAATCAGACTGT	TTGTGTCTCGAGGTTTGTATTTGTAAACGATGGTTCAAACA	1440
Db	1420	AGTGTCTTTAATCAAACTGT	TGTCGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAAACA	1479
Qy	1441	GATTAATACCTTAGAAGTGA	TCAATAAGCTTTATGGTAAATTAATCCTTAGGTTACGCATCATG	1500
Db	1480	GATAATACCTTAGAAGTGA	TCAATAAGCTTTATGGTAAATTAATCCTTAGGTTACGCATCATG	1539
Qy	1501	TCTAAACCAATGCGCAATAG	CTCAGCATCAAAATGCGCGCTTTCTTTTGTCTAAAGGT	1560
Db	1540	TCTAAACCAATGCGCGAATAG	CTCAGCATCAAAATGCGCGCTTTCTTTTGTCTAAAGGT	1599
Qy	1561	TATTACATTTGGCGAGTTAG	ATTACAGATGATTTATCTTGAGCCTGATGCAGTTGAATCTGTGT	1620
Db	1600	TATTACATTTGGCGAGTTAG	ATTACAGATGATTTATCTTGAGCCTGATGCAGTTGAATCTGTGT	1659
Qy	1621	TTAAAGAAATTTTAAAGATA	AAACCGCTAGCTTGTGTTATACCACTAATAGAAACGCTC	1680
Db	1660	TTAAAGAAATTTTAAAGATA	AAACCGCTAGCTTGTGTTATACCACTAATAGAAACGCTC	1719
Qy	1681	AATCCGGATGGTAGCTTAA	TTCGCTAAATGGTTTACAATGGCCAGCAATTTTCCACGAGAAAA	1740
Db	1720	AATCCGGATGGTAGCTTAA	TTCGCTAAATGGTTTACAATGGCCAGCAATTTTCCACGAGAAAA	1779
Qy	1741	CTCAACACGGCTATGAT	TGCTCACCATTTTAGAAATGTTTACAGATTAGAGCTTGGCATTTA	1800
Db	1780	CTCAACACGGCTATGAT	TGCTCACCATTTTAGAAATGTTTACAGATTAGAGCTTGGCATTTA	1839
Qy	1801	ACTGATGGAATCAATGAAAA	ATTTGAAAATGCGCTAGACTATGACATGTTTCTCAAACTC	1860
Db	1840	ACGGATGGATTTAACGAAAA	TATTTGAAAAATGCGCGTGGATTTATGACATGTTTCTTAAACTC	1899
Qy	1861	AGTGAAGTTCGAAAATTT	TAAACATCTTAAATAAAATCTGCTATACCCGTGTATTACATGGT	1920
Db	1900	AGTGAAGTTCGAAAATTT	TAAACATCTTAAATAAAATCTGCTATACCCGTGTATTACATGGT	1959
Qy	1921	GATAACACATCAATTAAG	AAACTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT	1980
Db	1960	GATAACACATCAATTAAG	AAACTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT	2019
Qy	1981	CAGTCATTTAAATAGACA	AGGCAATTTATTAATTTATGACAAATTTGATGATTAGAT	2040
Db	2020	CAGTCATTTAAATAGACA	AGGCAATTTATTAATTTATGACAAATTTGATGATTAGAT	2079
Qy	2041	GAAGTAGAAGTAGTATAT	TTTCAATAAAACCGCTCAATATCAAGAGAGAGATTGATATCTTA	2100
Db	2080	GAAGTAGAAGTAGTATAT	TTTCAATAAAACCGCTCAATATCAAGAGAGAGATTGATATCTTA	2139
Qy	2101	AAAGATATTTAAATCAT	CCAGATAAGATGCGCAAAATCGCAGTCAAGTATTTTCTATCCC	2160
Db	2140	AAAGATATTTAAATCAT	CCAGATAAGATGCGCAAAATCGCAGTCAAGTATTTTCTATCCC	2199
Qy	2161	AATACATTTAAACGGCT	TAGTGAAAAAACTTAAACAATTTATTTGAATATAATAAAAAATATA	2220
Db	2200	AATACATTTAAACGGCT	TAGTGAAAAAACTTAAACAATTTATTTGAATATAATAAAAAATATA	2259
Qy	2221	TTGCTTATTTGTTTACAT	GTGTTGATAAGAAATCATCTTTACACAGATATCAAAAAAGAAATA	2280
Db	2260	TTGCTTATTTTCTACAT	GTGTTGATAAGAAATCATCTTTACACAGATATCAAAAAAGAAATA	2319
Qy	2281	CTAGCCTCTATCATAA	ACATCAAGTGAATTTTTTACTTAATATGATATCTCATATTTAC	2340
Db	2320	TTGGCTTTTCTATCAT	AAGCAACAGTGAATTTTTTACTTAATATGATATCTCATATTTAC	2379
Qy	2341	ACGAGTAAATAGATTAA	TAAAAAACTGAGCGCATTTAAGTATATAATAATAATTAAGTCAG	2400

```

RESULT 12
US-10-184-485-4
; Sequence 4, Application US/10184485
; Publication No. US2003007763A1
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCE: 5820.551
; CURRENT APPLICATION NUMBER: US/10/184.485
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US/09/437,277
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 4
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-10-184-485-4

```

	Query Match	77.8%	Score 2271.2;	DB 5;	Length 2979;
	Best Local Similarity	86.5%;	Pred. No. 0;		
	Matches 2526;	Conservative 0;	Mismatches 373;	Indels 21;	Gaps 1;
QY	1	ATGAATACATTATCACAAGCAATAAAGCATATATAACAGCATGACTATCAATTAGCACTC	60		
Dd	61	ATGAATACATTATCACAAGCAATAAAGCATATATAACAGCATGACTATGAATTAGCACTC	120		
QY	61	AAATTTATTCGAAAAGTCGGCGGAANTCTATGAGCGGAAAAATTTGTGAATTTCAAATTTACC	120		
Dd	121	AAATTTATTCGAAAAGTCGTCTGAACCTACGGGGCAAAAATCGTTGAATTTCCAAATTTATC	180		
OY	121	AAATGCAGAAAGAAAACCTCTCAGCACATCTTCTGTTTAATTACGACCATCTTTTCTGTAAT	180		

```
QY 2401 TTAATCTAAATGTGAATACATCAATTTTGTGATATCATGACAGCCTATTGGTTAAAAAT 2460
Db 2401 TTAATCTAAATGTGAATACATCAATTTTGTGATATCATGACAGCCTATTGGTTAAAAAT 2460
QY 2461 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAACACAT 2520
Db 2461 GACAGCTATGCTTATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAACACAT 2520
QY 2521 GATTGGATCGAGAAAATCAATCGGCATCCACCATTTAAAAAGCTCATTTAAATCTTATTTT 2580
Db 2521 GATTGGATCGAGAAAATCAATCGGCATCCACCATTTAAAAAGCTCATTTAAATCTTATTTT 2580
QY 2581 AATGCAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGATATGTTTATGACG 2640
Db 2581 AATGCAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGATATGTTTATGACG 2640
QY 2641 TATGCGCTAGCGCATGAGCTTCTGAGGATTTTAAAGAAAGTCAATCAATCTTGGCAGTCA 2700
Db 2641 TATGCGCTAGCGCATGAGCTTCTGAGGATTTTAAAGAAAGTCAATCAATCTTGGCAGTCA 2700
QY 2701 ATTGATAGTGTGCCAGATATTAACACTGAGGATATTTGGTTCCTCAATTTGCACTTTTAAATC 2760
Db 2701 ATTGATAGTGTGCCAGATATTAACACTGAGGATATTTGGTTCCTCAATTTGCACTTTTAAATC 2760
QY 2761 TTAGAAAAAGAAACCGGCCATGTATTTAATAAAAAATCATGCCCTGACTTATATGCTTTGG 2820
Db 2761 TTAGAAAAAGAAACCGGCCATGTATTTAATAAAAAATCATGCCCTGACTTATATGCTTTGG 2820
QY 2821 GAACGAAATTAACATGGCAATGAACAAATTTGAAAGTGCAAAAGAGAGAGAAATATA 2880
Db 2821 GAACGAAATTAACATGGCAATGAACAAATTTGAAAGTGCAAAAGAGAGAGAAATATA 2880
QY 2881 CCTGTTAAACAGTTCAATTATTAATAGTATAACTCTA 2916
Db 2881 CCTGTTAAACAGTTCAATTATTAATAGTATAACTCTA 2916

RESULT 11
US-09-842-484A-1
; Sequence 1, Application US/09842484A
; Publication No. US20030104601A1
; GENERAL INFORMATION:
; APPLICANT: DEANGELIS, PAUL L.
; TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 4605.003
; CURRENT APPLICATION NUMBER: US/09/842,484A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-842-484A-1

Query Match 77.8%; Score 2271.2; DB 3; Length 2979;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2526; Conservative 0; Mismatches 373; Indels 21; Gaps 1;

QY 1 ATGAATACATTATCACAGCAATATAAGCATATAACAGCAATGACTATCAATTAGCAGCTC 60
Db 61 ATGAATACATTATCACAGCAATATAAGCATATAACAGCAATGACTATGAATTAGCAGCTC 120
QY 61 AAATTTTGAAGTCGCGGAAAATCTATGACGGAAAATTTGTAATTTCAAATTAACC 120
Db 121 AAATTTTGAAGTCGCTGAAAACCTACGGCGGAAAATTCGTTGAATTTCCAAATTAATC 180
QY 121 AATGCAAGAAAACCTCTCAGACATCTTCTGTTAATTCAGCACATCTTTCTGTTAAAT 180
Db 181 AATGTAAGAAAACCTCTCGAACATTC-----TTATGTAAGT 219
```

```
QY 181 AAAGAAAGAAAAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACAACTGTACTT 240
Db 220 GAAGATATAAAAAACAGTGTGCGTAGCTCATTAGATATCGCAACACAGCTCTTACTT 279
QY 241 TCCAACGTAAAAAAATTAGTACTTTCTGACTCGGAAAAAAAACAGTTTAAAAAATAAATGG 300
Db 280 TCCAACGTAAAAAAATTAACCTCTATCCGAATCAGAAAAAAAACAGTTTAAAAAATAAATGG 339
QY 301 AAATTGCTCAGTGAAGAAATCTGAAAAATCGGAGGTAAAGCGGTCCGCTTGTATCCA 360
Db 340 AAATCTATCACTCGGAAAAAATCGGAGAACCGAGAAATCAGAAAAAGGTGGAACCTAGTACCC 399
QY 361 AAAGATTTTCCCAAGAGTCTGTTTTAGCGCTTTTACCTGATCATGTTAAATGATTTTACA 420
Db 400 AAAGATTTTCTTAAGATCTTTGTTCTTGCTCATTTGCCAGATCATGTTAAATGATTTTACA 459
QY 421 TGGTACAAAAAGCGAAAAGAAAGACTTTGGCATATAAACTGAAACATCAACATGTTGGTCTT 480
Db 460 TGGTACAAAAATCGAAAAAAAAGCTTAGGTATAAAGCCTGTAAATAAGAAATATCGGTCTT 519
QY 481 TCTATTATCGTTTACAAATTCATTCGACCAGCAATTTTATCGATTTACATTTAGCTTGTATA 540
Db 520 TCTATTATTTCTTACATTTTAAATCGTAGCCGTATTTTAGATATATAACGTTAGCCTGTTG 579
QY 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600
Db 580 GTCAATCAGAAAAACAACTACCCATTTGAAAGTCTGTTGTGAGATGATGGTAGTAAGGAA 639
QY 601 GATCTATCACCGATCATTTCCGCAATATATGAAATATAAATTTGGATATTTCCGTCAGTCA 660
Db 640 AACTTACTTACCATTTGTGCAAAAATACGAAACAAAAAATTTGACATAAAGTATGTAAAGACA 699
QY 661 AAAGATAACGGTTTCAAGCCAGTCCCGCTCGGAATATGGGATTTAGCTTAGCAAAATAT 720
Db 700 AAAGATTTATGGATATCAATTTGTGTCAGTCAAGAACTTAGCTTTACGTACAGCAAAAGTAT 759
QY 721 GACTTTATTTGGCTTACTCGACTGTGATATGCGCCAAAATCCATTTAGGTTTCATTTCTTAT 780
Db 760 GATTTTGTCTCGATTTCTAGCTGCGATATGGCACCACAAATTTAGGTTTCATTTCTTAT 819
QY 781 GTTGACAGAGCTATTAGAAAGATGATGATTTAAACAATCATTTGGTCCAGAAAAATACATCGAT 840
Db 820 CTTACAGAACTATTAGAGACAATGATATGTTTTAAATTTGGACCTAGAAAAATATGTGGAT 879
QY 841 ACACAAATATTGACCCAAAAGACTTCTTTAAATAACGGAGTTTCTCTGAAATCAATFACCA 900
Db 880 ACTCATATAATTACCGCAGAACAAATTCCTTTACGATCCATATTTTAAATAGAATCAGTACCT 939
QY 901 GAAGTGAAAAACCAATAATAGTGTTCGCCCAAAAGGGGAGGAAACAGTTTCTCTGGAATCGG 960
Db 940 GAAACCGGTACAAAATAACAATCCITTCGATTTACATCAAAAGGAAATATATCTGTTGATTCG 999
QY 961 CGCTTTAGAACAAATTCGAAAAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTTCCGTTT 1020
Db 1000 AGATTTAGAACATTTCAAAAAAACCGATATCTACGCTATGTGATTTCTCGGTTCTGTTAT 1059
QY 1021 TTTGCGGCGGGTAAATGTTGCTTTCCTTAAAAATGGCTTAAATTAATTCGCGTTTCTTTGAT 1080
Db 1060 TTTGTTGCGGGTAAATGTTGCTATTTTCTAAAGAAATGGCTTAAATAAGTAGTGGTTGGTTCGAT 1119
QY 1081 GAGGAATTTAATCACTGGGTGAGAGATGTTGGAATTTTGGATATCGCTTTATTTCCGTTAC 1140
Db 1120 GAAGAAATTTAATCATTTGGGGGGGGAAGATGAGAAATTTGGTTCAGATATTTTGGCAAA 1179
QY 1141 GGTAGTTTCTTTAAAAACTATTGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200
Db 1180 GGCTGTTTTTTCAGAGTAATTTGACGGCGGAATGGCCATCCATCAAGAACCACTGGTAAA 1239
QY 1201 GAAAAATGAAACCGATCGTGAAGCGGAAAAAATATTTACGCTCGATATTTATGAGAGAAAAG 1260
Db 1240 GAAAAATGAAACAGAACCGGAAGCTGTGTAAGAGTATTACGCTTTAAAAATTTGTAAGAAAAG 1299
```

181 AAAGAGAAAGAGTCAATGTTTGGATAGTCCGTTAGATATTGCAACACAGTGTACTT 240  
241 TCCAAAGTAAAGAAATAGTACTTCTGACCTCGGAAAGAAACACGTTAAAGAAATAGG 300  
241 TCCAAAGTAAAGAAATAGTACTTCTGACCTCGGAAAGAAACACGTTAAAGAAATAGG 300  
301 AAATTTGCTCAGTGAAGAGAAATCTGAAATTCGCGAGGTAGAGCGGTGCGCTTGTACCA 360  
301 AAATTTGCTCAGTGAAGAGAAATCTGAAATTCGCGAGGTAGAGCGGTGCGCTTGTACCA 360  
361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
421 TGGTCAAAAAAGCGAAAGAAAGACTTGGCATATAAAACCTGAAACATCAACATGTTGGTCTT 480  
421 TGGTCAAAAAAGCGAAAGAAAGACTTGGCATATAAAACCTGAAACATCAACATGTTGGTCTT 480  
481 TCTATTATCGTTACAAACATTCATCGACCGCAATTTTATCGATTACATTAGCCCTGTTTA 540  
481 TCTATTATCGTTACAAACATTCATCGACCGCAATTTTATCGATTACATTAGCCCTGTTTA 540  
541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
601 GATCTATCACCGGATCATTCGGCAATATGAAATATAAATTTGGATATTCGCTAGTCAGACAA 660  
601 GATCTATCACCGGATCATTCGGCAATATGAAATATAAATTTGGATATTCGCTAGTCAGACAA 660  
661 AAAGATACCGTTTCAAGCCAGTGCCTCGGAATATGGGATATGGGATATGGGATATGGGATAT 720  
661 AAAGATACCGTTTCAAGCCAGTGCCTCGGAATATGGGATATGGGATATGGGATATGGGATAT 720  
721 GACTTTATGGCTTACTCGACTGTGATATGCGCAAAATCCATTATGGGTTTCACTTTAT 780  
721 GACTTTATGGCTTACTCGACTGTGATATGCGCAAAATCCATTATGGGTTTCACTTTAT 780  
781 GTTCAGAGCTATTAGAAAGATGATGATTTAAACATCATTTGTTGTCGAAAGAAATACATCGAT 840  
781 GTTCAGAGCTATTAGAAAGATGATGATTTAAACATCATTTGTTGTCGAAAGAAATACATCGAT 840  
841 ACACAAACATATTGACCCAAAGACTTCTTAATTAACCGAGTTGCTTGAATCATTACCA 900  
841 ACACAAACATATTGACCCAAAGACTTCTTAATTAACCGAGTTGCTTGAATCATTACCA 900  
901 GAAGTGAAGAACCAATAATAGTGTTCGCGCAAAAGGGAGGAAACAGTTTCTCTGGATTGG 960  
901 GAAGTGAAGAACCAATAATAGTGTTCGCGCAAAAGGGAGGAAACAGTTTCTCTGGATTGG 960  
961 CGCTTAGAACCAATTCGAAAGAACAGAAATCTCGCTTATCCGATTCGCTTTTCGCTTTT 1020  
961 CGCTTAGAACCAATTCGAAAGAACAGAAATCTCGCTTATCCGATTCGCTTTTCGCTTTT 1020  
1021 TTTGCGGCGGTAAATGTTGCTTTCGCTAAAGATGGCTAAATTAATCCGTTTCTTTGAT 1080  
1021 TTTGCGGCGGTAAATGTTGCTTTCGCTAAAGATGGCTAAATTAATCCGTTTCTTTGAT 1080  
1081 GAGGAATTTAATCACTCGGGTGGAGAAATGTGGAATTTGGATATCGCTTATTCGTTTAC 1140  
1081 GAGGAATTTAATCACTCGGGTGGAGAAATGTGGAATTTGGATATCGCTTATTCGTTTAC 1140  
1141 GGTAGTTTCTTTAAAGTATTGATGGCAATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200  
1141 GGTAGTTTCTTTAAAGTATTGATGGCAATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200  
1201 GAAATGAACCGATCGTGAAGCGGAAAGAAATATTAAGCTCGATTTATGAGAGAAAG 1260  
1201 GAAATGAACCGATCGTGAAGCGGAAAGAAATATTAAGCTCGATTTATGAGAGAAAG 1260  
1261 GTCCCTTATATCTATAGAAACCTTTTACCAATPAGAAAGTTCCGATATCAATAGAGTACCT 1320

1261 GTCCCTTATATCTATAGAAACCTTTTACCAATPAGAAAGTTCCGATATCAATAGAGTACCT 1320  
1321 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAAACGCTGCGTAGAT 1380  
1321 TTAGTTTCAATTTATATCCAGCTTATACTGTGCAAACTATATTCAAACGCTGCGTAGAT 1380  
1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTGTTATTTGTAACGATGGTTCAACA 1440  
1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTGTTATTTGTAACGATGGTTCAACA 1440  
1441 GATAATACCTTAGAAGTGATCAATAGCTTTATGGTAAATACTCTAGGGTACCCATCATG 1500  
1441 GATAATACCTTAGAAGTGATCAATAGCTTTATGGTAAATACTCTAGGGTACCCATCATG 1500  
1501 TCTAAACCAANTGCGGAATAGCTCAGCATCAAAATGCGAGCGTTCTTTTGTCTAAAGGT 1560  
1501 TCTAAACCAANTGCGGAATAGCTCAGCATCAAAATGCGAGCGTTCTTTTGTCTAAAGGT 1560  
1561 TATTACATTTGGGCGAGTTAGATTTCAGATGATTATCTTTGAGCCTGATGCGATTGAACCTGT 1620  
1561 TATTACATTTGGGCGAGTTAGATTTCAGATGATTATCTTTGAGCCTGATGCGATTGAACCTGT 1620  
1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTGTTGTTTATACCACTAATAGAAACGTC 1680  
1621 TTTAAAGAAATTTTAAAGATAAAACGCTAGCTGTTGTTTATACCACTAATAGAAACGTC 1680  
1681 AATCCGATGCTAGCTTAATCGCTTAATGTTTACAATTTGGCCAGAAATTTTCAAGAGAAAA 1740  
1681 AATCCGATGCTAGCTTAATCGCTTAATGTTTACAATTTGGCCAGAAATTTTCAAGAGAAAA 1740  
1741 CTCAACACGGCTATGATTTGCTCACCATTGTTAGAAATGTTTACGATTAGAGCTTGGCATTTA 1800  
1741 CTCAACACGGCTATGATTTGCTCACCATTGTTAGAAATGTTTACGATTAGAGCTTGGCATTTA 1800  
1801 ACTGATGGATCAATGAAGAAATTTGAAATGCGGTAGACTATGACATGTTTCTTCAAACTC 1860  
1801 ACTGATGGATCAATGAAGAAATTTGAAATGCGGTAGACTATGACATGTTTCTTCAAACTC 1860  
1861 AGTGAAGTTCGAAATTTTAAACATCTTAATAAATCTGCTATAACCGGTGATTACATGGT 1920  
1861 AGTGAAGTTCGAAATTTTAAACATCTTAATAAATCTGCTATAACCGGTGATTACATGGT 1920  
1921 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
1921 GATAACACATCAATTAAGAAACTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
1981 CAGTCATTAATAGACAAGGCATAAATTATATAATTTATGACGAAATTTGATTTAGAT 2040  
1981 CAGTCATTAATAGACAAGGCATAAATTATATAATTTATGACGAAATTTGATTTAGAT 2040  
2041 GAAAGTAGAAGTATATTTTCAATATAAACCGCTGAATATCAAGAAAGAGATTGATATCTTA 2100  
2041 GAAAGTAGAAGTATATTTTCAATATAAACCGCTGAATATCAAGAAAGAGATTGATATCTTA 2100  
2101 AAAGATATTAATATCATCCAGAAATAAGATGCGCAAAATCGCAGTCAGTATTTTATATCCC 2160  
2101 AAAGATATTAATATCATCCAGAAATAAGATGCGCAAAATCGCAGTCAGTATTTTATATCCC 2160  
2161 AATACATTAACCGCTTAGTGAAAAAACTAAACATATTTATGAAATATAAATAAATA 2220  
2161 AATACATTAACCGCTTAGTGAAAAAACTAAACATATTTATGAAATATAAATAAATA 2220  
2221 TTCGTTATGTTCTACATGTTGATAAGAAATCATCTTACACCGAGATATCAAAAAAGAAATA 2280  
2221 TTCGTTATGTTCTACATGTTGATAAGAAATCATCTTACACCGAGATATCAAAAAAGAAATA 2280  
2281 CTAGCTTCTATCATAAACATCAAGTGAATTTTACTAAATAATGATATCTCATATTTAC 2340  
2281 CTAGCTTCTATCATAAACATCAAGTGAATTTTACTAAATAATGATATCTCATATTTAC 2340  
2341 ACGAGTAAATAGATTAATAAATACTGAGCGGCAATTTAAGTGAATATAATAAATTAAGTCAG 2400  
2341 ACGAGTAAATAGATTAATAAATACTGAGCGGCAATTTAAGTGAATATAATAAATTAAGTCAG 2400

1381 AGTCGACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAACGATGGTTCAACA 1440  
Db |  
1381 AGTCGACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTAACGATGGTTCAACA 1440  
Qy |  
1441 GATAATACCTTAGAAGTGAATCAATAGCTTTTATGGTAAATAATCCTAGGGTAGCGATCATG 1500  
Db |  
1441 GATAATACCTTAGAAGTGAATCAATAGCTTTTATGGTAAATAATCCTAGGGTAGCGATCATG 1500  
Qy |  
1501 TCTAAACCAAATGGCGGAATACGCTCAGCATCAAAATGACGCGGTTCTTTTGTCTAAAGGT 1560  
Db |  
1501 TCTAAACCAAATGGCGGAATACGCTCAGCATCAAAATGACGCGGTTCTTTTGTCTAAAGGT 1560  
Qy |  
1561 TATTACATTTGGCGAGTTAGATTCAGATGATTAATCTTGAGCCCTGATGCAATCTGTGT 1620  
Db |  
1561 TATTACATTTGGCGAGTTAGATTCAGATGATTAATCTTGAGCCCTGATGCAATCTGTGT 1620  
Qy |  
1621 TTAAGAAGATTTTAAAGATATAAAGCGTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
Db |  
1621 TTAAGAAGATTTTAAAGATATAAAGCGTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
Qy |  
1681 AATCCGGATGGTAGCTTAATCGCTAATGCTTAACTGCTTCAAAATGGCCAGAAATTTTCACGAGAAAA 1740  
Db |  
1681 AATCCGGATGGTAGCTTAATCGCTAATGCTTAACTGCTTCAAAATGGCCAGAAATTTTCACGAGAAAA 1740  
Qy |  
1741 CTCACAAACGCTATGATGCTCACCACTTTAGAAATGCTTACAGATTTAGAGCTTGGCATTTA 1800  
Db |  
1741 CTCACAAACGCTATGATGCTCACCACTTTAGAAATGCTTACAGATTTAGAGCTTGGCATTTA 1800  
Qy |  
1801 ACTGATGGATTCAAATGAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCAAACTC 1860  
Db |  
1801 ACTGATGGATTCAAATGAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCAAACTC 1860  
Qy |  
1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAAACCGGTATTACATGGT 1920  
Db |  
1861 AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAAACCGGTATTACATGGT 1920  
Qy |  
1921 GATAACACATCAATTAAGAAAACTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Db |  
1921 GATAACACATCAATTAAGAAAACTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Qy |  
1981 CAGTCATTAATAGACAAGCATAACTTATTATAATTTATGACGAATTTGATGATTTAGAT 2040  
Db |  
1981 CAGTCATTAATAGACAAGCATAACTTATTATAATTTATGACGAATTTGATGATTTAGAT 2040  
Qy |  
2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100  
Db |  
2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAAGAGATTGATATCTTA 2100  
Qy |  
2101 AAGATATTAATAATCATCCAGAAATAAGATGCCAAAATCGCAGTCAAGTATTTTATCCG 2160  
Db |  
2101 AAGATATTAATAATCATCCAGAAATAAGATGCCAAAATCGCAGTCAAGTATTTTATCCG 2160  
Qy |  
2161 AATACATTAACCGCTTAGTGAATAAACTTAACAATATTATTGAATATAATAAAATATA 2220  
Db |  
2161 AATACATTAACCGCTTAGTGAATAAACTTAACAATATTATTGAATATAATAAAATATA 2220  
Qy |  
2221 TTGCTTATTTGTTCTACATGTTTGAATAAGATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
Db |  
2221 TTGCTTATTTGTTCTACATGTTTGAATAAGATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
Qy |  
2281 CTAGCCCTTCTATCAATAACATCAAGTGAATTTTTTACTAAATATGATATCTCATATTAC 2340  
Db |  
2281 CTAGCCCTTCTATCAATAACATCAAGTGAATTTTTTACTAAATATGATATCTCATATTAC 2340  
Qy |  
2341 ACAGATTAATAGATTAATAAACTGAGGCGCATTTAAGTAATATTAAATAAAGTCAAG 2400  
Db |  
2341 ACAGATTAATAGATTAATAAACTGAGGCGCATTTAAGTAATATTAAATAAAGTCAAG 2400  
Qy |  
2401 TTAATCTAAATTTGTAATACATCATTTTTTGTAAATCATGACAGCCTATTTCGTTAAAAAT 2460  
Db |  
2401 TTAATCTAAATTTGTAATACATCATTTTTTGTAAATCATGACAGCCTATTTCGTTAAAAAT 2460

2461 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAACACAT 2520  
Db |  
2461 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAACACAT 2520  
Qy |  
2521 GATTGGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAGACTCATTTAAACCTTATTTT 2580  
Db |  
2521 GATTGGATCGAGAAAAATCAATGCGCATCCACCATTTTAAAGACTCATTTAAACCTTATTTT 2580  
Qy |  
2581 AATGACATGACTTTAAAGAGTATGAATGTGAAGGGGCATCAAGAGGTATGTTTATGACG 2640  
Db |  
2581 AATGACATGACTTTAAAGAGTATGAATGTGAAGGGGCATCAAGAGGTATGTTTATGACG 2640  
Qy |  
2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAAGTCAATCTTGGCAGTCA 2700  
Db |  
2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTATTAAGAAAGTCAATCTTGGCAGTCA 2700  
Qy |  
2701 ATTGATAGTGTGCGAGAAATATAACA CTGAGGATATTTGGTCCAAATTTGCACTTTTAATC 2760  
Db |  
2701 ATTGATAGTGTGCGAGAAATATAACA CTGAGGATATTTGGTCCAAATTTGCACTTTTAATC 2760  
Qy |  
2761 TTAGAAAAGAAAACCGGCCATGTTTAAATAAAACATCGACCTGACTTATATGCTTTGG 2820  
Db |  
2761 TTAGAAAAGAAAACCGGCCATGTTTAAATAAAACATCGACCTGACTTATATGCTTTGG 2820  
Qy |  
2821 GAAAGAAAATTTACAAATGACAAATGAACAAATTTGAAAGTGCAAAAGAGGAGAAATATA 2880  
Db |  
2821 GAAAGAAAATTTACAAATGACAAATGAACAAATTTGAAAGTGCAAAAGAGGAGAAATATA 2880  
Qy |  
2881 CCTGTTAAACAAGTTCATTTTAAATAGTATAACTCTA 2916  
Db |  
2881 CCTGTTAAACAAGTTCATTTTAAATAGTATAACTCTA 2916

RESULT 10  
US-11-096-190-8  
; Sequence 8, Application US/11096190  
; Publication No. US20050221446A1  
; GENERAL INFORMATION:  
; APPLICANT: Widner, William  
; APPLICANT: Sloma, Alan  
; APPLICANT: Thomas, Michael D.  
; APPLICANT: Tang, Maria  
; TITLE OF INVENTION: Methods For Producing A Hyaluronic Acid In A Bacillus Cell  
; FILE REFERENCE: 10596.200-US  
; CURRENT FILING DATE: 2005-03-31  
; PRIOR FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-096-190-8

Query Match 99.8%; Score 2914.4; DB 10; Length 2916;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGATAACATATATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
Db 1 ATGATAACATATATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60  
Qy 61 AAATATTATTGAAAAGTCGCGGAAATCTATGGAACGGAATAATTTGTAATTTCAATTTACC 120  
Db 61 AAATATTATTGAAAAGTCGCGGAAATCTATGGAACGGAATAATTTGTAATTTCAATTTACC 120  
Qy 121 AAATGCAAGAAAACTCTCAGCACATCTCTCTGTTTAATTCAGCACATCTTTCTGTAAT 180  
Db 121 AAATGCAAGAAAACTCTCAGCACATCTCTCTGTTTAATTCAGCACATCTTTCTGTAAT 180  
Qy 181 AAAGAGAAAAAGTCAATGTTTGGCATAGTCGCTTAGATATATTGCAACACAACTGTTCATT 240

```
2641 QY TATGGCTAGCGCATGAGCTTCTGACGATTATTAAAGAGTCATCACATCTTGCCAGTCA 2700
2659 Db TATGGCTAGCGCATGAGCTTCTGACGATTATTAAAGAGTCATCACATCTTGCCAGTCA 2718
2701 QY ATTGATAGTGGCAGAGATATAACACACTGAGGATATTTGGTTCCAAATTGCACTTTTAATC 2760
2719 Db ATTGATAGTGGCAGAGATATAACACACTGAGGATATTTGGTTCCAAATTGCACTTTTAATC 2778
2761 QY TTAGAAAAGAAAACCGGCCATGTATTTAATAAATCGACCTTGACTTATATGCTTGG 2820
2779 Db TTAGAAAAGAAAACCGGCCATGTATTTAATAAATCGACCTTGACTTATATGCTTGG 2838
2821 QY GAACGAAATTTACAAATGACACAAATGAAACAAATTCGAAAGTGCAGAAAGAGGAGAAAATATA 2880
2839 Db GAACGAAATTTACAAATGACACAAATGAAACAAATTCGAAAGTGCAGAAAGAGGAGAAAATATA 2898
2881 QY CCTGTTAACAGTTTCATTATTAATAGTATATACTCTATAA 2919
2899 Db CCTGTTAACAGTTTCATTATTAATAGTATATACTCTATAA 2937

RESULT 9
US-10-326-185-94
; Sequence 94, Application US/10326185
; Publication No. US20030175902A1
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan
; APPLICANT: Behr, Regine
; APPLICANT: Widner, William
; APPLICANT: Tang, Maria
; APPLICANT: Sternberg, David
; APPLICANT: Brown, Stephen
; TITLE OF INVENTION: Methods for Producing Hyaluronan In a Recombinant Host Cell
; FILE REFERENCE: 10241.200-US
; CURRENT APPLICATION NUMBER: US/10/326.185
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/342,644
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 94
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2916)
; OTHER INFORMATION:
US-10-326-185-94

Query Match 99.8%; Score 2914.4; DB 6; Length 2916;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATACATTTATCAACAGCAATTAACGATATTAACGCAATGACTATCAATTAGCACTC 60
Db 1 ATGATACATTTATCAACAGCAATTAACGATATTAACGCAATGACTATCAATTAGCACTC 60
QY 61 AAATTTATTTGAAAGTCGCGGAAATCTATGGACGGAATTTGTTGAATTTCAAATTACC 120
Db 61 AAATTTATTTGAAAGTCGCGGAAATCTATGGACGGAATTTGTTGAATTTCAAATTACC 120
QY 121 AAATGCAAGAAAACCTCTCAGACATCCTTCTGTGTAATTCAGACATCTTCTGTAAAT 180
Db 121 AAATGCCAAGAAAACCTCTCAGACATCCTTCTGTGTAATTCAGACATCTTCTGTAAAT 180
QY 181 AAAGAGAAAAGTCAATGTTTGGATAGTCGTTAGATATTTGCAACACACTGTTACTT 240
Db 181 AAAGAGAAAAGTCAATGTTTGGATAGTCGTTAGATATTTGCAACACACTGTTACTT 240
QY 241 TCCAAAGTAAAAAAATTTAGTACTTCTGACTCGGAAAAAACACCGTTAAAAAATAAATGG 300
Db 241 TCCAAAGTAAAAAAATTTAGTACTTCTGACTCGGAAAAAACACCGTTAAAAAATAAATGG 300

241 TCCAAAGTAAAAAAATTTAGTACTTCTGACTCGGAAAAAACACCGTTAAAAAATAAATGG 300
301 AAATTTGCTCACTCAGAGAAATCTGAAATTCGGAGGTAGAGCGGTGCGCCCTTGTACCA 360
301 AAATTTGCTCACTCAGAGAAATCTGAAATTCGGAGGTAGAGCGGTGCGCCCTTGTACCA 360
361 AAAGATTTTCCCAAGATCTGGTTTATAGGCGCTTTACCTGATCATGTTAATGATTTTACA 420
361 AAAGATTTTCCCAAGATCTGGTTTATAGGCGCTTTACCTGATCATGTTAATGATTTTACA 420
421 TGGTACAAAAGCGGAAAGAAAGACCTTGGCATAAAACCTTGAAATCAATCAACATGTTGGTCTT 480
421 TGGTACAAAAGCGGAAAGAAAGACCTTGGCATAAAACCTTGAAATCAATCAACATGTTGGTCTT 480
481 TCTATTATCGTTACAAATTCATTCGACACAGCAATTTTATCGGATTACATTAGCTGTTTAA 540
481 TCTATTATCGTTACAAATTCATTCGACACAGCAATTTTATCGGATTACATTAGCTGTTTAA 540
541 GTAAACCAAAAAACACATTACCGTTTGAAGTTTATCGTGACAGATGATGTTAGTCAGGAA 600
541 GTAAACCAAAAAACACATTACCGTTTGAAGTTTATCGTGACAGATGATGTTAGTCAGGAA 600
601 GATCTATCACCGATCATTCGCCAATATGAAATTAATTTGGATATTCGCTACGTCAGACAA 660
601 GATCTATCACCGATCATTCGCCAATATGAAATTAATTTGGATATTCGCTACGTCAGACAA 660
661 AAAGATAACCGTTTTCAGGCCAGTGGCGCTCGGAATATGGAATTCGCTTAGCAAAATAT 720
661 AAAGATAACCGTTTTCAGGCCAGTGGCGCTCGGAATATGGAATTCGCTTAGCAAAATAT 720
721 GACTTTATTTGGCTTACTCGACTGTGATATGCGGCCAAATCCATTTATGGGTTCACTTTAT 780
721 GACTTTATTTGGCTTACTCGACTGTGATATGCGGCCAAATCCATTTATGGGTTCACTTTAT 780
781 GTTGACAGAGCTATTAGAGATGATGATTAAACATCATTCGTCCAAGAAAATACATCGAT 840
781 GTTGACAGAGCTATTAGAGATGATGATTAAACATCATTCGTCCAAGAAAATACATCGAT 840
841 ACACAACATATTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTGAATCATTAACCA 900
841 ACACAACATATTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTGAATCATTAACCA 900
901 GAAGTGAATAACCAATTAATAGTGTGCGCAAAAGGGGAAAGGAAACAGTTTCTCTGGATTGG 960
901 GAAGTGAATAACCAATTAATAGTGTGCGCAAAAGGGGAAAGGAAACAGTTTCTCTGGATTGG 960
961 CGCTTAGAACATTCGAAAAAACAGAAAATCTCGCTTATCCGATTCGCGCTTCCCGTTT 1020
961 CGCTTAGAACATTCGAAAAAACAGAAAATCTCGCTTATCCGATTCGCGCTTCCCGTTT 1020
1021 TTTGCGCGGGTAAATGTTGCTTTTTCGCTAAAAAATGGCTAAATAAATCCGGTTTCTTTTGTAT 1080
1021 TTTGCGCGGGTAAATGTTGCTTTTTCGCTAAAAAATGGCTAAATAAATCCGGTTTCTTTTGTAT 1080
1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1140
1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1140
1141 GGTAGTTTCTTTAAAACTATTGATGGCATTTAGCCCTACCATCAAGAGCCACCAAGTAAA 1200
1141 GGTAGTTTCTTTAAAACTATTGATGGCATTTAGCCCTACCATCAAGAGCCACCAAGTAAA 1200
1201 GAAATCAAAACCGATCGTGAAGCGGAAAAAATAATACGCTCGATATTTATGAGAGAAAAAG 1260
1201 GAAATCAAAACCGATCGTGAAGCGGAAAAAATAATACGCTCGATATTTATGAGAGAAAAAG 1260
1261 GTCCCTTATATCTATAGAAAATCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320
1261 GTCCCTTATATCTATAGAAAATCTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320
1321 TTAGTTTCAATTTATATCCAGCTTATAAATGTCGCAAACTATATTCAACGTTGCGTAGAT 1380
1321 TTAGTTTCAATTTATATCCAGCTTATAAATGTCGCAAACTATATTCAACGTTGCGTAGAT 1380
```



|||||  
439 TGGTACAAAGCGAAGAAAGACTTGGCATAAACCTGAACATCAACATGTTGGTCTT 498 Db  
481 TCTATTATCGTTACAACTCAATCGACAGCAATTTTATCGATTACATTTAGCCGTGTTTA 540 QY  
499 TCTATTATCGTTACAACTCAATCGACAGCAATTTTATCGATTACATTTAGCCGTGTTTA 558 Db  
541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600 QY  
559 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618 Db  
601 GATCTATCACCGCATCATTCGCCCAATATGAATAAATTTGAATTTTCGGTACGTGACAGCAA 660 QY  
619 GATCTATCACCGCATCATTCGCCCAATATGAATAAATTTGAATTTTCGGTACGTGACAGCAA 678 Db  
661 AAGAGTAACGGTTTTCAAGCCAGTCGCCCTCGGAATATGGGATTAACGTTAGCAAAAAATAT 720 QY  
679 AAGAGTAACGGTTTTCAAGCCAGTCGCCCTCGGAATATGGGATTAACGTTAGCAAAAAATAT 738 Db  
721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTTATGGGTTCAATCTTAT 780 QY  
739 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTTATGGGTTCAATCTTAT 798 Db  
781 GTTGCAGAGCTATTAGAAGATGATTTTAAACAATCATTTGGTCCCAAGAAAAATACATCGAT 840 QY  
799 GTTGCAGAGCTATTAGAAGATGATTTTAAACAATCATTTGGTCCCAAGAAAAATACATCGAT 858 Db  
841 ACAACAATATTGACCCAAAAGACTCTTTAAATAACGCGAGTTTTCGTTGAATCATTTACCA 900 QY  
859 ACAACAATATTGACCCAAAAGACTCTTTAAATAACGCGAGTTTTCGTTGAATCATTTACCA 918 Db  
901 GAAGTGAAACCAATAATAGTTGTGCGCAAAAGGGGAAGGAAAGTTCCTCTGGAATGG 960 QY  
919 GAAGTGAAACCAATAATAGTTGTGCGCAAAAGGGGAAGGAAAGTTCCTCTGGAATGG 978 Db  
961 CGCTTAGAACCAATTCGMAAAAACAGAAATCTCCGCTTATCCGATTTCCGCTTTCCGTTT 1020 QY  
979 CGCTTAGAACCAATTCGMAAAAACAGAAATCTCCGCTTATCCGATTTCCGCTTTCCGTTT 1038 Db  
1021 TTTTGGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATCCGGTTTCTTTGAT 1080 QY  
1039 TTTTGGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAAATCCGGTTTCTTTGAT 1098 Db  
1081 GAGGAATTTAATCACTGGGGTGAGAAAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1140 QY  
1099 GAGGAATTTAATCACTGGGGTGAGAAAGATGTGGAATTTGGATATCGCTTATTCGGTTAC 1158 Db  
1141 GGTAGTTTCTTTAAACTATTGATGGCATTTATGGCTTATCCATCAAGAGCCACAGTAA 1200 QY  
1159 GGTAGTTTCTTTAAACTATTGATGGCATTTATGGCTTATCCATCAAGAGCCACAGTAA 1218 Db  
1201 GAAATGAAACCGATCGTGAAGCGGAAAAATATTTACGCTCGATATTTAGAGAAAAAG 1260 QY  
1219 GAAATGAAACCGATCGTGAAGCGGAAAAATATTTACGCTCGATATTTAGAGAAAAAG 1278 Db  
1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320 QY  
1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1338 Db  
1321 TTAGTTTCAATTTATATCCAGCTTATACCTGTGCAAACTATATTCAGCGTTCCGTAGAT 1380 QY  
1339 TTAGTTTCAATTTATATCCAGCTTATATACCTGTGCAAACTATATTCAGCGTTCCGTAGAT 1398 Db  
1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGTTTGTATTTGTAAACGATGGTTCAACA 1440 QY  
1399 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGTTTGTATTTGTAAACGATGGTTCAACA 1458 Db  
1441 GATAATACCTTAGAAGTGAATCAATAAGCTTTATGGTAAATAATCCTAGGGTACGCATCATG 1500 QY  
1459 GATAATACCTTAGAAGTGAATCAATAAGCTTTATGGTAAATAATCCTAGGGTACGCATCATG 1518 Db  
1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAATGCGAGCCGTTCTTTTGTCTAAGGT 1560 QY  
|||||

1519 TCTAAACAAATGGCGGAATAGCCCTCAGCATCAAAATCGACCGCTTTCTTTTGTCTAAAGGT 1578 Db  
1561 TATTACATTCGGCAGTTAGATTAGATTAGATTATCTTGAGCCTGATGAGTTGAACCTGTGT 1620 QY  
1579 TATTACATTCGGCAGTTAGATTAGATTAGATTATCTTGAGCCTGATGAGTTGAACCTGTGT 1638 Db  
1621 TTAAAGAAATTTTAAAGAGATAAACCGCTAGCTTGTGTTTATACCACTTAATPAGAAACGTC 1680 QY  
1639 TTAAAGAAATTTTAAAGAGATAAACCGCTAGCTTGTGTTTATACCACTTAATPAGAAACGTC 1698 Db  
1681 AATCCGATGGTAGCTTAATCGCTTAATCGTTTACAAATTTGGCCGAGAAATTTTTCAGGAAAAA 1740 QY  
1699 AATCCGATGGTAGCTTAATCGCTTAATCGTTTACAAATTTGGCCGAGAAATTTTTCAGGAAAAA 1758 Db  
1741 CTCAACCGCTATGATTTGCTCACCACCTTTTGAATGTTTACGATTTAGAGCTTTGGCATTTA 1800 QY  
1759 CTCAACCGCTATGATTTGCTCACCACCTTTTGAATGTTTACGATTTAGAGCTTTGGCATTTA 1818 Db  
1801 ACTGATGGATTCAAATGAAAAAATTTGAAAAATGCCCGTAGACTATGACATGTTCTCTCAAACTC 1860 QY  
1819 ACTGATGGATTCAAATGAAAAAATTTGAAAAATGCCCGTAGACTATGACATGTTCTCTCAAACTC 1878 Db  
1861 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAATCTGCTATAAACCGGTGATTTACATGGT 1920 QY  
1879 AGTGAAGTTGAAAAATTTTAAACATCTTAAATAAATCTGCTATAAACCGGTGATTTACATGGT 1938 Db  
1921 GATAACACATCAATTTAGAAAACTTTGGCATTTCAAAGAAAAACCAATTTTGTGTAGTCAAT 1980 QY  
1939 GATAACACATCAATTTAGAAAACTTTGGCATTTCAAAGAAAAACCAATTTTGTGTAGTCAAT 1998 Db  
1981 CAGTCATTAAATAGAACGCGATAACTTATTTATTAATTTATGACGAATTTTGATGATTTAGAT 2040 QY  
1999 CAGTCATTAAATAGAACGCGATAACTTATTTATTAATTTATGACGAATTTTGATGATTTAGAT 2058 Db  
2041 GAAAGTGAAGATGATATTTTCAATAAACCCCTGAATATCAAGAGAGATTTGAATCTTTA 2100 QY  
2059 GAAAGTGAAGATGATATTTTCAATAAACCCCTGAATATCAAGAGAGATTTGAATCTTTA 2118 Db  
2101 AAAGATATTTAAATCATCCAGAAATAAGATGCCAAAAATCGCAGTCAGTATTTTATCC 2160 QY  
2119 AAAGATATTTAAATCATCCAGAAATAAGATGCCAAAAATCGCAGTCAGTATTTTATCC 2178 Db  
2161 AATCATTTAAACGGCTTAGTGAAAAAACTAAACAATATTTTGAATATAATAAAAAATATA 2220 QY  
2179 AATCATTTAAACGGCTTAGTGAAAAAACTAAACAATATTTTGAATATAATAAAAAATATA 2238 Db  
2221 TTCGTTATTTGTTCTACATGTTGATAAGAAATCATCTTACACGAGATPATAAAAAAGAAATA 2280 QY  
2239 TTCGTTATTTGTTCTACATGTTGATAAGAAATCATCTTACACGAGATPATAAAAAAGAAATA 2298 Db  
2281 CTAGCCCTTCTATCATATAAACATCAAGTGAATTTTCTAAATATGATATCTCATATTAC 2340 QY  
2299 CTAGCCCTTCTATCATATAAACATCAAGTGAATTTTCTAAATATGATATCTCATATTAC 2358 Db  
2341 ACGAGTATAGATTAATAAAAACTCAGCGCAATTTAAGTAAATTAATAAATAAAGTCAAG 2400 QY  
2359 ACGAGTATAGATTAATAAAAACTCAGCGCAATTTAAGTAAATTAATAAATAAAGTCAAG 2418 Db  
2401 TTAAATCTAAATTTGTAATAATCATCAATTTTGTGATAATCATGACAGCTATTTCGTTAAAAAT 2460 QY  
2419 TTAAATCTAAATTTGTAATAATCATCAATTTTGTGATAATCATGACAGCTATTTCGTTAAAAAT 2478 Db  
2461 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTTAACAT 2520 QY  
2479 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTTAACAT 2538 Db  
2521 GATTCGATCGGAAAAATCAATCGCGCATCCACATTTTAAAAAGCTCATTTAAAACTTATTTT 2580 QY  
2539 GATTCGATCGGAAAAATCAATCGCGCATCCACATTTTAAAAAGCTCATTTAAAACTTATTTT 2598 Db  
2581 AATGACATGACTTAAAAAGTATGAAATGTGAAAGGGGCATCAAGGATATGTTTATGACG 2640 QY  
2599 AATGACATGACTTAAAAAGTATGAAATGTGAAAGGGGCATCAAGGATATGTTTATGACG 2658 Db





```
QY 2821 GAACGAAATACATGACCAATGAAACAATGGAAGTGAAGGAGGAGGAGAAATATA 2880
DB 2839 GAACGAAATACATGACCAATGAAACAATGGAAGTGAAGGAGGAGGAGGAGAAATATA 2898
QY 2881 CCTGTTAAACAAGTTCATTTATTAATAGTATAACTCTATAA 2919
DB 2899 CCTGTTAAACAAGTTCATTTATTAATAGTATAACTCTATAA 2937

RESULT 7
US-10-172-527-9
; Sequence 9, Application US/10172527
; Publication No. US20030092118A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kshama
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: HYALURONAN SYNTHASE GENES AND EXPRESSION THEREOF IN BACILLUS SUBT
; FILE REFERENCE: 3554.048
; CURRENT APPLICATION NUMBER: US/10/172,527
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/297,788
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/297,744
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: pasteurella multocida
US-10-172-527-9

Query Match 99.9%; Score 2917.4; DB 5; Length 2937;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATACATTTATCACAAGCAATATAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60
DB 19 ATGAATACATTTATCACAAGCAATATAAAGCATATAAAGCAATGACTATCAATTAGCACTC 78
QY 61 AAATTTATTTGAAAGTCGGCGGAAATCTATGACGGAATAATGTTGAAATTTCAAAATTACC 120
DB 79 AAATTTATTTGAAAGTCGGCGGAAATCTATGACGGAATAATGTTGAAATTTCAAAATTACC 138
QY 121 AAATGCAAGAAAGAACTCTCAGCACATCTCTGTTTAAATTCAGCACATCTTTCTGTAAT 180
DB 139 AAATGCAAGAAAGAACTCTCAGCACATCTCTGTTTAAATTCAGCACATCTTTCTGTAAT 198
QY 181 AAAGAGAAAGAAAGTCAATGTTCCGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 240
DB 199 AAAGAGAAAGAAAGTCAATGTTCCGATAGTCCGTTAGATATTGCAACACAACTGTTACTT 258
QY 241 TCCAAAGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300
DB 259 TCCAAAGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 318
QY 301 AAATGCTCACTCAGAGAAATCTGAAATTCGGAGGTGAAGCGGTGCGCCCTGTGACCA 360
DB 319 AAATGCTCACTCAGAGAAATCTGAAATTCGGAGGTGAAGCGGTGCGCCCTGTGACCA 378
QY 361 AAAGATTTTCCAAAGATCTGGTTTATAGCCCTTTACCTGATCATGTTAATGATTTTACA 420
DB 379 AAAGATTTTCCAAAGATCTGGTTTATAGCCCTTTTACCTGATCATGTTAATGATTTTACA 438
QY 421 TGGTACAAAAGCGAAAGAAAGACTTTGGCATATAAAACCTCAACATCAACATGTTGGTCTT 480
DB 439 TGGTACAAAAGCGAAAGAAAGACTTTGGCATATAAAACCTCAACATCAACATGTTGGTCTT 498
```

```
QY 481 TCTATTATCGTTTACAAACATTCATCAATCGACCAAGCAATTTTATCGATTACATTAGCCTGTTTA 540
DB 499 TCTATTATCGTTTACAAACATTCATCAATCGACCAAGCAATTTTATCGATTACATTAGCCTGTTTA 558
QY 541 GTAAACCAAAAAACAATACCTGTTTGAAGTTATCGTGAAGATGATGTTAGTACAGAA 600
DB 559 GTAAACCAAAAAACAATACCTGTTTGAAGTTATCGTGAAGATGATGTTAGTACAGAA 618
QY 601 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGATATTCGCTACGTACAGACAA 660
DB 619 GATCTATCACCGATCATTCGCAATATGAAATTAATTTGGATATTCGCTACGTACAGACAA 678
QY 661 AAAGATTAACGGTTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGTTAGCAAAATPAT 720
DB 679 AAAGATTAACGGTTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGTTAGCAAAATPAT 738
QY 721 GACTTTATTTGCTTTACTCGACTGTGATATGCGGCAAAATCCATTATGGGTTCAATCTTTAT 780
DB 739 GACTTTATTTGCTTTACTCGACTGTGATATGCGGCAAAATCCATTATGGGTTCAATCTTTAT 798
QY 781 GTTCGAGAGCTATTAGAGATGATTTTAAACAATCATTTGTCCTCAAGAAAAATACATCGAT 840
DB 799 GTTCGAGAGCTATTAGAGATGATTTTAAACAATCATTTGTCCTCAAGAAAAATACATCGAT 858
QY 841 ACACAAACATATTGACCCCAAAAGACTTCTTAATAACGCGAGTTTTCGTTTGAATCATTAACA 900
DB 859 ACACAAACATATTGACCCCAAAAGACTTCTTAATAACGCGAGTTTTCGTTTGAATCATTAACA 918
QY 901 GAAGTGAAAAACCAATTAATAGTGTTCGCCCAAAAGGGGAAAGAAACAGTTTCTCTGATTTGG 960
DB 919 GAAGTGAAAAACCAATTAATAGTGTTCGCCCAAAAGGGGAAAGAAACAGTTTCTCTGATTTGG 978
QY 961 CGCTTAGAACCAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCCTTCCGTTT 1020
DB 979 CGCTTAGAACCAATTCGAAAAAACAAGAAATCTCCGCTTATCCGATTCGCCCTTCCGTTT 1038
QY 1021 TTTGCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAAAATTAATTCGGTTTCTTTGAT 1080
DB 1039 TTTGCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAAAATTAATTCGGTTTCTTTGAT 1098
QY 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTTAC 1140
DB 1099 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATTCGGTTTATTCGGTTTAC 1158
QY 1141 GGTAGTCTTTTAAACATTTATGATGGCATTTATGGCTACCATCAAGAGCCACAGGTA 1200
DB 1159 GGTAGTCTTTTAAACATTTATGATGGCATTTATGGCTACCATCAAGAGCCACAGGTA 1218
QY 1201 GAAATGAAACCGATCGTGAAGCGGAAAAAATAATTTAGCTCGATATTATGAGAGAAAAG 1260
DB 1219 GAAATGAAACCGATCGTGAAGCGGAAAAAATAATTTAGCTCGATATTATGAGAGAAAAG 1278
QY 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAGATTCGCATATCAATAGATACCT 1320
DB 1279 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAAGATTCGCATATCAATAGATACCT 1338
QY 1321 TTAGTTTCAATTTATATCCAGCTTTAATCTGTGCAAACTATATTCAAGCTTTCGCTAGAT 1380
DB 1339 TTAGTTTCAATTTATATCCAGCTTTAATCTGTGCAAACTATATTCAAGCTTTCGCTAGAT 1398
QY 1381 AGTGACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTGTAACGATGTTCAACA 1440
DB 1399 AGTGACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTGTAACGATGTTCAACA 1458
QY 1441 GATAAATACCTTAGAAGATGATCAATTAAGCTTTATGGTAATAATTCCTAGGGTACGCTCATG 1500
DB 1459 GATAAATACCTTAGAAGATGATCAATTAAGCTTTATGGTAATAATTCCTAGGGTACGCTCATG 1518
QY 1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAATGACAGCGTTTCTTTTGGTAAAGGT 1560
DB 1519 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAATGACAGCGTTTCTTTTGGTAAAGGT 1578
QY 1561 TATTACATTTGGCGAGTTAGATTTAGATTTAGATTTATCTTTGAGCCTGTAGTCACTGTTGAT 1620
```

Db 619 GATCTATCACCGATCATTTCCGCAATATGAAATAAAATTTGGATATTCGCTACGTCAGACAA 678  
Qy 661 AAAGATAACGGTTTTTCAAGCCAGTGGCCGCTCGGAATATGGATTTACGCTTTAGCAAAATAT 720  
Db 679 AAAGATAACGGTTTTTCAAGCCAGTGGCCGCTCGGAATATGGATTTACGCTTTAGCAAAATAT 738  
Qy 721 GACTTTATTTGGCTTTACTCGACTGTGATATGCGCCAAATCCATTTATGGGTTCATTTCTTAT 780  
Db 739 GACTTTATTTGGCTTTACTCGACTGTGATATGCGCCAAATCCATTTATGGGTTCATTTCTTAT 798  
Qy 781 GTTCAGAGCTATTAGAGATGATGATTTAACAATCATTTGGTCCAGAAATACATCGAT 840  
Db 799 GTTCAGAGCTATTAGAGATGATGATTTAACAATCATTTGGTCCAGAAATACATCGAT 858  
Qy 841 ACACAACATATTGACCCAAAGACTCTTAAATAACCGGAGTTTGGCTTTGAATCATTACCA 900  
Db 859 ACACAACATATTGACCCAAAGACTCTTAAATAACCGGAGTTTGGCTTTGAATCATTACCA 918  
Qy 901 GAAGTGAACCAATTAATAGTTTGGCCGCAAAAGGGGAAAGAACAGTTTCTCTGGATTGG 960  
Db 919 GAAGTGAACCAATTAATAGTTTGGCCGCAAAAGGGGAAAGAACAGTTTCTCTGGATTGG 978  
Qy 961 CGCTTAGAACCAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTTCCGCTTTCCGTTTT 1020  
Db 979 CGCTTAGAACCAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTTCCGCTTTCCGTTTT 1038  
Qy 1021 TTTGCGGGGTAAATGTTGCTTTCGCTAAAAAAATGGCTAAATAATCCGGTTTCTTTGAT 1080  
Db 1039 TTTGCGGGGTAAATGTTGCTTTCGCTAAAAAAATGGCTAAATAATCCGGTTTCTTTGAT 1098  
Qy 1081 GAGGAAATTAATCACTCGGGGTGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTTAC 1140  
Db 1099 GAGGAAATTAATCACTCGGGGTGAGAGATGTGAAATTTGGATATCGCTTATTCGGTTTAC 1158  
Qy 1141 GGTAGTTTCTTTAAAACTATTGATGGCAATATGCGCTTACCAATCAAGAGCCACAGGTAAA 1200  
Db 1159 GGTAGTTTCTTTAAAACTATTGATGGCAATATGCGCTTACCAATCAAGAGCCACAGGTAAA 1218  
Qy 1201 GAAATGAACCGATCGTGAAGCGGGGAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260  
Db 1219 GAAATGAACCGATCGTGAAGCGGGGAAAAATATTACGCTCGATATTATGAGAGAAAAG 1278  
Qy 1261 GTCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
Db 1279 GTCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1338  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATAA CTGTGCAAACTATATTCAACGTTGCGTAGAT 1380  
Db 1339 TTAGTTTCAATTTATATCCAGCTTATAA CTGTGCAAACTATATTCAACGTTGCGTAGAT 1398  
Qy 1381 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTCTGTAACGATGGTTCAACA 1440  
Db 1399 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTCTGTAACGATGGTTCAACA 1458  
Qy 1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATATCTCTAGGGTACGCATCATG 1500  
Db 1459 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATATCTCTAGGGTACGCATCATG 1518  
Qy 1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACGCGGTTCTTTTGGCTTAAAGGT 1560  
Db 1519 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGACGCGGTTCTTTTGGCTTAAAGGT 1578  
Qy 1561 TATTACATTTGGCGAGTTAGATTCAGATGATTTCTTGAGCCCTGATGCAATTTGAATCTGTG 1620  
Db 1579 TATTACATTTGGCGAGTTAGATTCAGATGATTTCTTGAGCCCTGATGCAATTTGAATCTGTG 1638  
Qy 1621 TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTTAATAGAAAAGCTC 1680  
Db 1639 TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACCACTTAATAGAAAAGCTC 1698  
Qy 1681 AATCCGGATGGTAGCTTAATCGCTTAATCGTTTACAAATGGCGCAGAAATTTTCAAGAAAAA 1740  
Db 1699 AATCCGGATGGTAGCTTAATCGCTTAATCGTTTACAAATGGCGCAGAAATTTTCAAGAAAAA 1758

Qy 1741 CTCAACAACGGCTATGATTTGCTCACCACCTTTTAGAATGTTCAAGATTAGAGCTTGGCAATTTA 1800  
Db 1759 CTCAACAACGGCTATGATTTGCTCACCACCTTTTAGAATGTTCAAGATTAGAGCTTGGCAATTTA 1818  
Qy 1801 ACTGATGGATTTCAATGAAAAAATTTGAAATGCCGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1819 ACTGATGGATTTCAATGAAAAAATTTGAAATGCCGTAGACTATGACATGTTCTCTCAAACTC 1878  
Qy 1861 AGTGAAGTTTGGAAAAATTTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1920  
Db 1879 AGTGAAGTTTGGAAAAATTTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGGT 1938  
Qy 1921 GATPAAACACATCAATTAAGAAAACTTGGCATTTCAAAAGAAAAAACCATTTTTGTGTAGTCAAT 1980  
Db 1939 GATPAAACACATCAATTAAGAAAACTTGGCATTTCAAAAGAAAAAACCATTTTTGTGTAGTCAAT 1998  
Qy 1981 CAGTCATTAATAGACAAAGGCATACTTATTATAAATTTATGACCAATTTGATGATTTAGAT 2040  
Db 1999 CAGTCATTAATAGACAAAGGCATACTTATTATAAATTTATGACCAATTTGATGATTTAGAT 2058  
Qy 2041 GAAAGTAGAAAGTATATTTTCAATAAAAAACCGCTGAATATCAAGAAAGAGATTGATATCTTA 2100  
Db 2059 GAAAGTAGAAAGTATATTTTCAATAAAAAACCGCTGAATATCAAGAAAGAGATTGATATCTTA 2118  
Qy 2101 AAAGATATTAAAAATCATCCAGAAATAAAGATGCCAAAAATCGCAGTCAGTATTTTTTATCCC 2160  
Db 2119 AAAGATATTAAAAATCATCCAGAAATAAAGATGCCAAAAATCGCAGTCAGTATTTTTTATCCC 2178  
Qy 2161 AATAACATTAACCGGCTTAGTGAAAAAAATCAAAACATATTATTGAAATATAATAAATAATA 2220  
Db 2179 AATAACATTAACCGGCTTAGTGAAAAAAATCAAAACATATTATTGAAATATAATAAATAATA 2238  
Qy 2221 TTGCTTATTGCTTCTACATGTTGATAAGAATCATCTTACACACAGATATCAAAAAAGAAATA 2280  
Db 2239 TTGCTTATTGCTTCTACATGTTGATAAGAATCATCTTACACACAGATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCCTTCTATCAATAACATCAAGTGAATTTTACTAAATTAATGATATCTCATATTAC 2340  
Db 2299 CTAGCCCTTCTATCAATAACATCAAGTGAATTTTACTAAATTAATGATATCTCATATTAC 2358  
Qy 2341 ACAGATTAATGATTAATAAAAACTGAGCGGCATTTAAGTAATATTATAAATTAAGTCAG 2400  
Db 2359 ACAGATTAATGATTAATAAAAACTGAGCGGCATTTAAGTAATATTATAAATTAAGTCAG 2418  
Qy 2401 TTAATCTRAATTTGGAATACATCATTTTGTAAATCATGACAGCCTTATTCGTTAAAAAT 2460  
Db 2419 TTAATCTRAATTTGGAATACATCATTTTGTAAATCATGACAGCCTTATTCGTTAAAAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAACACAT 2520  
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAACACAT 2538  
Qy 2521 GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTAAAAAGCTCATTTAAACATTTT 2580  
Db 2539 GATTGGATCGAGAAAAATCAATGCGCATCCACCAATTTAAAAAGCTCATTTAAACATTTT 2598  
Qy 2581 AATGACATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCAAAAGGTATGTTTATGACG 2640  
Db 2599 AATGACATGACTTTAAAAAGTATGAATGTGAAAGGGGCATCAAAAGGTATGTTTATGACG 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTTCTGACGATTTATTAAGAAGTCATCACATCTTGCAGTCA 2700  
Db 2659 TATGCGCTAGCGCATGAGCTTTCTGACGATTTATTAAGAAGTCATCACATCTTGCAGTCA 2718  
Qy 2701 ATTGATAGTGTGCAGAAATATAACATGAGGATATTGGTTCGAATTTGCACTTTTAAATC 2760  
Db 2719 ATTGATAGTGTGCAGAAATATAACATGAGGATATTGGTTCGAATTTGCACTTTTAAATC 2778  
Qy 2761 TTAGAAAAGAAACCGGCCATGTTTAAATAAACAATCGACCCCTGATTTATATGSCCTTGG 2820  
Db 2779 TTAGAAAAGAAACCGGCCATGTTTAAATAAACAATCGACCCCTGATTTATATATGCTTGG 2838

Db 1819 ACTGATGATTCATGAAAGAAATTTGAAATGCGGTAGACTATGACATGTTCTCTCAAACTC 1878

Qy 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAAATCTGCTATAAACCGGTGTAATTACATGGT 1920

Db 1879 AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAAATCTGCTATAAACCGGTGTAATTACATGGT 1938

Qy 1921 GATAACACATCAATTTAAGAACTTGGCAATTCARAAAGRAAAACCAATTTTGTGTGTAATCAAT 1980

Db 1939 GATAACACATCAATTTAAGAACTTGGCAATTCARAAAGRAAAACCAATTTTGTGTGTAATCAAT 1998

Qy 1981 CAGTCATTAAATAGACAAGGCAATCTTATTAATAATATGACGAATTTGATGATTTAGAT 2040

Db 1999 CAGTCATTAAATAGACAAGGCAATCTTATTAATAATATGACGAATTTGATGATTTAGAT 2058

Qy 2041 GAAAGTAGAAGTATATTTTCAATAAAAACCGTGAATATCAAGAAGAGATGATATCTTA 2100

Db 2059 GAAAGTAGAAGTATATTTTCAATAAAAACCGTGAATATCAAGAAGAGATGATATCTTA 2118

Qy 2101 AAAGATATTAATAATCATCCAGATTAAGATGCCAAATCGCAGTCAGTATTTTATCCC 2160

Db 2119 AAAGATATTAATAATCATCCAGATTAAGATGCCAAATCGCAGTCAGTATTTTATCCC 2178

Qy 2161 AATACATTAAACGGCTTAGTGAAGAACTTAAACAATATTTATGAATAATAAAAAATATA 2220

Db 2179 AATACATTAAACGGCTTAGTGAAGAACTTAAACAATATTTATGAATAATAAAAAATATA 2238

Qy 2221 TTTCGTTATTTCTACATGTTGATGAAGATCATCTTTACACCCAGATATCAAAAAAGAAATA 2280

Db 2239 TTTCGTTATTTCTACATGTTGATGAAGATCATCTTTACACCCAGATATCAAAAAAGAAATA 2298

Qy 2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTTAATTAATGATATCTCATATTAC 2340

Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTTAATTAATGATATCTCATATTAC 2358

Qy 2341 ACGAGTAAATAGATTAATAAAACTGAGGCGCAATTTAAGTAATTAATAAAATTAAGTCAG 2400

Db 2359 ACGAGTAAATAGATTAATAAAACTGAGGCGCAATTTAAGTAATTAATAAAATTAAGTCAG 2418

Qy 2401 TTAATATCTAAATTTGTGAATPACATCATTTTTTGATATCATGACAGCCTATTCGTTAAAAAT 2460

Db 2419 TTAATATCTAAATTTGTGAATPACATCATTTTTTGATATCATGACAGCCTATTCGTTAAAAAT 2478

Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAACACAT 2520

Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTGCGCATGAATTTCTCAGCATTAACACAT 2538

Qy 2521 GATTGGATCGAGAAATCAATCGCATCCACCAATTTAAAAAGCTCAATTAACCTTATTTT 2580

Db 2539 GATTGGATCGAGAAATCAATCGCATCCACCAATTTAAAAAGCTCAATTAACCTTATTTT 2598

Qy 2581 AATGACAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGACG 2640

Db 2599 AATGACAATGACTTAAAAAGTATGAATGTGAAAGGGGCATCAAGGTATGTTTATGACG 2658

Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTAATAAAGAGTCAATCATCTTGCAGTCA 2700

Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTAATAAAGAGTCAATCATCTTGCAGTCA 2718

Qy 2701 ATTGATAGTGTGCCAGATATAACACTGAGGATATTTGGTCCAAATTCACATTTTAAATC 2760

Db 2719 ATTGATAGTGTGCCAGATATAACACTGAGGATATTTGGTCCAAATTCACATTTTAAATC 2778

Qy 2761 TTAGAAAAGAAAACCGGCCATGTTATTTAATAAAACATCGACCTGACTTATATGCTTGG 2820

Db 2779 TTAGAAAAGAAAACCGGCCATGTTATTTAATAAAACATCGACCTGACTTATATGCTTGG 2838

Qy 2821 GAAACGAAAATTAACAATGGACAAATGAACAAATTTGAAAGTGCAAAAAGAGAGAAAATATA 2880

Db 2839 GAAACGAAAATTAACAATGGACAAATGAACAAATTTGAAAGTGCAAAAAGAGAGAAAATATA 2898

Qy 2881 CCTGTTAACAGTTCAATTTAATAGTATTAACCTATAA 2919

Db 2899 CCTGTTAACAGTTCAATTTAATAGTATTAACCTATAA 2937

RESULT 6

US-09-879-959-9  
; Sequence 9, Application US/09879959  
; Patent No. US20020160489A1

GENERAL INFORMATION:

; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Kshama  
; APPLICANT: Deangelis, Paul  
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION  
; TITLE OF INVENTION: IN BACILLUS SUBTILIS  
; FILE REFERENCE: 3554.049  
; CURRENT APPLICATION NUMBER: US/09/879,959  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: 09/469,200  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9

LENGTH: 2937

TYPE: DNA

ORGANISM: pasteurella multocida

US-09-879-959-9

Query Match 99.9%; Score 2917.4; DB 3; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGATATCATTTATCACAAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC 60

Db 19 ATGATATCATTTATCACAAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC 78

Qy 61 AAATTTATTTGAAAAGTCGGCGGAAATCTATGAGCGGAAAATTTGTGAATTTCAAATTACC 120

Db 79 AAATTTATTTGAAAAGTCGGCGGAAATCTATGAGCGGAAAATTTGTGAATTTCAAATTACC 138

Qy 121 AAATGCAAGAAAACTCTCAGCACATCCCTCTGTGTAATTCAGCACATCTTCTGTGTAAT 180

Db 139 AAATGCCAAGAAAACTCTCAGCACATCCCTCTGTGTAATTCAGCACATCTTCTGTGTAAT 198

Qy 181 AAAGAGAAAAAGTCAATGTTTGGATAGTCGGTATGATATTTGCAACACAACTGTACTTT 240

Db 199 AAAGAGAAAAAGTCAATGTTTGGATAGTCGGTATGATATTTGCAACACAACTGTACTTT 258

Qy 241 TCCACGCTAAAAAATTAAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300

Db 259 TCCACGCTAAAAAATTAAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 318

Qy 301 AAATGCTCCTCAGAGAAGAAATCTGAAAAATGCGGAGGTAAGAGCGGTGCGCCCTGTACCA 360

Db 319 AAATGCTCCTCAGAGAAGAAATCTGAAAAATGCGGAGGTAAGAGCGGTGCGCCCTGTACCA 378

Qy 361 AAAGATTTTCCAAAGATCTGGTTTACGGCTTTTACCTGATCATGTAAATGATTTTACA 420

Db 379 AAAGATTTTCCAAAGATCTGGTTTACGGCTTTTACCTGATCATGTAAATGATTTTACA 438

Qy 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAAACCTGAAACATCAACATGTTGGTCTTT 480

Db 439 TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAAAACCTGAAACATCAACATGTTGGTCTTT 498

Qy 481 TCTATTATCTGTTTAAACATTTCAATCGACCAAGCAATTTTATTCGATTTACATTTAGCCTGTTTA 540

Db 499 TCTATTATCTGTTTAAACATTTCAATCGACCAAGCAATTTTATTCGATTTACATTTAGCCTGTTTA 558

Qy 541 GTAACCAAAAAAACAATTTACCCGTTTGAAGTTTATCGTGACAGATGATGTTAGTCAGGAA 600

Db 559 GTAACCAAAAAAACAATTTACCCGTTTGAAGTTTATCGTGACAGATGATGTTAGTCAGGAA 618

Qy 601 GATCTATCACCGATCAATTCGCCCAATATGAAAAATAAATTTGGATATTTTCGCTACGTCAGACAA 660





841 ACAACAATATTGACCCAAAAGACTCTTAAATAACGGAGTTTCGTTGAATCATTTACCA 900  
 Db |  
 859 ACACAACATATTGACCCAAAAGACTCTTAAATAACGGAGTTTCGTTGAATCATTTACCA 918  
 Qy |  
 901 GAAGTGAACCAATAATAGTGTTCGCGCAAAAGGGAAGAAAGTTTCTCGATTGG 960  
 Db |  
 919 GAAGTGAACCAATAATAGTGTTCGCGCAAAAGGGAAGAAAGTTTCTCGATTGG 978  
 Qy |  
 961 CGCTTAGAACCAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTT 1020  
 Db |  
 979 CGCTTAGAACCAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTT 1038  
 Qy |  
 1021 TTTCGGGGGGAATTTGCTTTTCGCTAAAAAATGGCTAAATTAATTAATTCGCTTTCTTGAT 1080  
 Db |  
 1039 TTTCGGGGGGAATTTGCTTTTCGCTAAAAAATGGCTAAATTAATTAATTCGCTTTCTTGAT 1098  
 Qy |  
 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTTATTCGTTAC 1140  
 Db |  
 1099 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTTATTCGTTAC 1158  
 Qy |  
 1141 GGTAGTTTCTTTAAACTATTGATGGCATTATGGCCTACCATCAAGAGCCACAGGTAAA 1200  
 Db |  
 1159 GGTAGTTTCTTTAAACTATTGATGGCATTATGGCCTACCATCAAGAGCCACAGGTAAA 1218  
 Qy |  
 1201 GAAAAATGAACCCGATCGTGAAGCGGAAAAAATAATTACGCTCGATATTATGAGAGAAAG 1260  
 Db |  
 1219 GAAAAATGAACCCGATCGTGAAGCGGAAAAAATAATTACGCTCGATATTATGAGAGAAAG 1278  
 Qy |  
 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
 Db |  
 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1338  
 Qy |  
 1321 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGGTTGCGTAGAT 1380  
 Db |  
 1339 TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGGTTGCGTAGAT 1398  
 Qy |  
 1381 AGTGCACTGAATCAGACTGTGTGTGATCTCGAGTTTGTATTTGTAACGATGGTTCAACA 1440  
 Db |  
 1399 AGTGCACTGAATCAGACTGTGTGTGATCTCGAGTTTGTATTTGTAACGATGGTTCAACA 1458  
 Qy |  
 1441 GATAATACCTTAGAAGTGATCAATAGCTTTATGTTTAAATCCCTAGGCTAGGCATCATG 1500  
 Db |  
 1459 GATAATACCTTAGAAGTGATCAATAGCTTTATGTTTAAATCCCTAGGCTAGGCATCATG 1518  
 Qy |  
 1501 TCTAAACCAAAATGGCGGAATAGCTCAGCATCAATGCGAGCCGTTCTTTTGTCTAAAGGT 1560  
 Db |  
 1519 TCTAAACCAAAATGGCGGAATAGCTCAGCATCAATGCGAGCCGTTCTTTTGTCTAAAGGT 1578  
 Qy |  
 1561 TATTACATTTGGGCGAGTTAGATTCCAGATGATTTCTTTGAGCCTGATCGAGTTGAACGTGT 1620  
 Db |  
 1579 TATTACATTTGGGCGAGTTAGATTCCAGATGATTTCTTTGAGCCTGATCGAGTTGAACGTGT 1638  
 Qy |  
 1621 TTAAGAGAAATTTTAAAGATAAAGACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
 Db |  
 1639 TTAAGAGAAATTTTAAAGATAAAGACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1698  
 Qy |  
 1681 AATCCGGATGGTAGCTTAAATCGCTAATGTTTCAATTTGGCCAGAAATTTTACAGAGAAAA 1740  
 Db |  
 1699 AATCCGGATGGTAGCTTAAATCGCTAATGTTTCAATTTGGCCAGAAATTTTACAGAGAAAA 1758  
 Qy |  
 1741 CTCAACACGGCTATGATTTGCTACCACTTTTAGAATGTTTCAAGATTAGAGCTTGGCATTTA 1800  
 Db |  
 1759 CTCAACACGGCTATGATTTGCTACCACTTTTAGAATGTTTCAAGATTAGAGCTTGGCATTTA 1818  
 Qy |  
 1801 ACTGATGGATTCATAGAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTTCAAACTC 1860  
 Db |  
 1819 ACTGATGGATTCATAGAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTTCAAACTC 1878  
 Qy |  
 1861 AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAATCTGCTATTAACCGTGTATTACATGGT 1920  
 Db |  
 1879 AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAATCTGCTATTAACCGTGTATTACATGGT 1938

1921 GATAACACATCAATTAAGAAAACTTGGCATTCAAAAGAAAAAACCACTTTTGTGTAGTCAAT 1980  
 Db |  
 1939 GATAACACATCAATTAAGAAAACTTGGCATTCAAAAGAAAAAACCACTTTTGTGTAGTCAAT 1998  
 Qy |  
 1981 CAGTCATTTAAATAGACAAGGCATAACTTATTATTAATTAATGACGAATTTGATGATTTAGAT 2040  
 Db |  
 1999 CAGTCATTTAAATAGACAAGGCATAACTTATTATTAATTAATGACGAATTTGATGATTTAGAT 2058  
 Qy |  
 2041 GAAAGTAGAAGTATATTTTCAATAAABACCGCTGAATATCAAGAGACATTTGATATCTTA 2100  
 Db |  
 2059 GAAAGTAGAAGTATATTTTCAATAAABACCGCTGAATATCAAGAGACATTTGATATCTTA 2118  
 Qy |  
 2101 AAAGATATTTAAATATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTATCCC 2160  
 Db |  
 2119 AAAGATATTTAAATATCATCCAGATAAAGATGCCAAAATCGCAGTCAGTATTTTATCCC 2178  
 Qy |  
 2161 AATACATTTAAACGGCTTAGTGAAAAAATACTAAACAATATTTATTGAAATATAAATAATATA 2220  
 Db |  
 2179 AATACATTTAAACGGCTTAGTGAAAAAATACTAAACAATATTTATTGAAATATAAATAATATA 2238  
 Qy |  
 2221 TTTCGTATTGTTTACATGTTTGAAGAATCATCTTACCCAGATATCAAAAAAGAAATA 2280  
 Db |  
 2239 TTTCGTATTGTTTACATGTTTGAAGAATCATCTTACCCAGATATCAAAAAAGAAATA 2298  
 Qy |  
 2281 CTAGCCTTCTATCAATAAACAATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2340  
 Db |  
 2299 CTAGCCTTCTATCAATAAACAATCAAGTGAATATTTTACTAAATAATGATATCTCATATTAC 2358  
 Qy |  
 2341 ACGAGTAATAGATTAATAAATACTGAGCGCATTTAAGTAATTAATAAATAAAGTCAAG 2400  
 Db |  
 2359 ACGAGTAATAGATTAATAAATACTGAGCGCATTTAAGTAATTAATAAATAAAGTCAAG 2418  
 Qy |  
 2401 TTAATCTAAATTTGTAATACATCATTTTTGTAATATCATGACGCTATTCGTTAAAAAT 2460  
 Db |  
 2419 TTAATCTAAATTTGTAATACATCATTTTTGTAATATCATGACGCTATTCGTTAAAAAT 2478  
 Qy |  
 2461 GACACCTATGCTTATATGAAAAAATATCATGTCGCGCATGAAATTTCTCAGCATTTAACACAT 2520  
 Db |  
 2479 GACACCTATGCTTATATGAAAAAATATCATGTCGCGCATGAAATTTCTCAGCATTTAACACAT 2538  
 Qy |  
 2521 GATTGGATCGAGAAAAATCAATCGCATCCACATTTTAAAGAAAGCTCATTTAAAACTTATTTT 2580  
 Db |  
 2539 GATTGGATCGAGAAAAATCAATCGCATCCACATTTTAAAGAAAGCTCATTTAAAACTTATTTT 2598  
 Qy |  
 2581 AATGCAATAGCTTTAAAAAGTATGAATGTGAAGGGGCATCAAGGATGATTTATGACG 2640  
 Db |  
 2599 AATGCAATAGCTTTAAAAAGTATGAATGTGAAGGGGCATCAAGGATGATTTATGACG 2658  
 Qy |  
 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCAATCACAATCTTGGCCAGTCA 2700  
 Db |  
 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAAAGTCAATCACAATCTTGGCCAGTCA 2718  
 Qy |  
 2701 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAAATC 2760  
 Db |  
 2719 ATTGATAGTGTGCCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAAATC 2778  
 Qy |  
 2761 TTAGAAAAAGAAAAACCGGCCATGTTTAAATAAACAATCGACCTGATTTATATGCTCTGG 2820  
 Db |  
 2779 TTAGAAAAAGAAAAACCGGCCATGTTTAAATAAACAATCGACCTGATTTATATGCTCTGG 2838  
 Qy |  
 2821 GAACGAAATTAACAATGGACAAATGAACAAATTTGAAAGTGCANAAAGAGAGAGAAATATA 2880  
 Db |  
 2839 GAACGAAATTAACAATGGACAAATGAACAAATTTGAAAGTGCANAAAGAGAGAGAAATATA 2898  
 Qy |  
 2881 CCTGTTAAACAGTTTCATTTAATAGTATAAATCTATAA 2919  
 Db |  
 2899 CCTGTTAAACAGTTTCATTTAATAGTATAAATCTATAA 2937



```
Db 1999 CAGTCATTAAATAGACAAGGCATAACTTATTATAAATATGACGAATTTGATGATTTAGAT 2058
Qy 2041 GAAAGTGAAGATATATTTTCATTAACACCGCTGAATATCAAGAGAGATTTGATATCTTA 2100
Db 2059 GAAAGTGAAGATATATTTTCATTAACACCGCTGAATATCAAGAGAGATTTGATATCTTA 2118
Qy 2101 AAAGATATTAATTAATCAGCAATTAAGAGATGCGCAAAATCGCAGTCAGTATTTTATCCC 2160
Db 2119 AAAGATATTAATTAATCAGCAATTAAGAGATGCGCAAAATCGCAGTCAGTATTTTATCCC 2178
Qy 2161 AATACATTAACCGCTTAGTGAAAAAATACTAAACAATATTTATGATATTAATAAATAATA 2220
Db 2179 AATACATTAACCGCTTAGTGAAAAAATACTAAACAATATTTATGATATTAATAAATAATA 2238
Qy 2221 TTGCTTATGTTCTACATGTTGATAAGNATCATCTTACACAGATATCAAAAAAGAAATA 2280
Db 2239 TTGCTTATGTTCTACATGTTGATAAGNATCATCTTACACAGATATCAAAAAAGAAATA 2298
Qy 2281 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2340
Db 2299 CTAGCCTTCTATCATAAACATCAAGTGAATATTTTACTAAATATGATATCTCATATTAC 2358
Qy 2341 ACAGATTAATAGATTAATAAATACTGAGCGCATTTAAAGTAAATTAATAAATAAAGTCAG 2400
Db 2359 ACAGATTAATAGATTAATAAATACTGAGCGCATTTAAAGTAAATTAATAAATAAAGTCAG 2418
Qy 2401 TTAATCTAAATTTGATATACATCATTTTGTGATATCATGACAGCCTATTGTTAAATAAT 2460
Db 2419 TTAATCTAAATTTGATATACATCATTTTGTGATATCATGACAGCCTATTGTTAAATAAT 2478
Qy 2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2520
Db 2479 GACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACACAT 2538
Qy 2521 GATTGGATCGAGAAAAATCAATCGCATCCACCATTTTAAAGAGTCATTAATAACTTATTTT 2580
Db 2539 GATTGGATCGAGAAAAATCAATCGCATCCACCATTTTAAAGAGTCATTAATAACTTATTTT 2598
Qy 2581 AATGACATGACTTTAAAGATGATGATGTAAGAGGCGCATCAAGGTATGTTTATGACG 2640
Db 2599 AATGACATGACTTTAAAGATGATGATGTAAGAGGCGCATCAAGGTATGTTTATGACG 2658
Qy 2641 TATGCGCTAGCGCATGAGCTTCTGACGATTAATAAGAAAGTCATCACAATCTTGCCAGTCA 2700
Db 2659 TATGCGCTAGCGCATGAGCTTCTGACGATTAATAAGAAAGTCATCACAATCTTGCCAGTCA 2718
Qy 2701 ATTGATAGTGTGCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAATC 2760
Db 2719 ATTGATAGTGTGCAGAAATATAACACTGAGGATATTTGGTTCCAAATTTGCACTTTTAATC 2778
Qy 2761 TTAGAAAAGAAAACCGGCCATGTTTAAATAAACATCGACCTGACTTATATGCTTGG 2820
Db 2779 TTAGAAAAGAAAACCGGCCATGTTTAAATAAACATCGACCTGACTTATATGCTTGG 2838
Qy 2821 GAACGAAATTTACAAATGACAAATGAACAAATTTGAAAGTGCAAAAGAGGAGAAAATATA 2880
Db 2839 GAACGAAATTTACAAATGACAAATTTGAAAGTGCAAAAGAGGAGAAAATATA 2898
Qy 2881 CCTGTTAAACAAGTTCATTATTAATAGTATAACTCTATAA 2919
Db 2899 CCTGTTAAACAAGTTCATTATTAATAGTATAACTCTATAA 2937
```

## RESULT 4

```
US-10-011-771B-8
; Sequence 8, Application US/10011771B
; Publication No. US20030082780A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H.
; APPLICANT: DeAngelis, Paul
; APPLICANT: Kumari, Kshama
; TITLE OF INVENTION: Hvaluronan Synthase Gene and Uses Thereof
; FILE REFERENCE: 3554.011
```

```
; CURRENT APPLICATION NUMBER: US/10/011,771B
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 09/178,851
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: US 60/064,435
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Pasteurella Multocida
; US-10-011-771B-8
```

Query Match 100.0%; Score 2919; DB 5; Length 2937;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 ATGAATACATTATCAAGAACAATAAAGCATATATAACGCAATGACTATCAATTTAGCACTC 60
Db 19 ATGAATACATTATCAAGAACAATAAAGCATATATAACGCAATGACTATCAATTTAGCACTC 78
Qy 61 AAATTATTTCAAAAGTCGGCGGAATCTATGGACGGAATTTGTTGAATTTCAAAATTACC 120
Db 79 AAATTATTTGAAAAGTCGGCGGAATCTATGGACGGAATTTGTTGAATTTCAAAATTACC 138
Qy 121 AAATGCAAGAAAAAATCTTCAGCACATCTTCTGTTAAATTCAGCACATCTTCTGTTAAAT 180
Db 139 AAATGCAAGAAAAAATCTTCAGCACATCTTCTGTTAAATTCAGCACATCTTCTGTTAAAT 198
Qy 181 AAAGAAGAAAAAGTCAATTTTTCGGATAGTCCTGTTAGATATTTGCAACACAATCTTTACTT 240
Db 199 AAAGAAGAAAAAGTCAATTTTTCGGATAGTCCTGTTAGATATTTGCAACACAATCTTTACTT 258
Qy 241 TCCAACTAAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAAGTTTAAAAAATAAATGG 300
Db 259 TCCAACTAAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAAGTTTAAAAAATAAATGG 318
Qy 301 AAATTGCTCACTGAGAAGAAATCTGAAAATCGGAGAGTAAGAGCGGTCGCGCTTTGTACCA 360
Db 319 AAATTGCTCACTGAGAAGAAATCTGAAAATCGGAGAGTAAGAGCGGTCGCGCTTTGTACCA 378
Qy 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTTAATGATTTTACA 420
Db 379 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTTACCTGATCATGTTTAATGATTTTACA 438
Qy 421 TGGTACAAAAGCGAAGAAAAAGACTTTGGCATAAAACTGNAACATCAACATGTTTGGTCTT 480
Db 439 TGGTACAAAAGCGAAGAAAAAGACTTTGGCATAAAACTGNAACATCAACATGTTTGGTCTT 498
Qy 481 TCTATTATCGTTTACAACATTTCAATCGACAGCAATTTTATCGATTACATTTAGCCTGTTTA 540
Db 499 TCTATTATCGTTTACAACATTTCAATCGACAGCAATTTTATCGATTACATTTAGCCTGTTTA 558
Qy 541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600
Db 559 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 618
Qy 601 GATCTATCACCGATCATTCGCCAATATGAAAATAAATTTGGATATTCGCTAGCAGCAAA 660
Db 619 GATCTATCACCGATCATTCGCCAATATGAAAATAAATTTGGATATTCGCTAGCAGCAAA 678
Qy 661 AAAGATAACGGTTTTTCAAGCGCAGTCGCGTAATATGGGATTAATCGCTTAGCAAAATAT 720
Db 679 AAAGATAACGGTTTTTCAAGCGCAGTCGCGTAATATGGGATTAATCGCTTAGCAAAATAT 738
Qy 721 GACTTTTATGGCTTACTCGACTGTGATAATGCGCAAAATCCATTATGGGTTCACTTTAT 780
Db 739 GACTTTTATGGCTTACTCGACTGTGATAATGCGCAAAATCCATTATGGGTTCACTTTAT 798
Qy 781 GTTCGACAGCTATTAGAGATGATGATTTAAACAATCATTTGTTCCAGAAAATACATCAT 840
Db 799 GTTCGACAGCTATTAGAGATGATGATTTAAACAATCATTTGTTCCAGAAAATACATCAT 858
```

; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 2937  
; TYPE: DNA  
; ORGANISM: Pastuerella Multocida  
US-10-011-768B-8

Query Match 100.0%; Score 2919; DB 5; Length 2937;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAATACATTTATCAGACGATTAAGCATATTAACGCAATGACTATCAATTAGCACTC	60
Db	19	ATGAATACATTTATCAGACGATTAAGCATATTAAGCAATGACTATCAATTAGCACTC	78
Qy	61	AAATTTATTTGAAAGCTCGGCGGAAATCTATGACCGGAAATTTGTTGAAATTTCAAAATTACC	120
Db	79	AAATTTATTTGAAAGCTCGGCGGAAATCTATGACCGGAAATTTGTTGAAATTTCAAAATTACC	138
Qy	121	AAATGCAAGAAAACTCTCAGCACATCCTTCTGTTAATTCAGCACATCTTTCTGTAAT	180
Db	139	AAATGCAAGAAAACTCTCAGCACATCCTTCTGTTAATTCAGCACATCTTTCTGTAAT	198
Qy	181	AAAGAAAGAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACACTGTTACTT	240
Db	199	AAAGAAAGAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACACTGTTACTT	258
Qy	241	TCCACGTTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG	300
Db	259	TCCACGTTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG	318
Qy	301	AAATTTGCTCACTGAGAGAAATCTGAAAAATGCGGAGGTAAAGACGCGTCCGCTTGTAACA	360
Db	319	AAATTTGCTCACTGAGAGAAATCTGAAAAATGCGGAGGTAAAGACGCGTCCGCTTGTAACA	378
Qy	361	AAAGATTTTCCAAAGATCTGGTTTGGGCTTTTACCTGATCATGTTAATGATTTTACA	420
Db	379	AAAGATTTTCCAAAGATCTGGTTTGGGCTTTTACCTGATCATGTTAATGATTTTACA	438
Qy	421	TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTTGAACATCAACATGTTGCTCTT	480
Db	439	TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACCTTGAACATCAACATGTTGCTCTT	498
Qy	481	TCTATTATCGTTTCAACATTTCAATCGACGAGCAATTTTATCGATTACATTTAGCCTGTTTA	540
Db	499	TCTATTATCGTTTCAACATTTCAATCGACGAGCAATTTTATCGATTACATTTAGCCTGTTTA	558
Qy	541	GTAACCAAAAAACACATTTACCGGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	600
Db	559	GTAACCAAAAAACACATTTACCGGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA	618
Qy	601	GATCTATCACCGCATCATTCGCAATATGAATAAATTCGATATTCGCTACGTCAGACAA	660
Db	619	GATCTATCACCGCATCATTCGCAATATGAATAAATTCGATATTCGCTACGTCAGACAA	678
Qy	661	AAAGATAACCGGTTTTCAAGCCAGTGCCTCGGAATATGGGATTTAGCTTTAGCAAAATAT	720
Db	679	AAAGATAACCGGTTTTCAAGCCAGTGCCTCGGAATATGGGATTTAGCTTTAGCAAAATAT	738
Qy	721	GACTTTATTTGGCTTACTCGAATGATGATTTAACAATCATTTGGTCCAAATTCATTCCTTAT	780
Db	739	GACTTTATTTGGCTTACTCGAATGATGATTTAACAATCATTTGGTCCAAATTCATTCCTTAT	798
Qy	781	GTTCGAGCTATTAGAAGTATGATTTAACAATCATTTGGTCCAAAGAAATACATCGAT	840
Db	799	GTTCGAGCTATTAGAAGTATGATTTAACAATCATTTGGTCCAAAGAAATACATCGAT	858
Qy	841	ACACAAACATATTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTGGCTGAATCAATTACCA	900
Db	859	ACACAAACATATTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTGGCTGAATCAATTACCA	918
Qy	901	GAAGTGAACCAATTAATAGTGTTCGGCCAAAGGGGAGGAACAGTTTCTCTGGATTGG	960

Db	919	GAAGTGAACCAATAATAGTGTTCGCCAAAAAGGGAAGGAACAGTTTCTCTGGATTGG	978
Qy	961	CGCTTAGAACCAATTCGAAAAACAGAAATCTCGCTTATCCGATTCGCTTTCCGTTTT	1020
Db	979	CGCTTAGAACCAATTCGAAAAACAGAAATCTCGCTTATCCGATTCGCTTTCCGTTTT	1038
Qy	1021	TTTCGGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAATCCGGTTTCTTTGAT	1080
Db	1039	TTTCGGCGGGTAATGTTGCTTTTCGCTAAAAAATGGCTAAATAATCCGGTTTCTTTGAT	1098
Qy	1081	GAGGAATTTAATCACTCGGGTGGAGAAAGATGTGAAATTTGGATATTCGCTTATTCGGTTAC	1140
Db	1099	GAGGAATTTAATCACTCGGGTGGAGAAAGATGTGAAATTTGGATATTCGCTTATTCGGTTAC	1158
Qy	1141	GGTAGTTTCTTTAAAACTATTGATGGCATTTATGCGCTACCATCAAGACCCACAGGTAAA	1200
Db	1159	GGTAGTTTCTTTAAAACTATTGATGGCATTTATGCGCTACCATCAAGACCCACAGGTAAA	1218
Qy	1201	GAAATGAACCCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG	1260
Db	1219	GAAATGAACCCGATCGTGAAGCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAAG	1278
Qy	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT	1320
Db	1279	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAAGATTCGCATATCAATAGAGTACCT	1338
Qy	1321	TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGGTAGAT	1380
Db	1339	TTAGTTTCAATTTATATCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGGTAGAT	1398
Qy	1381	AGTCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTGAAACGATGGTTCAACA	1440
Db	1399	AGTCACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTGTTGAAACGATGGTTCAACA	1458
Qy	1441	GATATACTTTAGAAAGTATCAATAAGCTTTATGTTAAATAATCTCTAGGGTAGCATCATG	1500
Db	1459	GATATACTTTAGAAAGTATCAATAAGCTTTATGTTAAATAATCTCTAGGGTAGCATCATG	1518
Qy	1501	TCTAAACCAATGGCGGAATAGCTCAGCATCAAAATGCAGCGGTTCTTTTGTCTAAGGT	1560
Db	1519	TCTAAACCAATGGCGGAATAGCTCAGCATCAAAATGCAGCGGTTCTTTTGTCTAAGGT	1578
Qy	1561	TATTAACATTTGGCGAGTTAGATTAGATGATTTATCTTGAGCTGTAGTGAATCTGTGT	1620
Db	1579	TATTAACATTTGGCGAGTTAGATTAGATGATTTATCTTGAGCTGTAGTGAATCTGTGT	1638
Qy	1621	TTAAAAAGAAATTTTAAAAAGATAAAAAACGCTAGCTGTGTGTTTATACCACTAATAGAAACGTC	1680
Db	1639	TTAAAAAGAAATTTTAAAAAGATAAAAAACGCTAGCTGTGTGTTTATACCACTAATAGAAACGTC	1698
Qy	1681	AATCGGATGGTAGCTTAATCGTAACTAATGGTTTAACTGGTTCAGGAGAAAAA	1740
Db	1699	AATCGGATGGTAGCTTAATCGTAACTAATGGTTCAGGAGAAAAA	1758
Qy	1741	CTCAACACGGCTATCATTTGCTCACCACCTTTAGAAATGTTACAGATTAGAGCTTTGGCATTTA	1800
Db	1759	CTCAACACGGCTATCATTTGCTCACCACCTTTAGAAATGTTACAGATTAGAGCTTTGGCATTTA	1818
Qy	1801	ACTGATGGAATCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC	1860
Db	1819	ACTGATGGAATCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC	1878
Qy	1861	AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAACTGCTATAAATCGGTGTTTACATGGT	1920
Db	1879	AGTGAAGTTGGAAAAATTTAAACATCTTAAATAAACTGCTATAAATCGGTGTTTACATGGT	1938
Qy	1921	GATAACATCAATTTAAGAACTTCGCAATTTCAAAAGAAAAACATTTTGTGTGATGCAAT	1980
Db	1939	GATAACATCAATTTAAGAACTTCGCAATTTCAAAAGAAAAACATTTTGTGTGATGCAAT	1998
Qy	1981	CAGTCATTAATAGCAAGGCATACTTATTATAATTTATGACGAATTTGATGATTTAGAT	2040

1021 TTTCGGCGGTAATGTTGCTTTTCGCTAAATAATGGCTAAATAATCCGGTTCCTTTGAT 1080  
1021 TTTCGGCGGGAATGTTGCTTTTCGCTAAATAATGGCTAAATAATCCGGTTCCTTTGAT 1080  
1081 GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATCCGTTAC 1140  
1081 GAGGAATTTAATCACTCGGGTGGAGAGATGTGGAAATTTGGATATCGCTTATCCGTTAC 1140  
1141 GGTAGTTTCTTTAAACCTATTTGATGCGCATTTATGCGCTTACCCTCAAGAGCCACGAGTAAA 1200  
1141 GGTAGTTTCTTTAAACCTATTTGATGCGCATTTATGCGCTTACCCTCAAGAGCCACGAGTAAA 1200  
1201 GAAATGAACCCGATCGTGAAGCGGGGAAAAATATTACGCTCGATATTTATGAGAGAAAAG 1260  
1201 GAAATGAACCCGATCGTGAAGCGGGGAAAAATATTACGCTCGATATTTATGAGAGAAAAG 1260  
1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTGCGCATATCAATAGAGTACCT 1320  
1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTGCGCATATCAATAGAGTACCT 1320  
1321 TTAGTTTCAATTTATATCCAGCTTATACTGTCGCAACTATATTCAACGTTGCGGTAGAT 1380  
1321 TTAGTTTCAATTTATATCCAGCTTATACTGTCGCAACTATATTCAACGTTGCGGTAGAT 1380  
1381 AGTCGACTGAATCAGACTGTTGTTGATCTCGAGGTTTGATTTGTAACGATGGTTCAACA 1440  
1381 AGTCGACTGAATCAGACTGTTGTTGATCTCGAGGTTTGATTTGTAACGATGGTTCAACA 1440  
1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATATCTAGGGTACGCATCATG 1500  
1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATATCTAGGGTACGCATCATG 1500  
1501 TCTAAACCAATGCGGAATAGCTCAGCATCAATGCGAGCGGTTCTTTTGTCTAAAGGT 1560  
1501 TCTAAACCAATGCGGAATAGCTCAGCATCAATGCGAGCGGTTCTTTTGTCTAAAGGT 1560  
1561 TATTACATGCGGAGTTAGATTGAGTCAATGATTTCTGAGCCTGATGAGTTGAACTGTG 1620  
1561 TATTACATGCGGAGTTAGATTGAGTCAATGATTTCTGAGCCTGATGAGTTGAACTGTG 1620  
1621 TTTAAAGAAATTTTAAAGATATAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
1621 TTTAAAGAAATTTTAAAGATATAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1680  
1681 AATCCGGATGTAAGTTAATCGCTTAATGGTTTCAATGCGGCAAGATTTTCAAGAGAAAA 1740  
1681 AATCCGGATGTAAGTTAATCGCTTAATGGTTTCAATGCGGCAAGATTTTCAAGAGAAAA 1740  
1741 CTCACACCGCTATGATTGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
1741 CTCACACCGCTATGATTGCTCACCCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
1801 ACTGATGATTCAATGAAAAAATGAAAAATGCGGCTAGACTATGACATGTTCTCAAACTC 1860  
1801 ACTGATGATTCAATGAAAAAATGAAAAATGCGGCTAGACTATGACATGTTCTCAAACTC 1860  
1861 AGTGAAGTTGGAAAAATTTTAAACATCTTAAATAATCTGCTATAACCGGTGATTACATGGT 1920  
1861 AGTGAAGTTGGAAAAATTTTAAACATCTTAAATAATCTGCTATAACCGGTGATTACATGGT 1920  
1921 GATACACATCAATTTAAGAACTTGGCAATTTCAAGAGAAAAACCAATTTTGTGTAGTCAAT 1980  
1921 GATACACATCAATTTAAGAACTTGGCAATTTCAAGAGAAAAACCAATTTTGTGTAGTCAAT 1980  
1981 CAGTCATTAAATAGACAGGATACCTTATTATATATGATGAGATTTGATGATTAGAT 2040  
1981 CAGTCATTAAATAGACAGGATACCTTATTATATATGATGAGATTTGATGATTAGAT 2040  
2041 GAAAGTAGAAGATATATTTTCAATAAAAACCGCTGATATCAAGAGAGATTGATATCTTA 2100  
2041 GAAAGTAGAAGATATATTTTCAATAAAAACCGCTGATATCAAGAGAGATTGATATCTTA 2100

2101 AAAGATATTAAATATCATCCAGATAAAGATGCCAAATCGCAGTCAGTATTTTTTATCCC 2160  
2101 AAAGATATTAAATATCATCCAGATAAAGATGCCAAATCGCAGTCAGTATTTTTTATCCC 2160  
2161 AATACATTAACCGCTTAGTGAAGAACTAAACAATATTATTGAATATAATAAAAAATATA 2220  
2161 AATACATTAACCGCTTAGTGAAGAACTAAACAATATTATTGAATATAATAAAAAATATA 2220  
2221 TTCTGTTATTGTTCTCATCATGTTGATAAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
2221 TTCTGTTATTGTTCTCATCATGTTGATAAGAATCATCTTACACCAGATATCAAAAAAGAAATA 2280  
2281 CTAGCCTTCTATCATAAAAATCAAGTGAATATTTTACTAAATTAATCATATCTCATATTAC 2340  
2281 CTAGCCTTCTATCATAAAAATCAAGTGAATATTTTACTAAATTAATCATATCTCATATTAC 2340  
2341 ACCAGTAATAGATTAAATAAACTGAGGCGCATTTAAGTAATATTAAATAATTAAGTCAG 2400  
2341 ACCAGTAATAGATTAAATAAACTGAGGCGCATTTAAGTAATATTAAATAATTAAGTCAG 2400  
2401 TTAATCTAAATTTGTAATACATCATTTTGTGATAATCATGACAGCCTTATTCGTTAAAAAT 2460  
2401 TTAATCTAAATTTGTAATACATCATTTTGTGATAATCATGACAGCCTTATTCGTTAAAAAT 2460  
2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGCAATGAATTTCTCAGCATTAACACAT 2520  
2461 GACAGCTATGCTTATATGAAAAAATATGATGTCGCAATGAATTTCTCAGCATTAACACAT 2520  
2521 GATTGATCGAGAAATCAATGCGCATCCACCTTTTAAAGAGCTCATTAAGCTTATTTT 2580  
2521 GATTGATCGAGAAATCAATGCGCATCCACCTTTTAAAGAGCTCATTAAGCTTATTTT 2580  
2581 AATGACAACTGACTTAAAGAGTATGAATGTGAAAGGGGCATCAAGAGTATGTTTATGACG 2640  
2581 AATGACAACTGACTTAAAGAGTATGAATGTGAAAGGGGCATCAAGAGTATGTTTATGACG 2640  
2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGCTCATCAATCTTGCCAGTCA 2700  
2641 TATGCGCTAGCGCATGAGCTTCTGACGATTTTAAAGAGCTCATCAATCTTGCCAGTCA 2700  
2701 ATTGATAGTGTGCGAGATATAACACTGAGGATATTGGTTCCCAATTTGCACTTTTAATC 2760  
2701 ATTGATAGTGTGCGAGATATAACACTGAGGATATTGGTTCCCAATTTGCACTTTTAATC 2760  
2761 TTAGAAAGAAAAACCGGCCATGATTTTAAACAATCGACCTGACTTATATGCTTTGG 2820  
2761 TTAGAAAGAAAAACCGGCCATGATTTTAAACAATCGACCTGACTTATATGCTTTGG 2820  
2821 GAACGAAAAATTACAAATGGACAAATGAACAAATTTGAAAGTGCMAAAGAGGAGAAAAATATA 2880  
2821 GAACGAAAAATTACAAATGGACAAATGAACAAATTTGAAAGTGCMAAAGAGGAGAAAAATATA 2880  
2881 CCTGTTAAAGTTTCAATTTATTAAGTATACTCTATAA 2920  
2881 CCTGTTAAAGTTTCAATTTATTAAGTATACTCTATAA 2920

## RESULT 3

US-10-011-768B-8  
; Sequence 8, Application US/10011768B  
; Publication No. US20030073221A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H.  
; APPLICANT: Deangelis, Paul  
; APPLICANT: Kumari, Kehana  
; TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
; FILE REFERENCE: 3554.011  
; CURRENT APPLICATION NUMBER: US/10/011,768B  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: US 60/064,435  
; PRIOR FILING DATE: 1997-10-31

QY 2461 GACAGCTATGCTTATATGAAAAATATGATGTCGCGCATGAATTTCTCAGCAATTAACACAT 2520  
Db 2461 GACAGCTATGCTTATGAAAAAATATGATGTCGCGCATGAATTTCTCAGCAATTAACACAT 2520  
QY 2521 GATTGGATCGAGAAAATCAATGCGCATCCACCATTAAAAAGCTCATTTAAAACTTATTTT 2580  
Db 2521 GATTGGATCGAGAAAATCAATGCGCATCCACCATTAAAAAGCTCATTTAAAACTTATTTT 2580  
QY 2581 AATGCAATAGCTTAAAAAGTATGAATGTGAAAAGGGCGCATCAAGGTATGTTTATGACG 2640  
Db 2581 AATGCAATAGCTTAAAAAGTATGAATGTGAAAAGGGCGCATCAAGGTATGTTTATGACG 2640  
QY 2641 TATGGCTAGCGCATGAGCTTCTGAGCATATTAAGAAGTCAATCAATCTTGGCAGTCA 2700  
Db 2641 TATGGCTAGCGCATGAGCTTCTGAGCATATTAAGAAGTCAATCAATCTTGGCAGTCA 2700  
QY 2701 ATTGATAGTGTGCCAGATATAAACAATGAGGATATTTGTTCCAAATTTGCACTTTTAATC 2760  
Db 2701 ATTGATAGTGTGCCAGATATAAACAATGAGGATATTTGTTCCAAATTTGCACTTTTAATC 2760  
QY 2761 TTAGAAAAAGAAACCGGCCATGTATTTAATAAACAATCGACCTGACTTATATGCTTTGG 2820  
Db 2761 TTAGAAAAAGAAACCGGCCATGTATTTAATAAACAATCGACCTGACTTATATGCTTTGG 2820  
QY 2821 GAACGAAAATTACAATGAGCAAAATGAACAAATTTGAAAGTGCAAAAGAGGAGAAAATATA 2880  
Db 2821 GAACGAAAATTACAATGAGCAAAATGAACAAATTTGAAAGTGCAAAAGAGGAGAAAATATA 2880  
QY 2881 CCTGTTACAGTTCATTATTAATAGTATTAACCTATATAA 2920  
Db 2881 CCTGTTACAGTTCATTATTAATAGTATTAACCTATATAA 2920

RESULT 2

US-10-642-248-1  
; Sequence 1, Application US/10642248  
; Publication No. US20040132143A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; APPLICANT: Jing, Wei  
; TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METHOD  
; TITLE OF INVENTION: MAKING AND USING SAME  
; FILE REFERENCE: 3554.097  
; CURRENT APPLICATION NUMBER: US/10/642,248  
; CURRENT FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/842,484  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2920  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida

US-10-642-248-1

Query Match 100.0%; Score 2920; DB 7; Length 2920;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGATAATCATTTATCAAGCAATAAAAAAGCATATATAACAGCAATGACTATCAATTAGCACTC 60  
Db 1 ATGATAATCATTTATCAAGCAATATAAAGCATATAAAGCAATGACTATCAATTAGCACTC 60  
QY 61 AAATTTATTTGAAAAGTCGCGGGAATCTATGAGCGGAAAATTTGTTGAAATTTCAAATTACC 120  
Db 61 AAATTTATTTGAAAAGTCGCGGGAATCTATGAGCGGAAAATTTGTTGAAATTTCAAATTACC 120  
QY 121 AAATGCAAGAAAACCTCTCAGCACATCTCTCTGTTAATTTTCAGCACATCTTTCTGTTAAAT 180  
Db 121 AAATGCAAGAAAACCTCTCAGCACATCTCTCTGTTAATTTTCAGCACATCTTTCTGTTAAAT 180  
QY 181 AAAGAAGAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACAACTGTTACTT 240  
Db 181 AAAGAAGAAAAGTCAATGTTTGGCATAGTCCGTTAGATATTGCAACACAACTGTTACTT 240  
QY 241 TCCAACGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300  
Db 241 TCCAACGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300  
QY 301 AAATTTGCTCACTGAGAGAAAATCTGAAAATTCGCGAGGTAAAGCGGTCGCCCTTTGTACCA 360  
Db 301 AAATTTGCTCACTGAGAGAAAATCTGAAAATTCGCGAGGTAAAGCGGTCGCCCTTTGTACCA 360  
QY 361 AAAGATTTTCCCAAGATCTGTTTTTAGCGCTTTTACTGATCATGTTAAATGATTTTACA 420  
Db 361 AAAGATTTTCCCAAGATCTGTTTTTAGCGCTTTTACTGATCATGTTAAATGATTTTACA 420  
QY 421 TGGTACAAAAAGCGAAAAGAAAGACTTTGGCATATAAAACCTGAAATCAACATGTTGGTCTT 480  
Db 421 TGGTACAAAAAGCGAAAAGAAAGACTTTGGCATATAAAACCTGAAATCAACATGTTGGTCTT 480  
QY 481 TCTATTATCGTTACAAACATTCATCGACCAGCAATTTTATCGATTACATTTAGCCCTGTTTA 540  
Db 481 TCTATTATCGTTACAAACATTCATCGACCAGCAATTTTATCGATTACATTTAGCCCTGTTTA 540  
QY 541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db 541 GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
QY 601 GATCTATCACCGATCATTTCCGCAATATGAAAATAAATTTGGAATATTCGCTACGTCAGACAA 660  
Db 601 GATCTATCACCGATCATTTCCGCAATATGAAAATAAATTTGGAATATTCGCTACGTCAGACAA 660  
QY 661 AAAGATAACGGTTTTTCAAGCCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAAATAT 720  
Db 661 AAAGATAACGGTTTTTCAAGCCAGTCCGCTCGGAATATGGGATTTACGCTTAGCAAAAATAT 720  
QY 721 GACTTTATTTGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGTTTCATTTTAT 780  
Db 721 GACTTTATTTGGCTTACTCGACTGTGATATGCGCCAAATCCATTTATGGTTTCATTTTAT 780  
QY 781 GTTGACAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGTTCCAAAGAAAATACATCGAT 840  
Db 781 GTTGACAGAGCTATTAGAAGATGATGATTTAAACAATCATTTGTTCCAAAGAAAATACATCGAT 840  
QY 841 ACACAACATATTTGACCCCAAAAAGACTTTCTTAATAAACCGGAGTTTGTCTTGAATCATTACCA 900  
Db 841 ACACAACATATTTGACCCCAAAAAGACTTTCTTAATAAACCGGAGTTTGTCTTGAATCATTACCA 900  
QY 901 GAAGTGAAGAAACCAATTAATAGTTGTTCCGCAAAAGGGAGGAAAGAGTTTCTCTGATTTGG 960  
Db 901 GAAGTGAAGAAACCAATTAATAGTTGTTCCGCAAAAGGGAGGAAAGAGTTTCTCTGATTTGG 960  
QY 961 CGCTTTAGAAACAATTCGAAAAAACAAGAAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTTT 1020  
Db 961 CGCTTTAGAAACAATTCGAAAAAACAAGAAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTTT 1020

Db 241 TCCAAACGTAAAAAATAGTACTTCTGACTCGGAAAAAACAACGTTAAAAAATAAATGG 300  
Qy 301 AATTTGCTCACTGAGAGAAATCTGAANAATCGGAGGTAGAGCGGTGCGCTTGTACCA 360  
Db 301 AATTTGCTCACTGAGAGAAATCTGAANAATCGGAGGTAGAGCGGTGCGCTTGTACCA 360  
Qy 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTACCTGATCATGTTAATGATTTTACA 420  
Db 361 AAAGATTTTCCAAAGATCTGGTTTATAGCGCTTTA CTTGATCATGTTAATGATTTTACA 420  
Qy 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAAACTGAAACATCAACATGTTGGTCTT 480  
Db 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAAACTGAAACATCAACATGTTGGTCTT 480  
Qy 481 TCTATTATCGTTACAAATCAATCGACCGCAATTTTATCGATTACATTAATGAGCTGTTA 540  
Db 481 TCTATTATCGTTACAAATCAATCGACCGCAATTTTATCGATTACATTAATGAGCTGTTA 540  
Qy 541 GTAAACCAAAAAACACATTAACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db 541 GTAAACCAAAAAACACATTAACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Qy 601 GATCTATCACCGATCATTTGCGCAATATGAANAATTAATTTGGATATTCGCTACGTCAGACAA 660  
Db 601 GATCTATCACCGATCATTTGCGCAATATGAANAATTAATTTGGATATTCGCTACGTCAGACAA 660  
Qy 661 AAGATTAACGGTTTTTCAAGCCAGTGGCGCTCGGAATATGGGATTAACGCTTAGCAANAAT 720  
Db 661 AAGATTAACGGTTTTTCAAGCCAGTGGCGCTCGGAATATGGGATTAACGCTTAGCAANAAT 720  
Qy 721 GACTTTATTTGCTTACTCGACTGTGATGATGCGCAAAATCCATTAATGGGTTCACTCTTAT 780  
Db 721 GACTTTATTTGCTTACTCGACTGTGATGATGCGCAAAATCCATTAATGGGTTCACTCTTAT 780  
Qy 781 GTTCGAGAGCTATTAGAGATGATGA TTTAAACAATCATTTGGTCCAAAGAAATAATCGAT 840  
Db 781 GTTCGAGAGCTATTAGAGATGATGA TTTAAACAATCATTTGGTCCAAAGAAATAATCGAT 840  
Qy 841 ACACAACATATTGACCCAAAGACTTCTTAATAACCGAGTTTGGTGAATCATTAACCA 900  
Db 841 ACACAACATATTGACCCAAAGACTTCTTAATAACCGAGTTTGGTGAATCATTAACCA 900  
Qy 901 GAAGTGAACCAATATAGTGTTCGCGCAAAAGCGGAAGAACAGTTCTCTCGATTGG 960  
Db 901 GAAGTGAACCAATATAGTGTTCGCGCAAAAGCGGAAGAACAGTTCTCTCGATTGG 960  
Qy 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020  
Db 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTTCCGTTTT 1020  
Qy 1021 TTTGGCGGGTAAATGTTGCTTTCGCTAAAAAATGGCTAAATAATCCGTTTTCTTTGAT 1080  
Db 1021 TTTGGCGGGTAAATGTTGCTTTCGCTAAAAAATGGCTAAATAATCCGTTTTCTTTGAT 1080  
Qy 1081 GAGGAATTTAATCACTGGGTGGAGAGATGTGNAATTTGGATATCGCTTATTCGTTAC 1140  
Db 1081 GAGGAATTTAATCACTGGGTGGAGAGATGTGNAATTTGGATATCGCTTATTCGTTAC 1140  
Qy 1141 GGTAGTTTTCTTTAAACATTTGATGGCATTATGGCCTAACATCAAGAGCCACCGAGTAA 1200  
Db 1141 GGTAGTTTTCTTTAAACATTTGATGGCATTATGGCCTAACATCAAGAGCCACCGAGTAA 1200  
Qy 1201 GAAATGAACCGATCGTGAACCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260  
Db 1201 GAAATGAACCGATCGTGAACCGGAAAAAATATTACGCTCGATATTATGAGAGAAAAG 1260  
Qy 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
Db 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATTAACCTGTGCAAACTATATTCAACGTTGGGTAGAT 1380

Db 1321 TTAGTTTCAATTTATATCCAGCTTATATACTGTGCAAACTATATTCAACGTTGGGTAGAT 1380  
Qy 1381 AGTGCACCTAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1440  
Db 1381 AGTGCACCTAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1440  
Qy 1441 GATAAATACCTTTAGAAAGTGATCAATAAGCTTTATGGTAATTAATCTTAGGGTAGCATCATG 1500  
Db 1441 GATAAATACCTTTAGAAAGTGATCAATAAGCTTTATGGTAATTAATCTTAGGGTAGCATCATG 1500  
Qy 1501 TCTAARACCAATGCGGAAATAGCCTCAGCATCAAAATGACGCGTTCTTTTGTCTTAAAGGT 1560  
Db 1501 TCTAARACCAATGCGGAAATAGCCTCAGCATCAAAATGACGCGTTCTTTTGTCTTAAAGGT 1560  
Qy 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTTGAGCCTGATGCAAGTTGAACCTGT 1620  
Db 1561 TATTACATTTGGCGAGTTAGATTTCAGATGATTATCTTTGAGCCTGATGCAAGTTGAACCTGT 1620  
Qy 1621 TTTAAAGAAATTTTAAAGATATAAAACGCTAGCTTGTGTTTATACCCTAATATAGAAACGTC 1680  
Db 1621 TTTAAAGAAATTTTAAAGATATAAAACGCTAGCTTGTGTTTATACCCTAATATAGAAACGTC 1680  
Qy 1681 AATCCGAGTGGTAAATCGCTTAATCGCTAAATGGTTTACAATTTGGCCAGAAATTTTCAAGAGAAA 1740  
Db 1681 AATCCGAGTGGTAAATCGCTTAATCGCTAAATGGTTTACAATTTGGCCAGAAATTTTCAAGAGAAA 1740  
Qy 1741 CTCAACACGCTATGATTGCTCACCACTTTAGAAATGTTTACGATTAGAGCTTGGCAATTTA 1800  
Db 1741 CTCAACACGCTATGATTGCTCACCACTTTAGAAATGTTTACGATTAGAGCTTGGCAATTTA 1800  
Qy 1801 ACTGATGGATTCAATGAAAAATTTGAAATGCGCTAGCTATGACATGTTCTCTCAAACTC 1860  
Db 1801 ACTGATGGATTCAATGAAAAATTTGAAATGCGCTAGCTATGACATGTTCTCTCAAACTC 1860  
Qy 1861 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATACCGTGTATTACATGGT 1920  
Db 1861 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATACCGTGTATTACATGGT 1920  
Qy 1921 GATTAACACATCAATTAAGAAATCTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Db 1921 GATTAACACATCAATTAAGAAATCTTGGCATTTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Qy 1981 CAGTCATTAAATAGAACGATTAACCTTTATTAATTAATGACGAAATTTGATGATTTAGAT 2040  
Db 1981 CAGTCATTAAATAGAACGATTAACCTTTATTAATTAATGACGAAATTTGATGATTTAGAT 2040  
Qy 2041 GAAAGTGAAGTATATTTTCAATTAACACGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
Db 2041 GAAAGTGAAGTATATTTTCAATTAACACGCTGAATATCAAGAGAGATTTGATATCTTA 2100  
Qy 2101 AAAGATATTAAAAATCAATCCAGAAATAAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2160  
Db 2101 AAAGATATTAAAAATCAATCCAGAAATAAAGATGCCAAAATCGCAGTCAGTATTTTATATCCC 2160  
Qy 2161 AATAACATTAAACGCTTAGTGAATAAAAACTAAACCAATATTATTTGAATATAATAAAAAATA 2220  
Db 2161 AATAACATTAAACGCTTAGTGAATAAAAACTAAACCAATATTATTTGAATATAATAAAAAATA 2220  
Qy 2221 TTGCTTATTTGTTCTACATGTTGATTAAGAAATCATCTTACACGATATCAAAAAAGAAATA 2280  
Db 2221 TTGCTTATTTGTTCTACATGTTGATTAAGAAATCATCTTACACGATATCAAAAAAGAAATA 2280  
Qy 2281 CTAGCCTTCTATCATAAACATCAAGTGAATTTTAACTAAATATGATATCTCATATTTAC 2340  
Db 2281 CTAGCCTTCTATCATAAACATCAAGTGAATTTTAACTAAATATGATATCTCATATTTAC 2340  
Qy 2341 ACAGATTAATAGATTAATAAAAACTGAGCGCATTTAAGTAAATATAATAAATTAAGTCAG 2400  
Db 2341 ACAGATTAATAGATTAATAAAAACTGAGCGCATTTAAGTAAATATAATAAATTAAGTCAG 2400  
Qy 2401 TTAATCTAAATTTGTTGAATACATCATTTTGTGATTAATCATGACGCTTATTCGTTTAAAT 2460  
Db 2401 TTAATCTAAATTTGTTGAATACATCATTTTGTGATTAATCATGACGCTTATTCGTTTAAAT 2460

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 10:04:45 ; Search time 2070 Seconds

(without alignments)  
11665.016 Million cell updates/sec

Title: US-10-642-248-1

Perfect score: 2920

Sequence: 1 atgaatacattatcacagc.....taatagataactctataaa 2920

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2920	100.0	2920	5	US-10-217-613-2
2	2920	100.0	2920	7	US-10-642-248-1
3	2919	100.0	2937	5	US-10-011-768B-8
4	2919	100.0	2937	5	US-10-011-771B-8
5	2919	100.0	2937	10	US-11-109-855-8
6	2917.4	99.9	2937	3	US-09-879-959-9
7	2917.4	99.9	2937	5	US-10-172-527-9
8	2917.4	99.9	2937	6	US-10-309-560-7
9	2914.4	99.8	2916	6	US-10-326-185-94
10	2914.4	99.8	2916	10	US-11-096-190-8
11	2271.2	77.8	2979	3	US-09-842-484A-1
12	2271.2	77.8	2979	5	US-10-184-485-4
13	2271.2	77.8	2979	10	US-11-042-530-1
14	2269.4	77.7	2271	7	US-10-642-248-20
15	2266.4	77.6	2979	3	US-09-842-484A-3
16	2266.4	77.6	2979	7	US-10-642-248-3
17	2266.4	77.6	2979	9	US-10-197-153-4
18	2266.4	77.6	2979	10	US-11-042-530-3
19	2110.4	72.3	2112	7	US-10-642-248-71
20	2110.4	72.3	2112	9	US-10-197-153-2
21	2108.8	72.2	2112	5	US-10-184-485-2
22	2108.8	72.2	2112	7	US-10-642-248-11
23	2108.8	72.2	2112	7	US-10-642-248-12

24	2108.8	72.2	2112	7	US-10-642-248-16	Sequence 16, Appl
25	2108.8	72.2	2112	7	US-10-642-248-18	Sequence 18, Appl
26	2108.8	72.2	2112	7	US-10-642-248-33	Sequence 33, Appl
27	2108.8	72.2	2112	7	US-10-642-248-34	Sequence 34, Appl
28	2108.8	72.2	2112	7	US-10-642-248-36	Sequence 36, Appl
29	2108.8	72.2	2112	7	US-10-642-248-37	Sequence 37, Appl
30	2108.8	72.2	2112	7	US-10-642-248-39	Sequence 39, Appl
31	2108.8	72.2	2112	7	US-10-642-248-40	Sequence 40, Appl
32	2108.8	72.2	2112	7	US-10-642-248-42	Sequence 42, Appl
33	2108.8	72.2	2112	7	US-10-642-248-43	Sequence 43, Appl
34	2108.8	72.2	2112	7	US-10-642-248-45	Sequence 45, Appl
35	2108.8	72.2	2112	7	US-10-642-248-46	Sequence 46, Appl
36	2108.8	72.2	2112	7	US-10-642-248-48	Sequence 48, Appl
37	2108.8	72.2	2112	7	US-10-642-248-49	Sequence 49, Appl
38	2107.2	72.2	2112	7	US-10-642-248-17	Sequence 17, Appl
39	2107.2	72.2	2112	7	US-10-642-248-19	Sequence 19, Appl
40	2107.2	72.2	2112	7	US-10-642-248-35	Sequence 35, Appl
41	2107.2	72.2	2112	7	US-10-642-248-38	Sequence 38, Appl
42	2107.2	72.2	2112	7	US-10-642-248-41	Sequence 41, Appl
43	2107.2	72.2	2112	7	US-10-642-248-44	Sequence 44, Appl
44	2107.2	72.2	2112	7	US-10-642-248-47	Sequence 47, Appl
45	2107.2	72.2	2112	7	US-10-642-248-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1

US-10-217-613-2  
; Sequence 2, Application US/10217613  
; Publication No. US20030113845A1  
; GENERAL INFORMATION:  
; APPLICANT: DEANGELIS, PAUL  
; TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND US  
; FILE REFERENCE: 35541.081  
; CURRENT APPLICATION NUMBER: US/10/217,613  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 09/178,851  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 2920  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-10-217-613-2

Query Match	100.0%	Score 2920;	DB 5;	Length 2920;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2920;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAATACATTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC	60	
Db	1	ATGAATACATTATCAAGCAATAAAGCATATAACAGCAATGACTATCAATTAGCACTC	60	
QY	61	AAATTTTGAAGTCGCGGAAATCTATGACGAAATTTGTCGAAATTTCAAATTAACC	120	
Db	61	AAATTTTGAAGTCGCGGAAATCTATGACGAAATTTGTCGAAATTTCAAATTAACC	120	
QY	121	AAATGCAAGAAAAAATCTCTCAGCACATCTCTGTTTAATTCAGCACATCTTTCTGTAAT	180	
Db	121	AAATGCAAGAAAAAATCTCTCAGCACATCTCTGTTTAATTCAGCACATCTTTCTGTAAT	180	
QY	181	AAAGAAGAAAAAGTCAATGTTTCCGATAGTCGTTAGATATTCGCAACACACTGTTACTT	240	
Db	181	AAAGAAGAAAAAGTCAATGTTTCCGATAGTCGTTAGATATTCGCAACACACTGTTACTT	240	
QY	241	TCCACGTAAGAAAAATAGTACTTCTGACTCGAAAAAACAACGTTAAAAATAAATG	300	



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2006, 12:56:41 ; Search time 388 Seconds  
(without alignments)  
5485.817 Million cell updates/sec

Title: US-10-642-248-1

Perfect score: 2920

Sequence: 1 atgaatcacatcacacaagc.....taataagcacaactcctacaa 2920

Scoring table: IDENTITY NUC  
Gapop 10.0', Gapext 1.0

Searched: 4637609 seqs, 364468668 residues

Total number of hits satisfying chosen parameters: 9275218

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_NA\_New:\*  
1: /cgn2\_6/ptocdata/2/pubpna/US06\_NEW\_PUB.seq:\*  
2: /cgn2\_6/ptocdata/2/pubpna/US07\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptocdata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptocdata/2/pubpna/US07\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptocdata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptocdata/2/pubpna/US10\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptocdata/2/pubpna/US11\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptocdata/2/pubpna/US11\_NEW\_PUB.seq:\*  
9: /cgn2\_6/ptocdata/2/pubpna/US11\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptocdata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2920	100.0	2920	7	US-11-172-145-1
2	2917.4	99.9	2937	7	US-11-124-215-2
3	2917.4	99.9	2937	7	US-11-120-422-9
4	2266.4	77.6	2979	7	US-11-172-145-3
5	2110.4	72.3	2112	7	US-11-172-145-11
6	2108.8	72.2	2112	7	US-11-172-145-17
7	2108.8	72.2	2112	7	US-11-172-145-18
8	2108.8	72.2	2112	7	US-11-172-145-19
9	2108.8	72.2	2112	7	US-11-172-145-20
10	1975.4	67.7	1980	7	US-11-172-145-13
11	1898.4	65.0	1902	7	US-11-172-145-14
12	1826.8	62.6	1830	7	US-11-172-145-15
13	1759.4	60.3	1764	7	US-11-172-145-16
14	173.6	2.5	49979	6	US-10-995-561-13443
15	68.6	2.3	171486	7	US-11-121-086-105
16	65.2	2.2	6156	6	US-10-240-708-60
17	65.2	2.2	173602	6	US-11-121-086-25
18	65	2.2	119036	6	US-10-995-561-13314
19	64	2.1	6507	6	US-10-485-517-75
20	62.2	2.1	26772	6	US-10-995-561-13313
21	62.2	2.1	54946	6	US-10-995-561-13479
22	62.2	2.1	10467	6	US-10-240-708-2
23	61.6	2.1	10467	6	US-10-240-708-2

24	60.8	2.1	171486	7	US-11-121-086-105	Sequence 105, App
25	60.6	2.1	49979	6	US-10-995-561-13443	Sequence 13443, A
26	60	2.1	26772	6	US-10-995-561-13313	Sequence 13313, A
27	60	2.1	54946	6	US-10-995-561-13479	Sequence 13479, A
28	60	2.1	201990	6	US-10-995-561-13303	Sequence 13303, A
29	59.6	2.0	6866	6	US-10-240-708-20	Sequence 20, App1
30	59	2.0	5152	6	US-10-240-708-74	Sequence 74, App1
31	58.6	2.0	119036	6	US-10-995-561-13314	Sequence 13314, A
32	57.6	2.0	1299	6	US-10-793-626-779	Sequence 779, App
33	57.6	2.0	3119	6	US-10-793-626-4270	Sequence 4270, App
34	57.6	2.0	3645	6	US-10-793-626-4110	Sequence 4110, App
35	57.4	2.0	5455	6	US-10-240-708-33	Sequence 33, App1
36	57.2	2.0	5076	6	US-11-077-550-135	Sequence 135, App
37	56.8	1.9	2509	6	US-10-750-185-27479	Sequence 27479, A
38	56.8	1.9	2509	6	US-10-750-623-37479	Sequence 37479, A
39	56.8	1.9	135054	7	US-11-121-086-96	Sequence 96, App1
40	56.6	1.9	6583	6	US-10-240-708-26	Sequence 26, App1
41	55.8	1.9	6656	6	US-10-240-708-75	Sequence 75, App1
42	55.2	1.9	139054	7	US-11-121-086-96	Sequence 96, App1
43	55	1.9	6113	6	US-10-240-708-13	Sequence 13, App1
44	54.2	1.9	6669	6	US-10-240-708-6	Sequence 6, App1
45	53.8	1.8	2739	9	US-11-077-550-115	Sequence 115, App1

#### ALIGNMENTS

```
RESULT 1
US-11-172-145-1
; Sequence 1, Application US/11172145
; Publication No. US20050272696A1
; GENERAL INFORMATION:
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISORDERS WITH SPECIFIC
; FILE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS
; FILE REFERENCE: 3554.104
; CURRENT APPLICATION NUMBER: US/11/172,145
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/584,442
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 10/642,248
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/404,356
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 60/491,362
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/479,432
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 10/195,908
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/437,277
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 60/107,929
; PRIOR FILING DATE: 1998-11-11
; PRIOR APPLICATION NUMBER: 09/283,402
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/080,414
; PRIOR FILING DATE: 1999-04-02
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patencin version 3.3
; SEQ ID NO 1
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-1
Query Match      100.0%; Score 2920; DB 7; Length 2920;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAATACATTAATCAACAGCAATTAAGCATTAACAGCAAGCAATTAATTAAGCACTC 60
|||||
```

Dh 1 ATGATACATTATGCAACAACATATAAAGCATATAACAGCAATGACTATCATTAATAGCACTC 60  
Qy AAAATTTATTTGAAAAGTGGCGGAAAATCTATAGACGGAAAATTTGTGAATTTTCAAAATTAAC 120  
Dh 61 AAAATTTATTTGAAAAGTGGCGGAAAATCTATAGACGGAAAATTTGTGAATTTTCAAAATTAAC 120  
Qy 121 AAATGCAAAAGAAAACCTCAGACACATCCTTCTGTAAATTCAGACACATCTTTCTGTAAAT 180  
Dh 121 AAATGCAAAAGAAAACCTCAGACACATCCTTCTGTAAATTCAGACACATCTTTCTGTAAAT 180  
Qy 181 AAAGAGAAAAGTCAATGTTTGGCAGATGTCGTTAGATTTGCAACAACTGTACTT 240  
Dh 181 AAAGAGAAAAGTCAATGTTTGGCAGATGTCGTTAGATTTGCAACAACTGTACTT 240  
Qy 241 TCCAAACGTAAAAAATTTGTACTTCTTCTGACCTCGAAAAAACAAGTTAAAAAATTAATGG 300  
Dh 241 TCCAAACGTAAAAAATTTGTACTTCTTCTGACCTCGAAAAAACAAGTTAAAAAATTAATGG 300  
Qy 301 AAATGCTCAGTGAAGAAATCTGAAAATGCGAGATGAAGCGGTGCGCTTGTACCA 360  
Dh 301 AAATGCTCAGTGAAGAAATCTGAAAATGCGAGATGAAGCGGTGCGCTTGTACCA 360  
Qy 361 AAAGATTTTCCCAAGATCTGGTTTTCAGCCTTTTACCTGATCATGTTAATGATTTTACA 420  
Dh 361 AAAGATTTTCCCAAGATCTGGTTTTCAGCCTTTTACCTGATCATGTTAATGATTTTACA 420  
Qy 421 TGGTACAAAAGCGGAAAAGAAAGACTTGGCATTAACCTGAACATCAACATGTTGCTT 480  
Dh 421 TGGTACAAAAGCGGAAAAGAAAGACTTGGCATTAACCTGAACATCAACATGTTGCTT 480  
Qy 481 TCTATATCGTTACCAACATTCGACAGCAATTTTATGATTCATTAAGCTGTTT 540  
Dh 481 TCTATATCGTTACCAACATTCGACAGCAATTTTATGATTCATTAAGCTGTTT 540  
Qy 541 GTAAAACCAAAAAACCATTAACCCGTTTGAAGTTATGTCAGATGATGTAAGTCAGAA 600  
Dh 541 GTAAAACCAAAAAACCATTAACCCGTTTGAAGTTATGTCAGATGATGTAAGTCAGAA 600  
Qy 601 GATCTATACCGGATTCATTCGCGCAATATGAAAATTAATGGATTCGCTAGTCAGACAA 660  
Dh 601 GATCTATACCGGATTCATTCGCGCAATATGAAAATTAATGGATTCGCTAGTCAGACAA 660  
Qy 661 AAAGATTAACCGGTTTCAAGCCAGTCCGCTCGAATATGAGATTACGCTTACGCAAAATAT 720  
Dh 661 AAAGATTAACCGGTTTCAAGCCAGTCCGCTCGAATATGAGATTACGCTTACGCAAAATAT 720  
Qy 721 GACTTATTTGGCTTACTCGACTGTGATATGGCGCAATTCATTAATGAGGTTCAATCTTAT 780  
Dh 721 GACTTATTTGGCTTACTCGACTGTGATATGGCGCAATTCATTAATGAGGTTCAATCTTAT 780  
Qy 781 GTTGCAGAGCTATTTGAAGATGATGATTAACAATCATTTGTCGCAAGAAATTAATCATGAT 840  
Dh 781 GTTGCAGAGCTATTTGAAGATGATGATTAACAATCATTTGTCGCAAGAAATTAATCATGAT 840  
Qy 841 ACACAACATATTTGACCCAAAAGACTTCTTAAATACGCGAGTTTGTCTTGGAATCATTAACA 900  
Dh 841 ACACAACATATTTGACCCAAAAGACTTCTTAAATACGCGAGTTTGTCTTGGAATCATTAACA 900  
Qy 901 GAAAGTGAAGAACCAATATATAGTGTGCGCAAAAGGGGAGAGAACAGTTTCTCTGGATTTG 960  
Dh 901 GAAAGTGAAGAACCAATATATAGTGTGCGCAAAAGGGGAGAGAACAGTTTCTCTGGATTTG 960  
Qy 961 CGCTTGAAGAACATTTGAAAAACAGAAAAATCTCCCTTATCCGATTCCTCTTCCGTTTT 1020  
Dh 961 CGCTTGAAGAACATTTGAAAAACAGAAAAATCTCCCTTATCCGATTCCTCTTCCGTTTT 1020  
Qy 1021 TTTGGCGGGGTAATGTTGCTTTGCTTAAAAAATGGCTAAATTAATTCGGGTTCTTTGAT 1080  
Dh 1021 TTTGGCGGGGTAATGTTGCTTTGCTTAAAAAATGGCTAAATTAATTCGGGTTCTTTGAT 1080  
Qy 1081 GAGGATTTTAATCACTGGGGTGGAGAAAGATGTGGAATTTGGAATTCGCTTATTCGGTTAC 1140  
Dh 1081 GAGGATTTTAATCACTGGGGTGGAGAAAGATGTGGAATTTGGAATTCGCTTATTCGGTTAC 1140

Qy 1141 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGACCAACAGTTAAA 1200  
Dh 1141 GGTAGTTTCTTTAAAACTATTGATGGCATTTATGGCTTACCATCAAGACCAACAGTTAAA 1200  
Qy 1201 GAAAATGAACCGATCTGTGAAGCGGAAAATTAATTCGCTCGATTAATTAAGAGAAAAG 1260  
Dh 1201 GAAAATGAACCGATCTGTGAAGCGGAAAATTAATTCGCTCGATTAATTAAGAGAAAAG 1260  
Qy 1261 GTCCCTTAATCTATAGAAAACCTTTTACAAATGAAATTCGCAATATCAATAGAGTACCT 1320  
Dh 1261 GTCCCTTAATCTATAGAAAACCTTTTACAAATGAAATTCGCAATATCAATAGAGTACCT 1320  
Qy 1321 TTAGTTCAATTTATATCCAGCTTATTAACCTGTGCAACATATATTCACGTTGCGTAGAT 1380  
Dh 1321 TTAGTTCAATTTATATCCAGCTTATTAACCTGTGCAACATATATTCACGTTGCGTAGAT 1380  
Qy 1381 AGTGCATGAATCAGACTGTTGTTGATCTCGAGGTTGTATTTGTAAAGATGTTCAACA 1440  
Dh 1381 AGTGCATGAATCAGACTGTTGTTGATCTCGAGGTTGTATTTGTAAAGATGTTCAACA 1440  
Qy 1441 GATTAATCTTTAAGAGATCAATTAAGCTTTATGTTAATTAATCCTAGGTACCGATCATG 1500  
Dh 1441 GATTAATCTTTAAGAGATCAATTAAGCTTTATGTTAATTAATCCTAGGTACCGATCATG 1500  
Qy 1501 TCTAAAACCAATGGCGGAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGT 1560  
Dh 1501 TCTAAAACCAATGGCGGAATAGCCTCAGCATCAAAATGACGCGTTTCTTTTGTCTAAAGT 1560  
Qy 1561 TATTAATGCGCAGTTAGATTCAGATGATTAATCTTGAAGCTGATGCAAGTTGAACTGTGT 1620  
Dh 1561 TATTAATGCGCAGTTAGATTCAGATGATTAATCTTGAAGCTGATGCAAGTTGAACTGTGT 1620  
Qy 1621 TTAAAAAGATTTTAAAAAGATTAAGACCTTGTGTGTTTATACCACTAATAGAAAAGTGC 1680  
Dh 1621 TTAAAAAGATTTTAAAAAGATTAAGACCTTGTGTGTTTATACCACTAATAGAAAAGTGC 1680  
Qy 1681 AATCCGATGGTATGCTTAATCGCTAATGCTTAAACAATGGCCAGAAATTTTCAAGAAAAA 1740  
Dh 1681 AATCCGATGGTATGCTTAATCGCTAATGCTTAAACAATGGCCAGAAATTTTCAAGAAAAA 1740  
Qy 1741 CTCACAAACGGCTATGATTTGCTCACACTTATAGAAATGTTCAAGATTAAGCTTGGCAATTA 1800  
Dh 1741 CTCACAAACGGCTATGATTTGCTCACACTTATAGAAATGTTCAAGATTAAGCTTGGCAATTA 1800  
Qy 1801 ACTGATGATTCATTAAGAAAATTTGAAAATGCGCTTAACATTAAGCAATGTTCTCAAACTC 1860  
Dh 1801 ACTGATGATTCATTAAGAAAATTTGAAAATGCGCTTAACATTAAGCAATGTTCTCAAACTC 1860  
Qy 1861 AGTGAAGTGGAAAAATTTAAACATCTTAATTAATGCTTAACAGGATTAATCATAGT 1920  
Dh 1861 AGTGAAGTGGAAAAATTTAAACATCTTAATTAATGCTTAACAGGATTAATCATAGT 1920  
Qy 1921 GATTAACATCAATTAAGAAAATTTGCAATCTTAAATTAATGCTTAACAGGATTAATCATAGT 1980  
Dh 1921 GATTAACATCAATTAAGAAAATTTGCAATCTTAAATTAATGCTTAACAGGATTAATCATAGT 1980  
Qy 1981 CAGTCATTAATTAAGCAAGCAATTAATTAATTAATTAATTAAGCAATTTGATGATTTAGAT 2040  
Dh 1981 CAGTCATTAATTAAGCAAGCAATTAATTAATTAATTAATTAAGCAATTTGATGATTTAGAT 2040  
Qy 2041 GAAAGTGAAGAAATTAATTTTCAATTAAGAAACGCTGAATATCAAGAAAGATTAATCATCTTA 2100  
Dh 2041 GAAAGTGAAGAAATTAATTTTCAATTAAGAAACGCTGAATATCAAGAAAGATTAATCATCTTA 2100  
Qy 2101 AAAGATATTAATTAATCATCAAGATTAAGATGCAAAATTCGACAGTCAAGATTTTATATCC 2160  
Dh 2101 AAAGATATTAATTAATCATCAAGATTAAGATGCAAAATTCGACAGTCAAGATTTTATATCC 2160  
Qy 2161 AATACATTTAAACGGCTTAAGTGAAGAAAATTAACATATTAATTAATTAATTAATTAATTA 2220  
Dh 2161 AATACATTTAAACGGCTTAAGTGAAGAAAATTAACATATTAATTAATTAATTAATTAATTA 2220



Db 979 CGCTTAGAACATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTT 1038  
Qy 1021 TTTCGGGGGGTAAATGTTGCTTTGCTTAAATAATGGCTAAATATCGGTTCTTTGAT 1080  
Db 1039 TTTCGGGGGGTAAATGTTGCTTTGCTTAAATAATGGCTAAATATCGGTTCTTTGAT 1098  
Qy 1081 GAGGAATTTAATCACTGGGGTGAAGAGATGTGAAATTTGGATATCGCTTAATCCGTTAC 1140  
Db 1099 GAGGAATTTAATCACTGGGGTGAAGAGATGTGAAATTTGGATATCGCTTAATCCGTTAC 1158  
Qy 1141 GGTATGTTCTTTAAACTATTTGATGGCAATTTGGCTTACCATCAAGAGCCCAAGGTAAA 1218  
Db 1159 GGTATGTTCTTTAAACTATTTGATGGCAATTTGGCTTACCATCAAGAGCCCAAGGTAAA 1218  
Qy 1201 GAAATGAAACCGATTCGGAAGCGGGAAAAAATATTCGCTCGATPATATTAGAGAAAG 1260  
Db 1219 GAAATGAAACCGATTCGGAAGCGGGAAAAAATATTCGCTCGATPATATTAGAGAAAG 1278  
Qy 1261 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAATTCGCATATCAATAGATACCT 1320  
Db 1279 GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAATTCGCATATCAATAGATACCT 1338  
Qy 1321 TTAGTTCAATTTATATCCAGCTTATATAGTGCATATTTCAACGTTGGCTAGAT 1380  
Db 1339 TTAGTTCAATTTATATCCAGCTTATATAGTGCATATTTCAACGTTGGCTAGAT 1398  
Qy 1381 AGTCACTGAATCAAGCTGTTGATCTGAGGGTTGTATTTGTAAGATGTTCAACA 1440  
Db 1399 AGTCACTGAATCAAGCTGTTGATCTGAGGGTTGTATTTGTAAGATGTTCAACA 1458  
Qy 1441 GATAATACCTTAGAAGTATCAATAGCTTTATGTTATATTCCTAGGGTACGATCATG 1500  
Db 1459 GATAATACCTTAGAAGTATCAATAGCTTTATGTTATATTCCTAGGGTACGATCATG 1518  
Qy 1501 TCTAACCATAATGGCGGAATAGCTCAGCATCAAAATGCAAGCCGTTCTTTGCTAAAGT 1560  
Db 1519 TCTAACCATAATGGCGGAATAGCTCAGCATCAAAATGCAAGCCGTTCTTTGCTAAAGT 1578  
Qy 1561 TATTAATATGGGAGTTGATTCAGATGATATCTGAGCCGATGAGCTGAACTGAGT 1620  
Db 1579 TATTAATATGGGAGTTGATTCAGATGATATCTGAGCCGATGAGCTGAACTGAGT 1638  
Qy 1621 TTTAAAGAAATTTTAAAGATTAACGCTAGCTGTGTTTATACCACTAATAGAAACGTC 1680  
Db 1639 TTTAAAGAAATTTTAAAGATTAACGCTAGCTGTGTTTATACCACTAATAGAAACGTC 1698  
Qy 1681 AATCCGATGAGTGAATGCTTATGCTTATAGCTTAAATGGCCGAATTTTCAAGAAAA 1740  
Db 1699 AATCCGATGAGTGAATGCTTATGCTTATAGCTTAAATGGCCGAATTTTCAAGAAAA 1758  
Qy 1741 CTCACAAAGGCTATGATTCACCACTTTAGAAATGTTCAAGATTAAGAGCTTGACATTA 1800  
Db 1759 CTCACAAAGGCTATGATTCACCACTTTAGAAATGTTCAAGATTAAGAGCTTGACATTA 1818  
Qy 1801 ACTGATGATTCATGAAAAAATGAAAAATGCGGTAGACTATGACATGTTCTCTCAACCTC 1860  
Db 1819 ACTGATGATTCATGAAAAAATGAAAAATGCGGTAGACTATGACATGTTCTCTCAACCTC 1878  
Qy 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATAAAATCTGCTATACCGGTATATACATGCT 1920  
Db 1879 AGTGAAGTTGAAAAATTTAAACATCTTAATAAAATCTGCTATACCGGTATATACATGCT 1938  
Qy 1921 GATAACATCAATTAAGAAATTTGGCAATTCAAAAAGAAAAACATTTGTTGATGTCAT 1980  
Db 1939 GATAACATCAATTAAGAAATTTGGCAATTCAAAAAGAAAAACATTTGTTGATGTCAT 1998  
Qy 1981 CAGTATTAATAATAGCAAGGCTAATCTTATTAATTAATTAATGAAGATTTGATAGAT 2040  
Db 1999 CAGTATTAATAATAGCAAGGCTAATCTTATTAATTAATTAATGAAGATTTGATAGAT 2058  
Qy 2041 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATGATATCTTA 2100  
Db 2059 GAAAGTAGAAGTATATTTTCAATAAAACCGCTGAATATCAAGAGAGATGATATCTTA 2118

Qy 2101 AAGATATTAATAATCCAGAAATTAAGATGCCAAAATCCAGTACATATTTTATCCC 2160  
Db 2119 AAGATATTAATAATCCAGAAATTAAGATGCCAAAATCCAGTACATATTTTATCCC 2178  
Qy 2161 AATACATTAACGGCTTAATGAAAAAATCTAAACATATTTTGAATTAATTAATAATTA 2220  
Db 2179 AATACATTAACGGCTTAATGAAAAAATCTAAACATATTTTGAATTAATTAATAATTA 2238  
Qy 2221 TTGGTATGTTCTACATGTTGATTAAGAAATCATCTTACACCAATATCAAAAAAGAAATA 2280  
Db 2239 TTGGTATGTTCTACATGTTGATTAAGAAATCATCTTACACCAATATCAAAAAAGAAATA 2298  
Qy 2281 CTAGCCTTCTATCAATCAATCAAGTGAATATTTTCTAAATAATGATATCTCATATAC 2340  
Db 2299 CTAGCCTTCTATCAATCAATCAAGTGAATATTTTCTAAATAATGATATCTCATATAC 2358  
Qy 2341 ACAGATATATGATTAATAAAATCTGAGCCGCTTTAAGTAATTAATAATTAAGTCAG 2400  
Db 2359 ACAGATATATGATTAATAAAATCTGAGCCGCTTTAAGTAATTAATAATTAAGTCAG 2418  
Qy 2401 TTTAATCTAATTTGTAATATCATATTTTATATATCATGACAGCCATTCGTTAAAT 2460  
Db 2419 TTTAATCTAATTTGTAATATCATATTTTATATATCATGACAGCCATTCGTTAAAT 2478  
Qy 2461 GACAGCTATGCTTATATGAAAAAATATATGATGTGGCAATGATTTCTGAGATTAACAT 2520  
Db 2479 GACAGCTATGCTTATATGAAAAAATATATGATGTGGCAATGATTTCTGAGATTAACAT 2538  
Qy 2521 GATTGATCGAAGAAATCAATGCGCATCCACATTTAAAAAGCTCAATTAATTAATTTT 2580  
Db 2539 GATTGATCGAAGAAATCAATGCGCATCCACATTTAAAAAGCTCAATTAATTAATTTT 2598  
Qy 2581 AATGACAATGACTTAAAAAGTATGAATGTAAGAGGGGATCACAAAGGTATGTTATAGC 2640  
Db 2599 AATGACAATGACTTAAAAAGTATGAATGTAAGAGGGGATCACAAAGGTATGTTATAGC 2658  
Qy 2641 TATGCGCTAGCGCATGAGCTTTCGACGATTTTAAAGATGATCATCATCTTGCAGTCA 2700  
Db 2659 TATGCGCTAGCGCATGAGCTTTCGACGATTTTAAAGATGATCATCATCTTGCAGTCA 2718  
Qy 2701 ATTGATATGTTGCCAGAAATTAACATGAGATATTTGGTTCCAAATTTGCACTTTATATC 2760  
Db 2719 ATTGATATGTTGCCAGAAATTAACATGAGATATTTGGTTCCAAATTTGCACTTTATATC 2778  
Qy 2761 TTGAAAAAGAAACCGGCAATGATTTAATTAATAACATCGAACCTGACTTATATGCTTGG 2820  
Db 2779 TTGAAAAAGAAACCGGCAATGATTTAATTAATAACATCGAACCTGACTTATATGCTTGG 2838  
Qy 2821 GAACGAAAAATTAACATGAGCAATGAACAAATGGAAGTGCAAAAGAGAGAAAAATATA 2880  
Db 2839 GAACGAAAAATTAACATGAGCAATGAACAAATGGAAGTGCAAAAGAGAGAAAAATATA 2898  
Qy 2881 CCTGTTAACAACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2919  
Db 2899 CCTGTTAACAACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2937

RESULT 3  
US-11-120-422-9  
; Sequence 9, Application US/11120422  
; Publication No. US20050287646A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul H  
; APPLICANT: Kumari, Khama  
; APPLICANT: Deangelis, Paul  
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESSION  
; FILE REFERENCE: 3554, 049  
; CURRENT APPLICATION NUMBER: US/11/120,422  
; CURRENT FILING DATE: 2005-05-02  
; PRIOR APPLICATION NUMBER: US/09/879,959  
; PRIOR FILING DATE: 2001-09-12

; PRIOR APPLICATION NUMBER: 09/469,200  
 ; PRIOR FILING DATE: 1999-12-21  
 ; PRIOR APPLICATION NUMBER: 09/178,851  
 ; PRIOR FILING DATE: 1998-10-26  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 2937  
 ; TYPE: DNA  
 ; ORGANISM: pasteurella multocida  
 ; US-11-120-422-9

Query Match 99.9%; Score 2917.4; DB 7; Length 2937;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGAATACATTATCACAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC	60
Db	19	ATGAATACATTATCACAGCAATAAAGCATATTAACAGCAATGACTATCAATTAGCACTC	78
Qy	61	AAATTTATTTAAAGTCGGCGGAATCTATCGACGGAATAATGTTGAAATTTCAAAATTACC	120
Db	79	AAATTTATTTGAAAGTCGGCGGAATCTATCGACGGAATAATGTTGAAATTTCAAAATTACC	138
Qy	121	AAATGCAAGAAAAAATCTCTAGCATATCTTCTGTTAATTCAGCACATCTTTCTGTAAAT	180
Db	139	AAATGCCAAGAAAAAATCTCTAGCATATCTTCTGTTAATTCAGCACATCTTTCTGTAAAT	198
Qy	181	AAAGAAGAAAAAGTCAATGTTTGGGATAGTCCGTTAGATATGCAACAACAATCTGTACTT	240
Db	199	AAAGAAGAAAAAGTCAATGTTTGGGATAGTCCGTTAGATATGCAACAACAATCTGTACTT	258
Qy	241	TCCAAAGTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAAGTAAAAAATAAATGG	300
Db	259	TCCAAAGTAAAAAATTTAGTACTTCTGACTCGGAAAAAACAAGTAAAAAATAAATGG	318
Qy	301	AAATGCTCAGTACAGCAAAATCTGAAATGCGAGGTAAGAGCGGTCGCCCTTGTACCA	360
Db	319	AAATGCTCAGTACAGCAAAATCTGAAATGCGAGGTAAGAGCGGTCGCCCTTGTACCA	378
Qy	361	AAAGATTTTCCCAAGATCTGGTTTTAGCGCTTTACCTGATCATGTTAAATGATTTTACA	420
Db	379	AAAGATTTTCCCAAGATCTGGTTTTAGCGCTTTACCTGATCATGTTAAATGATTTTACA	438
Qy	421	TGGTACAAAAAGCGAAGAAAGACTTGGCATAAAACTTGAACATCAACATGTTGCTT	480
Db	439	TGGTACAAAAAGCGAAGAAAGACTTGGCATAAAACTTGAACATCAACATGTTGCTT	498
Qy	481	TCTATTATCGTTTACCAACATTCATCGACGCAATTTTATCGATTACATTTAGCCCTGTTTA	540
Db	499	TCTATTATCGTTTACCAACATTCATCGACGCAATTTTATCGATTACATTTAGCCCTGTTTA	558
Qy	541	GTAAACCAAAAAACATTTACCGGTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA	600
Db	559	GTAAACCAAAAAACATTTACCGGTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA	618
Qy	601	GATCTATCAACCGATCATTCGCGCAATATGAAATTAATTTGGATATTCGCTACGACAA	660
Db	619	GATCTATCAACCGATCATTCGCGCAATATGAAATTAATTTGGATATTCGCTACGACAA	678
Qy	661	AAAGATACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATATCGCTTAGCAAAATAT	720
Db	679	AAAGATACGGTTTTCAAGCCAGTCCGCTCGGAATATGGGATATCGCTTAGCAAAATAT	738
Qy	721	GACTTTATGGGTTACTCGACTGTGATATGGCGCAAAATCCCAATTTGGGTTCAATCTTAT	780
Db	739	GACTTTATGGGTTACTCGACTGTGATATGGCGCAAAATCCCAATTTGGGTTCAATCTTAT	798
Qy	781	GTTGAGAGCTATTAGAAGATGATGATTTAAACAATCAATTTGGTCCCAAGAAAAATACATCGAT	840
Db	799	GTTGAGAGCTATTAGAAGATGATGATTTAAACAATCAATTTGGTCCCAAGAAAAATACATCGAT	858
Qy	841	ACACAACATATTTGACCCAAAAGACTTCTTAAATAACGCGAGTTTGTCTTGAATCATTTACCA	900

Db	859	ACACAACATATTGACCCAAAAGACTTCTTAAATAACCGAGTTTGTCTGAATCATTTACCA	918
Qy	901	GAAGTGAACCAATATAGTGTTCGCGCAAAAGGGGAAGGAAACAGTTTCTCTGGATTGG	960
Db	919	GAAGTGAACCAATATAGTGTTCGCGCAAAAGGGGAAGGAAACAGTTTCTCTGGATTGG	978
Qy	961	CGCTTAGAACCAATTCGAAAAACAGAAAAATCTCCGCTTATCCCGATTCCGCTTTCCGTTTT	1020
Db	979	CGCTTAGAACCAATTCGAAAAACAGAAAAATCTCCGCTTATCCCGATTCCGCTTTCCGTTTT	1038
Qy	1021	TTTCCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGCGCTAAATAATCCGTTTCTTTGAT	1080
Db	1039	TTTCCGCGGGTAAATGTTGCTTTTCGCTAAAAAATGCGCTAAATAATCCGTTTCTTTGAT	1098
Qy	1081	GAGGAAATTTAATCACTCGGGTGGAGAGATGTGGAATTTTGATATCGCTTATTCGCTTAC	1140
Db	1099	GAGGAAATTTAATCACTCGGGTGGAGAGATGTGGAATTTTGATATCGCTTATTCGCTTAC	1158
Qy	1141	GGTAGTTTTCTTTAAAACTATTGATGGCATTTATGCGCTTACCATCAAGAGCCACAGGTAAA	1200
Db	1159	GGTAGTTTTCTTTAAAACTATTGATGGCATTTATGCGCTTACCATCAAGAGCCACAGGTAAA	1218
Qy	1201	GAATAAGAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG	1260
Db	1219	GAATAAGAACCGATCGTGAAGCGGGAATAATATTACGCTCGATATTATGAGAGAAAAG	1278
Qy	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT	1320
Db	1279	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT	1338
Qy	1321	TTAGTTTTCAATTTATATCCCAAGCTTTATACTGTGCAAACTATATTCAACGTTGCGTAGAT	1380
Db	1339	TTAGTTTTCAATTTATATCCCAAGCTTTATACTGTGCAAACTATATTCAACGTTGCGTAGAT	1398
Qy	1381	AGTGACCTGAATCAGACTGTTGTTGATCTCAGAGTTTGTATTGTTAAACGATGGTTCAACA	1440
Db	1399	AGTGACCTGAATCAGACTGTTGTTGATCTCAGAGTTTGTATTGTTAAACGATGGTTCAACA	1458
Qy	1441	GATTAATCTTTAGAGTGTGATCAATAAGCTTTATGTTAATAATCTTAGGGTACGCATCATG	1500
Db	1459	GATTAATCTTTAGAGTGTGATCAATAAGCTTTATGTTAATAATCTTAGGGTACGCATCATG	1518
Qy	1501	TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCGCGGTTCTTTTGTCTAAAGGT	1560
Db	1519	TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAAAATGCGCGGTTCTTTTGTCTAAAGGT	1578
Qy	1561	TATTACATGGCGAGTTAGATTGATGATGATTTTCTTGAGCCCTGATGCGAGTTGAACTGTGT	1620
Db	1579	TATTACATGGCGAGTTAGATTGATGATTTTCTTGAGCCCTGATGCGAGTTGAACTGTGT	1638
Qy	1621	TTAAAGAAATTTTAAAGATAAAAACGCTAGCTGTGTTTATACCACTAAATAGAAAACGTC	1680
Db	1639	TTAAAGAAATTTTAAAGATAAAAACGCTAGCTGTGTTTATACCACTAAATAGAAAACGTC	1698
Qy	1681	AATCCGATGGTAGCTTAAATCGCTAAATGTTTACAAATGGCCAGAAATTTTTCACGAGAAAA	1740
Db	1699	AATCCGATGGTAGCTTAAATCGCTAAATGTTTACAAATGGCCAGAAATTTTTCACGAGAAAA	1758
Qy	1741	CTCAACACGGCTGATGATTGCTCACCATTTTGAATGTTTCAAGATTAGAGCTTTGGCATTTTA	1800
Db	1759	CTCAACACGGCTGATGATTGCTCACCATTTTGAATGTTTCAAGATTAGAGCTTTGGCATTTTA	1818
Qy	1801	ACTGATGATTTCAATGAAAAAATTCAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC	1860
Db	1819	ACTGATGATTTCAATGAAAAAATTCAAAATGCGGTAGACTATGACATGTTCTCTCAAACTC	1878
Qy	1861	AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGTGTTATTACATGCT	1920
Db	1879	AGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGTGTTATTACATGCT	1938
Qy	1921	GATAACACATCAATTAAGAAAACTTGGCATTTCAAAAAAGAAAAACCATTTTGTGTAGTCAAT	1980

1939	GATAACACATCAATTAAGAAACCTGGCAATTCAAAGAGAAAAACCATTTGTTGTAGTCAAT	1999
Qy	CAGTCATTAAATAGACAAGGCATAAATTATTAATAATTTATGACGAATTTGATGATTTAGAT	2040
	1981	1999
	1999	CAGTCATTAAATAGACAAGGCATAAATTATTAATAATTTATGACGAATTTGATGATTTAGAT
Qy	2041	2100
	2059	2118
	2101	2160
Db	2101	2160
	2119	2178
	2161	2220
Qy	2161	2220
	2179	2238
	2221	2280
Db	2239	2298
	2281	2340
	2299	2358
Qy	2341	2400
	2359	2418
	2401	2460
Db	2419	2478
	2461	2520
	2479	2538
Qy	2521	2580
	2539	2598
	2581	2640
Db	2599	2658
	2641	2700
	2659	2718
Qy	2701	2760
	2719	2778
	2761	2820
Db	2779	2838
	2821	2880
	2839	2898
Qy	2881	2919
	2899	2937
	Db	

## RESULT 4

REGOUT 4  
US-11-172-145-3

US-11-172-143-3 : Sequence 3 Application US/11172145

; sequence 3, Application US/III/

; Publication No. US20

; GENERAL INFORMATION:



QY 541 GTAAACCAAAACACATTTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
DB |||||  
QY 580 GTCAATCAGAAACAACTACCCATTTGAGTCGTTGTTGAGATGATGGTAGTAAGAA 639  
DB |||||  
QY 601 GATCTATCACCAGATCATTTGCGCAATATGAAATATAAATTTGGATATTCGGCTACGTCAGACAA 660  
DB |||||  
QY 640 AACTTACTTACCATTTGTCAGAAATACGAAACAAAACTTGACATAAAGATATGTAAGACA 699  
DB |||||  
QY 661 AAAGATACGGTTTCAAGCCAGTCGCCCTCGGAATATGGGATTTAGCGTTAGCAAAATAT 720  
DB |||||  
QY 700 AAAGATATGAGATATCAATTTGTTGTCAGTCAGAACTTAGGTTTACGTACAGCAAGATAT 759  
DB |||||  
QY 721 GACTTTATTTGCTTACTCGATCTGATATGGCGCAAAATCAATTTAGGTTTCATTTCTTAT 780  
DB |||||  
QY 760 GATTTTGTCTGATTTCTAGATCTGGAATATGGCAACAAATTTATGGTTTCATTTCTTAT 819  
DB |||||  
QY 781 GTTGACAGATCTATTAGAAAGATGATGATTTAAACAATCATTTGTTGCCAGAAATATACATCAT 840  
DB |||||  
QY 820 CTTACAGAACTATTAGAAAGACATGATATTTGTTTTAAATTTGGACCTTAGAAATATGTCGAT 879  
DB |||||  
QY 841 ACACAAATATTGACCCAAAGACTTTCTTAATAACGGAGTTTTCGTTGGAATCATTTACCA 900  
DB |||||  
QY 880 ACTCATAATATTACCGCAGAACTATTCCTTAAACGATCCATATTTAATAGAATCACTACCT 939  
DB |||||  
QY 901 GAAGTGAAACCAATAATAGTTTCCGCAAAAGGGAGGAACAGTTTCTCTGATTTGG 960  
DB |||||  
QY 940 GAAACCGCTACAAATTAACAATCTTTCGATTAATCAAAAGGAATATATCGTTGGATTTGG 999  
DB |||||  
QY 961 CGCTTAGAACCAATTCGAAACCAACAGAAATCTCCGCTTATCCGATTCGCCCTTTCCGTTT 1020  
DB |||||  
QY 1000 AGATTTAGAACATTTCAAAACCAACGATATCTACGTCATGATGATTCCTCGTTTGGTTAT 1059  
DB |||||  
QY 1021 TTTGCGGGGGTAATGTTGCTTTCCCTTAAATAACGCTTAATAATAATCCGTTTCTTTGAT 1080  
DB |||||  
QY 1060 TTTAGTTGCGGTAATGTTGCAATTTCTAAAGAAATGGCTAAATAAAGTAGTTGGTTGCGAT 1119  
DB |||||  
QY 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTTGGAATTTGGATATCGCTTATTTCCGTTAC 1140  
DB |||||  
QY 1120 GAAGAAATTTAAATCATTTGGGGGGCGAGATGATGAGATTTGGTTACAGATATTTGCCAAA 1179  
DB |||||  
QY 1141 GGTAGTTTCTTTAAACATTTATGATGGCATTTATGGCTTACCATCAAGAGCCACAGGTAAA 1200  
DB |||||  
QY 1180 GCTGTTTTCAGAGTAATTTGACGGCGGAATGGCATACCATCAAGAACCACCTGGTAAA 1239  
DB |||||  
QY 1201 GAAATAGAAACCGATCGTGAAGCGGGGAAAAATATATACCTCGATATTTATGAGAGAAAG 1260  
DB |||||  
QY 1240 GAAATGAAACAGACCGCGAAGCTGTTAAAGATTTACGCTTTAAATTTGTGAAAGAAAG 1299  
DB |||||  
QY 1261 GTCCCTTATATCTATAGAAAATTTTACCAATAGAGATTTCCGATATCAATAGAGTACCT 1320  
DB |||||  
QY 1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAGATTTACATATTTATAGATATACCT 1359  
DB |||||  
QY 1321 TTATGTTTCAATTTATATCCAGCTTATTAACCTGTGCAAACTATATTTCAACGTTGCGTAGAT 1380  
DB |||||  
QY 1360 TTAGTTTCTATTTTATATCCCGCTTATTAACCTGTGCAAACTATTTCAAGATGTTGATAT 1419  
DB |||||  
QY 1381 AGTGCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1440  
DB |||||  
QY 1420 AGTGCTCTTAACTCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAAACGATGGTTCAACA 1479  
DB |||||  
QY 1441 GATAATACCTTAGAGATGATCAATAGCTTTATGTTATTAATTCCTAGGGTACGCATCATG 1500  
DB |||||  
QY 1480 GATAATACCTTAGAGATGATCAATAGCTTTATGTTATTAATTCCTAGGGTACGCATCATG 1539  
DB |||||  
QY 1501 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAATGCAAGCGGTTTCTTTTGTCTAAAGGT 1560  
DB |||||  
QY 1540 TCTAAACCAAAATGGCGGAATAGCCTCAGCATCAATGCAAGCGGTTTCTTTTGTCTAAAGGT 1599  
DB |||||  
QY 1561 TATTTACATTTGGGCGATTAGATTTAGATGATTTCTTTGAGCCCTGATGACGTTGACTGTGT 1620  
DB |||||  
QY 1600 TATTACATTTGGGCGATTAGATTTAGATGATTTCTTTGAGCCCTGATGACGTTGACTGTGT 1659  
DB |||||

QY 1621 TTAAGAGAAATTTTAAAGATATAAACCGTAGCTGTGTGTTTATACCACTAATAGAAAACGTC 1680  
DB |||||  
QY 1660 TTAAGAGAAATTTTAAAGATATAAACCGTAGCTGTGTGTTTATACCACTAATAGAAAACGTC 1719  
DB |||||  
QY 1681 AATCCGGATGTTAGCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTACAGAGAAAA 1740  
DB |||||  
QY 1720 AATCCGGATGTTAGCTTAATCGCTAATGTTTACAAATTTGGCCAGAAATTTTACAGAGAAAA 1779  
DB |||||  
QY 1741 CTCAAAACGGCTATGATTTGCTCACCACTTTTAAAGATTTTACGATTTAGAGCTTTGGCATTTA 1800  
DB |||||  
QY 1780 CTCAAAACGGCTATGATTTGCTCACCACTTTTAAAGATTTTACGATTTAGAGCTTTGGCATTTA 1839  
DB |||||  
QY 1801 ACTGATGATTTCAATAGAAATTTGAAATTTGCCGTAGACTATGACATGTTCTCAAACTC 1860  
DB |||||  
QY 1840 ACGGATGATTTAAACGAAATATTTGAAACCGCGGATTTATGACATGTTCTTTAAACTC 1899  
DB |||||  
QY 1861 AGTCAGTTGGAAATTTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTTACATGGT 1920  
DB |||||  
QY 1900 AGTGAAGTTGGAAATTTTAAACATCTTAATAAAATCTGCTATAACCGGTGATTTACATGGT 1959  
DB |||||  
QY 1921 GATAACACATCAATTTAAGAAAATTTGGCACTTCAAAAGAAAAACCAATTTTGTGTGATCAAT 1980  
DB |||||  
QY 1960 GATAACACATCAATTTAAGAAAATTTGGCACTTCAAAAGAAAAACCAATTTTGTGTGATCAAT 2019  
DB |||||  
QY 1981 CAGTCATTTAAATAGACAAAGGCATTAATTTATTAATTTATGACGATTTTGTGATTTAGAT 2040  
DB |||||  
QY 2020 CAGTCATTTAAATAGACAAAGGCATTAATTTATTAATTTATGACAAATTTTGTGATTTAGAT 2079  
DB |||||  
QY 2041 GAAAGTAGAAATGATTTTCAATAAAACCGCTGAATATCAAGAAGAGATGATATCTTTA 2100  
DB |||||  
QY 2080 GAAAGTAGAAATGATTTTCAATAAAACCGCTGAATATCAAGAAGAAATGATATTTTAA 2139  
DB |||||  
QY 2101 AAAGATATTTAAATCATCCAGAAATAAGATGCAAAATCGCAGTCAGTATTTTATATCCC 2160  
DB |||||  
QY 2140 AAAGATCTTAACTCATTTCAAAATAAGATGCCAAATCGCAGTCAGTATTTTCTATCCC 2199  
DB |||||  
QY 2161 AATCAATTTAAACGGCTTAGTGAAACCACTAAACAAATTTATTTGAATTAATAAATAATA 2220  
DB |||||  
QY 2200 AATCAATTTAAACGGCTTAGTGAAACCACTAAACAAATTTATTTGAATTAATAAATAATA 2259  
DB |||||  
QY 2221 TTCGTTATTTCTACATGTTGATGAAGATCATCTTACACCAAGATATCAAAAAAGAAATA 2280  
DB |||||  
QY 2260 TTCGTTATTTCTACATGTTGATGAAGATCATCTTACACCAAGATATCAAAAAAGAAATA 2319  
DB |||||  
QY 2281 CTAGCTTTCTATCAATAACATCAAGTGAATATTTTACTAAATAATGATATCTCATATTTAC 2340  
DB |||||  
QY 2320 TTGGCTTTCTATCATTAAGCAACCAAGTGAATTTTACTAAATAATGACATCTCATATTTAC 2379  
DB |||||  
QY 2341 ACGAGTAATAGATTAATAAATACTGAGCGCATTTTAAAGTAATTAATAAATAATGATCAG 2400  
DB |||||  
QY 2380 ACGAGTAATAGACTAATAAATACTGAGGCACATTTTAAAGTAATTAATAAATAATGATCAG 2439  
DB |||||  
QY 2401 TTAATCTTAAATTTGTAATGATCATCTTTTGAATATCATGACAGCTATTTCTGTTAAAAAT 2460  
DB |||||  
QY 2440 TTAATCTTAAATTTGTAATGATCATCTTTTGAATATCATGACAGCTATTTCTGTTAAAAAT 2499  
DB |||||  
QY 2461 GACAGCTATCTTATATGAAAAATATGATGTCGGCATGAAATTTCTCAGCATTAAACACAT 2520  
DB |||||  
QY 2500 GACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAAATTTCTCAGCATTAAACACAT 2559  
DB |||||  
QY 2521 GATTTGATCGGAAAAATCAATCGGCATCCACATTTTAAAAAGCTCATTTAAAACTTATTTT 2580  
DB |||||  
QY 2560 GATTTGATCGGAAAAATCAATCGGCATCCACCATTTTAAAAAGCTGATTTAAAACTTATTTT 2619  
DB |||||  
QY 2581 AATGCAATGACTTTAAAAAGTATGATGTAAGGGGCATCAACAGGATGATTTATGACG 2640  
DB |||||  
QY 2620 AATGCAATGACTTTAAGAGATGATGATGTAAGGGGCATCAACAGGATGATTTATGAAG 2679  
DB |||||  
QY 2641 TATGCGCTAGCCCATGAGCTTCTGACGATTTTAAAGAGTATCATCATCTTCTGCCAGTCA 2700  
DB |||||  
QY 2680 TATGCGCTAGCCCATGAGCTTCTGACGATTTTAAAGAGTATCATCATCTTCTGCCAGTCA 2739  
DB |||||  
QY 2701 ATTGATAGTGTGCCAGATATAACACTGAGGATATTTGGTTCCAAATTTTGCACTTTTAAATC 2760  
DB |||||



Db 1261 GTCCCTTATCTATAGAAAACCTTTTACCAATAGAGATTCCGATATCAATPAGAGTACCT 1320  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATTAACCTGTCGCAACTATATTTCAACGTTGCGTAGAT 1380  
Db 1321 TTAGTTTCAATTTATATCCAGCTTATTAACCTGTCGCAACTATATTTCAACGTTGCGTAGAT 1380  
Qy 1381 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTGTAACGATGTTTCAACA 1440  
Db 1381 AGTCACCTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTGTAACGATGTTTCAACA 1440  
Qy 1441 GATAATACCTTTAGAGTGATCAATAAGCTTTATGTTATATATATCTAGGTTAGGTTAGCATG 1500  
Db 1441 GATAATACCTTTAGAGTGATCAATAAGCTTTATGTTATATATATCTAGGTTAGGTTAGCATG 1500  
Qy 1501 TCTAAACCAATGGGGAATAGCCTCAGCATCAATGCGCGTTCCTTTGCTTAAAGGT 1560  
Db 1501 TCTAAACCAATGGGGAATAGCCTCAGCATCAATGCGCGTTCCTTTGCTTAAAGGT 1560  
Qy 1561 TATTACATTTGGCAGTTAGATTGATGATGATTTATCTTGAGCCTGATGCAAGTTGAACTGTGT 1620  
Db 1561 TATTACATTTGGCAGTTAGATTGATGATGATTTATCTTGAGCCTGATGCAAGTTGAACTGTGT 1620  
Qy 1621 TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACACTAATAGAAACGTC 1680  
Db 1621 TTAAAGAAATTTTAAAGATAAAACGCTAGCTTGTGTTTATACACTAATAGAAACGTC 1680  
Qy 1681 AATCCGGATGGTAGCTTAATGCTTAATGTTTACAAATGGCCAGAAATTTTCACGAGAAAA 1740  
Db 1681 AATCCGGATGGTAGCTTAATGCTTAATGTTTACAAATGGCCAGAAATTTTCACGAGAAAA 1740  
Qy 1741 CTCACACGGCTATGATTTGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
Db 1741 CTCACACGGCTATGATTTGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
Qy 1801 ACTGATGGATTCAATGAAAAAATGAAAAATGCGTAGACTATGACATGTTCTCTCAAACTC 1860  
Db 1801 ACTGATGGATTCAATGAAAAAATGAAAAATGCGTAGACTATGACATGTTCTCTCAAACTC 1860  
Qy 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGTT 1920  
Db 1861 AGTGAAGTTGAAAAATTTAAACATCTTAATAAATCTGCTATAACCGTGTATTACATGTT 1920  
Qy 1921 GATACACATCAATTAAGAACTTGCATTTCAAAAGAAAAACCAATTTGTTGTAGTCAAT 1980  
Db 1921 GATACACATCAATTAAGAACTTGCATTTCAAAAGAAAAACCAATTTGTTGTAGTCAAT 1980  
Qy 1981 CAGTCATTAATAGACAGGCAATACTTATTAATTAATGACGAATTTGATGATTTAGAT 2040  
Db 1981 CAGTCATTAATAGACAGGCAATACTTATTAATTAATGACGAATTTGATGATTTAGAT 2040  
Qy 2041 GAAAGTAGAAAGTATATTTTCAATAAACCCTGATATCAAGAAGAGATTGATATCTTA 2100  
Db 2041 GAAAGTAGAAAGTATATTTTCAATAAACCCTGATATCAAGAAGAGATTGATATCTTA 2100  
Qy 2101 AAAGATATTAA 2112  
Db 2101 AAAGATATTAA 2112

RESULT 6  
US-11-172-145-17  
; Sequence 17, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248

; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17  
; LENGTH: 2112  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-17  
  
Query Match 72.2%; Score 2108.8; DB 7; Length 2112;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 ATGAATACATTTATCACAAGCAATTAAGACATATTAACAGCAATGACTATCAATTAGCACTC 60  
Db 1 ATGAATACATTTATCACAAGCAATTAAGACATATTAACAGCAATGACTATCAATTAGCACTC 60  
  
Qy 61 AAATTTATTTGAAGTTCGGCGGAATCTATCGACGGAATTTGTTGAATTTCAAATACC 120  
Db 61 AAATTTATTTGAAGTTCGGCGGAATCTATCGACGGAATTTGTTGAATTTCAAATACC 120  
  
Qy 121 AAATGCAAGAAAAAATCTCTCAGCACATCTTCTGTTAATTCAGCACATCTTTCTGTAAT 180  
Db 121 AAATGCAAGAAAAAATCTCTCAGCACATCTTCTGTTAATTCAGCACATCTTTCTGTAAT 180  
  
Qy 181 AAAGAAGAAAAAGTCAATGTTTGGGATAGTCCGTTAGATATTTGCAACAACATGTTACTT 240  
Db 181 AAAGAAGAAAAAGTCAATGTTTGGGATAGTCCGTTAGATATTTGCAACAACATGTTACTT 240  
  
Qy 241 TCCAAAGTAAAAAATTTAGTACTTCTGACCTCGGAAAAAACAACCTTAAAAAATAAATGG 300  
Db 241 TCCAAAGTAAAAAATTTAGTACTTCTGACCTCGGAAAAAACAACCTTAAAAAATAAATGG 300  
  
Qy 301 AAATTTGCTCAGTGAAGAAATCTGAAAAATGCGGAGGTAGAGCGGTGCGCCCTGTACCA 360  
Db 301 AAATTTGCTCAGTGAAGAAATCTGAAAAATGCGGAGGTAGAGCGGTGCGCCCTGTACCA 360  
  
Qy 361 AAAGAATTTTCCCAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
Db 361 AAAGAATTTTCCCAAGATCTGTTTTAGCGCTTTTACCTGATCATGTTAATGATTTTACA 420  
  
Qy 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACTGAACATCAACATGTTGGTCTT 480  
Db 421 TGGTACAAAAGCGAAAGAAAGACTTGGCATAAAACTGAACATCAACATGTTGGTCTT 480  
  
Qy 481 TCTATTATCGTTTACAACTTCAATCGACAGCAATTTTATCGATTACATTAGCCTGTTTAA 540  
Db 481 TCTATTATCGTTTACAACTTCAATCGACAGCAATTTTATCGATTACATTAGCCTGTTTAA 540  
  
Qy 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA 600  
Db 541 GTAAACCAAAAAACACATTTACCCGTTTGAAGTTTATCGTGACAGATGATGGTAGTCAGGAA 600  
  
Qy 601 GATCTATCACCCGATCAATTCGCGCAATATGAAATTAATTTGGATATTCGCTACCTCAGACAA 660  
Db 601 GATCTATCACCCGATCAATTCGCGCAATATGAAATTAATTTGGATATTCGCTACCTCAGACAA 660

Qy 661 AAAGATAAACGGTTTCAAGCCAGTGCCTCGGAATATGGATTAACGTTAGCAAAATAT 720  
Db |||||  
Qy 661 AAAGATAACGGTTTCAAGCCAGTGCCTCGGAATATGGATTAACGTTAGCAAAATAT 720  
Db |||||  
Qy 721 GACTTTATGGCTTACTCGACTGTGATATGCGCAAAATCCATTATGGTTCATTCTTAT 780  
Db |||||  
Qy 721 GACTTTATGGCTTACTCGACTGTGATATGCGCAAAATCCATTATGGTTCATTCTTAT 780  
Db |||||  
Qy 781 GTTCAGAGCTATTAGAGATGATGATTTAAACAATCATTTGGTCCAAGAAAATACATCGAT 840  
Db |||||  
Qy 841 ACACAACATATTAGACCAAAAGACTTCTTAATAAATGCGGAGTTTGGCTTGAATCATACCA 900  
Db |||||  
Qy 841 ACACAACATATTAGACCAAAAGACTTCTTAATAAATGCGGAGTTTGGCTTGAATCATACCA 900  
Db |||||  
Qy 901 GAAGTGAACCAATAATAGTGTTCGCGCAAAAGGGAAGCAACAGTTTCTCTCGATTGG 960  
Db |||||  
Qy 901 GAAGTGAACCAATAATAGTGTTCGCGCAAAAGGGAAGCAACAGTTTCTCTCGATTGG 960  
Db |||||  
Qy 961 CGCTTAGAACCAATTCGAAAAACAGAAAATCTCGCTTATCCGATTCCGCTTTCCGTTTT 1020  
Db |||||  
Qy 961 CGCTTAGAACCAATTCGAAAAACAGAAAATCTCGCTTATCCGATTCCGCTTTCCGTTTT 1020  
Db |||||  
Qy 1021 TTTCCGCGGGTAATGTTGCTTTTCGCTAAAAATGCGTAATAATCGGTTCTTTTGAT 1080  
Db |||||  
Qy 1021 TTTCCGCGGGTAATGTTGCTTTTCGCTAAAAATGCGCTAAATAATCGGTTCTTTTGAT 1080  
Db |||||  
Qy 1081 GAGCAATTTAATCACTCGGGTGGAGAGATCTGGAATTTGGATATCGCTTATCCGTTAC 1140  
Db |||||  
Qy 1081 GAGCAATTTAATCACTCGGGTGGAGAGATCTGGAATTTGGATATCGCTTATCCGTTAC 1140  
Db |||||  
Qy 1141 GGTAGTTCTTTAAAACTATTGATGGCAATATGCGCTACCATCAAGAGCCACCAAGTAAA 1200  
Db |||||  
Qy 1141 GGTAGTTCTTTAAAACTATTGATGGCAATATGCGCTACCATCAAGAGCCACCAAGTAAA 1200  
Db |||||  
Qy 1201 GAAATGAACCGATCTGTAAGCGGGGAAAAAATATTAGCTCGATATTATGAGAGAAAAG 1260  
Db |||||  
Qy 1201 GAAATGAACCGATCTGTAAGCGGGGAAAAAATATTAGCTCGATATTATGAGAGAAAAG 1260  
Db |||||  
Qy 1261 GTCCCTTATATCTATAGAAAATTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
Db |||||  
Qy 1261 GTCCCTTATATCTATAGAAAATTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT 1320  
Db |||||  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATAAATCTGTGCAAACTATATTCAAGTTGGGTAGAT 1380  
Db |||||  
Qy 1321 TTAGTTTCAATTTATATCCAGCTTATAAATCTGTGCAAACTATATTCAAGTTGGGTAGAT 1380  
Db |||||  
Qy 1381 AGTGACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1440  
Db |||||  
Qy 1381 AGTGACATGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA 1440  
Db |||||  
Qy 1441 GATAATACCTTAGAGTCAATCAATGCTTTATGTAATATCTTAGGTTAGCATCATG 1500  
Db |||||  
Qy 1441 GATAATACCTTAGAGTCAATCAATGCTTTATGTAATATCTTAGGTTAGCATCATG 1500  
Db |||||  
Qy 1501 TCTAAACCAATGCGGAATAGCTTCAGCATCAATGCAAGCGGTTCTTTTGTGCTAAAGGT 1560  
Db |||||  
Qy 1501 TCTAAACCAATGCGGAATAGCTTCAGCATCAATGCAAGCGGTTCTTTTGTGCTAAAGGT 1560  
Db |||||  
Qy 1561 TATTACATGGGCGAGTTAGATTAGATGATTTATCTTTGAGCCGTGATGCAAGTTGATGTGT 1620  
Db |||||  
Qy 1561 TATTACATGGGCGAGTTAGATTAGATGATTTATCTTTGAGCCGTGATGCAAGTTGATGTGT 1620  
Db |||||  
Qy 1621 TTTAAAGAAATTTTAAAGATAAAGCGCTAGCTGTGTTTATACCACTAATAGAAAAGTTC 1680  
Db |||||  
Qy 1621 TTTAAAGAAATTTTAAAGATAAAGCGCTAGCTGTGTTTATACCACTAATAGAAAAGTTC 1680  
Db |||||  
Qy 1681 AATCCGATGGTGTGTTAATCGCTAATGGTTTACAAATGCGCAGAAATTTTACGAGAAAAA 1740  
Db |||||  
Qy 1681 AATCCGATGGTGTGTTAATCGCTAATGGTTTACAAATGCGCAGAAATTTTACGAGAAAAA 1740  
Db |||||

Qy 1741 CTCACAAGCGCTATGCTCACCACCTTTAGAAATGTTACAGATTAGAGCTTGGCATTTTA 1800  
Db |||||  
Qy 1741 CTCACAAGCGCTATGCTCACCACCTTTAGAAATGTTACAGATTAGAGCTTGGCATTTTA 1800  
Db |||||  
Qy 1801 ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCAAACCTC 1860  
Db |||||  
Qy 1801 ACTGATGGATTCAATGAAAAAATTTGAAATGCGGTAGACTATGACATGTTCTCAAACCTC 1860  
Db |||||  
Qy 1861 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT 1920  
Db |||||  
Qy 1861 AGTGAAGTTGGAATAATTTAAACATCTTAATAAATCTGCTATTAACCGTGTATTACATGGT 1920  
Db |||||  
Qy 1921 GATAACACATCAATTAAGAAACTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Db |||||  
Qy 1921 GATAACACATCAATTAAGAAACTTGGCATTCAAAAGAAAAACCAATTTTGTGTAGTCAAT 1980  
Db |||||  
Qy 1981 CAGTCATTAAATAGACAGGCATTAATTAATAATTAATGACGAATTTGATGATTTAGAT 2040  
Db |||||  
Qy 1981 CAGTCATTAAATAGACAGGCATTAATTAATAATTAATGACGAATTTGATGATTTAGAT 2040  
Db |||||  
Qy 2041 GAAAGTAGAAAGTATATTTTCAATAAACCCTGGAATATCAAGAAGAGATTGATATCTTA 2100  
Db |||||  
Qy 2041 GAAAGTAGAAAGTATATTTTCAATAAACCCTGGAATATCAAGAAGAGATTGATATCTTA 2100  
Db |||||  
Qy 2101 AAAGATATTAAA 2112  
Db |||||  
Qy 2101 AAAGATATTAAA 2112  
Db |||||

RESULT 7

US-11-172-145-18  
; Sequence 18, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 18  
; LENGTH: 2112  
; TYPE: DNA  
; ORGANISM: Paeteurella multocida  
US-11-172-145-18

Query Match 72.2%; Score 2108.8; DB 7; Length 2112;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAATACATTTATCAAGCAATAAAGCATATATAACAGCAATGACTACTCAATTAGCACTC 60  
DB 1 ATGAATACATTTATCAAGCAATAAAGCATATATAACAGCAATGACTACTCAATTAGCACTC 60  
QY 61 AAATTTATTTGAAAGTCGGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAATTTACC 120  
DB 61 AAATTTATTTGAAAGTCGGCGGAAATCTATGGACGGAAATTTGTTGAATTTCAAATTTACC 120  
QY 121 AAATGCAAGAAACCTCTAGCACATCTTCTGTTAATTCAGCACATCTTCTGTTAAAT 180  
DB 121 AAATGCAAGAAACCTCTAGCACATCTTCTGTTAATTCAGCACATCTTCTGTTAAAT 180  
QY 181 AAAGAAGAAAGTCAATTTTGGATAGTCCGTTAGATATTGCAACAACACTGTTACTT 240  
DB 181 AAAGAAGAAAGTCAATTTTGGATAGTCCGTTAGATATTGCAACAACACTGTTACTT 240  
QY 241 TCCAACGTAAATAAATTAGTACTTCTGATCTCGGAAAGAAACACGTTAAATAAATGG 300  
DB 241 TCCAACGTAAATAAATTAGTACTTCTGATCTCGGAAAGAAACACGTTAAATAAATGG 300  
QY 301 AAATTTGCTCACTGAGAGAAATCTGAAATATCGGAGGTAAAGCGGTGCGCCCTGTACCA 360  
DB 301 AAATTTGCTCACTGAGAGAAATCTGAAATATCGGAGGTAAAGCGGTGCGCCCTGTACCA 360  
QY 361 AAAGATTTTCCAAAGATCTGTTTACGCGCTTTACCTGATCATGTTAAATGATTTTACA 420  
DB 361 AAAGATTTTCCAAAGATCTGTTTACGCGCTTTACCTGATCATGTTAAATGATTTTACA 420  
QY 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAATCTGAAACATCAACATGTTGGTCTT 480  
DB 421 TGGTACAAAAAGCGAAAGAAAGACTTGGCATAAATCTGAAACATCAACATGTTGGTCTT 480  
QY 481 TCTATTATCGTTAACAACATTCATCGACGACCAATTTTATCGATTACATTTAGCCTGTTTA 540  
DB 481 TCTATTATCGTTAACAACATTCATCGACGACCAATTTTATCGATTACATTTAGCCTGTTTA 540  
QY 541 GTAAACAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
DB 541 GTAAACAAAAACACATTTACCCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAA 600  
QY 601 GATCTATCACCGATCATTTGCGCAATATCAAAATAAATTTGGATATTGCGTACGTCAGACAA 660  
DB 601 GATCTATCACCGATCATTTGCGCAATATCAAAATAAATTTGGATATTGCGTACGTCAGACAA 660  
QY 661 AAAGATAACGGTTTCAAGCCAGTCGCGTCGGAATATGGATATTGCGTACGTCAGACAA 720  
DB 661 AAAGATAACGGTTTCAAGCCAGTCGCGTCGGAATATGGATATTGCGTACGTCAGACAA 720  
QY 721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAATTCATTTATGGTTTCAATCTTTAT 780  
DB 721 GACTTTATTTGGCTTACTCGACTGTGATATGGCGCAATTCATTTATGGTTTCAATCTTTAT 780  
QY 781 GTTCAGAGCTATTAGAAGATGATGATTTTAAACATCATTTGGTCCAAAGAAATACATCGAT 840  
DB 781 GTTCAGAGCTATTAGAAGATGATGATTTTAAACATCATTTGGTCCAAAGAAATACATCGAT 840  
QY 841 ACACAAATATTGACCCAAAGACTTCTTAATAACGCGAGTTTTCGTTGAATCATTTACCA 900  
DB 841 ACACAAATATTGACCCAAAGACTTCTTAATAACGCGAGTTTTCGTTGAATCATTTACCA 900  
QY 901 GAAGTGAAACCAATAATAGTCTCGCAAGGAGGAAAGGAAAGGTTCTCTCGATTGG 960  
DB 901 GAAGTGAAACCAATAATAGTCTCGCAAGGAGGAAAGGAAAGGTTCTCTCGATTGG 960  
QY 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTCCGCTTTT 1020  
DB 961 CGCTTAGAACCAATTCGAAAAACAGAAATCTCCGCTTATCCGATTCGCTTCCGCTTTT 1020  
QY 1021 TTTGGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAATTAATTCGGTTTCTTTGAT 1080  
DB 1021 TTTGGCGGGTAAATGTTGCTTTTCGCTAAAAAATGGCTAAATTAATTCGGTTTCTTTGAT 1080  
QY 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTTAC 1140

DB 1081 GAGGAATTTAATCACTGGGGTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTTAC 1140  
QY 1141 GGTAGTTTCTTTAAACATATTGATGGCATTTATGCCCTTACCATCAAGAGCCACCAGGTAAA 1200  
DB 1141 GGTAGTTTCTTTAAACATATTGATGGCATTTATGCCCTTACCATCAAGAGCCACCAGGTAAA 1200  
QY 1201 GAAAAAGAAACCGATCGTGAAGCGGGAAAAAATAATTATAGCTCGATATTATGAGAGAAAAG 1260  
DB 1201 GAAAAAGAAACCGATCGTGAAGCGGGAAAAAATAATTATAGCTCGATATTATGAGAGAAAAG 1260  
QY 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
DB 1261 GTCCCTTATATCTATAGAAAACCTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT 1320  
QY 1321 TTAGTTTCAATTTATATCCAGCTTTATAAATGTGTCAAAATATATTCAACGTTGCGTAGAT 1380  
DB 1321 TTAGTTTCAATTTATATCCAGCTTTATAAATGTGTCAAAATATATTCAACGTTGCGTAGAT 1380  
QY 1381 AGTSCACTGAATCAGACTGTTGTTGATCTGAGGTTTGTATTGTTAAGATGGTTCAACA 1440  
DB 1381 AGTSCACTGAATCAGACTGTTGTTGATCTGAGGTTTGTATTGTTAAGATGGTTCAACA 1440  
QY 1441 GATTAATACCTTAGAAGTGAATCAAGCTTTATGGTAATATCTAGGGTACGCATCATG 1500  
DB 1441 GATTAATACCTTAGAAGTGAATCAAGCTTTATGGTAATATCTAGGGTACGCATCATG 1500  
QY 1501 TCTAAACCAATGCGGAAATAGCCTCAGCATCAAAATGCAGCGGTTCTTTTGTGCTAAAGGT 1560  
DB 1501 TCTAAACCAATGCGGAAATAGCCTCAGCATCAAAATGCAGCGGTTCTTTTGTGCTAAAGGT 1560  
QY 1561 TATTACATTTGGCAGTTAGATTTCAGATGATTTATCTGAGCCTGATGAGTTGAACTGTGT 1620  
DB 1561 TATTACATTTGGCAGTTAGATTTCAGATGATTTATCTGAGCCTGATGAGTTGAACTGTGT 1620  
QY 1621 TTTAAAGAAATTTTAAAGATATAACCGTAGCTTGTGTTTATACCATTAATAGAAACGTC 1680  
DB 1621 TTTAAAGAAATTTTAAAGATATAACCGTAGCTTGTGTTTATACCATTAATAGAAACGTC 1680  
QY 1681 AATCCGATGTAGCTTAATCGCTTAATGTTTACAAATGGCCAGAAATTTTTCACGAGAAAA 1740  
DB 1681 AATCCGATGTAGCTTAATCGCTTAATGTTTACAAATGGCCAGAAATTTTTCACGAGAAAA 1740  
QY 1741 CTCACACGCGTATGATTTGCTCACCATTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
DB 1741 CTCACACGCGTATGATTTGCTCACCATTTAGAAATGTTTACGATTTAGAGCTTGGCATTTA 1800  
QY 1801 ACTGATGATTTCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCTCAACCTC 1860  
DB 1801 ACTGATGATTTCAATGAAAAAATTTGAAAAATGCGGTAGACTATGACATGTTCTCTCAACCTC 1860  
QY 1861 AGTGAAGTTGGAATAATTTAAACATCTTAAATAAATCTGCTATTAACCGTGTATTACATGTT 1920  
DB 1861 AGTGAAGTTGGAATAATTTAAACATCTTAAATAAATCTGCTATTAACCGTGTATTACATGTT 1920  
QY 1921 GATTAACATCAATTAAGAAAACTTTGGCATTTCAAAAGAAAAAACCAATTTTGTGTAGTCAAT 1980  
DB 1921 GATTAACATCAATTAAGAAAACTTTGGCATTTCAAAAGAAAAAACCAATTTTGTGTAGTCAAT 1980  
QY 1981 CAGTCATTTAAATAGACAAAGGCAATTAATTAATTAATAGCAATTTTGTAGTATTAGAT 2040  
DB 1981 CAGTCATTTAAATAGACAAAGGCAATTAATTAATTAATAGCAATTTTGTAGTATTAGAT 2040  
QY 2041 GAAAGTGAAGATATTTTCAATAAACCCTGTAATTAAGAGAGAGATTTGATATCTTTA 2100  
DB 2041 GAAAGTGAAGATATATTTTCAATAAACCCTGTAATTAAGAGAGAGATTTGATATCTTTA 2100  
QY 2101 AAAGATATTTAA 2112  
DB 2101 AAAGATATTTAA 2112



US-11-172-145-19		US-11-172-145-19	
; Sequence 19, Application US/11172145		; Sequence 19, Application US/11172145	
; Publication No. US20050272696A1		; Publication No. US20050272696A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: DeAngelis, Paul		; APPLICANT: DeAngelis, Paul	
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC		; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC	
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS		; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS	
; FILE REFERENCE: 3554.104		; FILE REFERENCE: 3554.104	
; CURRENT APPLICATION NUMBER: US/11172.145		; CURRENT APPLICATION NUMBER: US/11172.145	
; CURRENT FILING DATE: 2005-06-30		; CURRENT FILING DATE: 2005-06-30	
; PRIOR FILING DATE: 60/584,442		; PRIOR FILING DATE: 60/584,442	
; PRIOR FILING DATE: 2004-06-30		; PRIOR FILING DATE: 2004-06-30	
; PRIOR APPLICATION NUMBER: 10/642,248		; PRIOR APPLICATION NUMBER: 10/642,248	
; PRIOR FILING DATE: 2003-08-15		; PRIOR FILING DATE: 2003-08-15	
; PRIOR APPLICATION NUMBER: 60/404,356		; PRIOR APPLICATION NUMBER: 60/404,356	
; PRIOR FILING DATE: 2002-08-16		; PRIOR FILING DATE: 2002-08-16	
; PRIOR APPLICATION NUMBER: 60/479,432		; PRIOR APPLICATION NUMBER: 60/479,432	
; PRIOR FILING DATE: 2003-06-18		; PRIOR FILING DATE: 2003-06-18	
; PRIOR APPLICATION NUMBER: 60/491,362		; PRIOR APPLICATION NUMBER: 60/491,362	
; PRIOR FILING DATE: 2003-07-31		; PRIOR FILING DATE: 2003-07-31	
; PRIOR APPLICATION NUMBER: 10/195,908		; PRIOR APPLICATION NUMBER: 10/195,908	
; PRIOR FILING DATE: 2002-07-15		; PRIOR FILING DATE: 2002-07-15	
; PRIOR APPLICATION NUMBER: 09/437,277		; PRIOR APPLICATION NUMBER: 09/437,277	
; PRIOR FILING DATE: 1999-11-01		; PRIOR FILING DATE: 1999-11-01	
; PRIOR APPLICATION NUMBER: 60/107,929		; PRIOR APPLICATION NUMBER: 60/107,929	
; PRIOR FILING DATE: 1998-11-11		; PRIOR FILING DATE: 1998-11-11	
; PRIOR APPLICATION NUMBER: 09/283,402		; PRIOR APPLICATION NUMBER: 09/283,402	
; PRIOR FILING DATE: 1999-04-01		; PRIOR FILING DATE: 1999-04-01	
; PRIOR APPLICATION NUMBER: 60/080,414		; PRIOR APPLICATION NUMBER: 60/080,414	
; PRIOR FILING DATE: 1998-04-02		; PRIOR FILING DATE: 1998-04-02	
; Remaining Prior Application data removed - See File Wrapper or PALM.		; Remaining Prior Application data removed - See File Wrapper or PALM.	
; NUMBER OF SEQ ID NOS: 25		; NUMBER OF SEQ ID NOS: 25	
; SOFTWARE: PatentIn version 3.3		; SOFTWARE: PatentIn version 3.3	
; SEQ ID NO 19		; SEQ ID NO 19	
; LENGTH: 2112		; LENGTH: 2112	
; TYPE: DNA		; TYPE: DNA	
; ORGANISM: Pasteurella multocida		; ORGANISM: Pasteurella multocida	
US-11-172-145-19		US-11-172-145-19	
Query Match 72.2%; Score 2108.8; DB 7; Length 2112;		Query Match 72.2%; Score 2108.8; DB 7; Length 2112;	
Best Local Similarity 99.9%; Pred. No. 0;		Best Local Similarity 99.9%; Pred. No. 0;	
Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Matches 2110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1	ATGAATACATTATCAACGCAATAAAGCATATATAACAGCAATGACTATCAATTAGCACTC	60
Db	1	ATGAATACATTATCAACGCAATAAAGCATATATAACAGCAATGACTATCAATTAGCACTC	60
Qy	61	AAATTATTGAAAGTCGGCGGAATCTATCGACGGAATTTGTTGAATTCBAATTACC	120
Db	61	AAATTATTGAAAGTCGGCGGAATCTATCGACGGAATTTGTTGAATTCBAATTACC	120
Qy	121	AAATGCAAGAAAACTCTCAGCACATCCTTCTGTTAATTCAGCACATCTTTCTGTAAAT	180
Db	121	AAATGCAAGAAAACTCTCAGCACATCCTTCTGTTAATTCAGCACATCTTTCTGTAAAT	180
Qy	181	AAAGAAGAAAAAGTCAATGTTTGGATAGTCGGTTAGATATATGCAACACAACTGTACTT	240
Db	181	AAAGAAGAAAAAGTCAATGTTTGGATAGTCGGTTAGATATATGCAACACAACTGTACTT	240
Qy	241	TCCACGTAAAAAATAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATAATGG	300
Db	241	TCCACGTAAAAAATAGTACTTCTGACTCGGAAAAAACAAGTTAAAAAATAATGG	300
Qy	301	AAATTTGCTCACTGAGAAGAAATCTGAAATTCGGAGGTAAAGCGGTGCTGTACCA	360
Db	301	AAATTTGCTCACTGAGAAGAAATCTGAAATTCGGAGGTAAAGCGGTGCTGTACCA	360
Qy	361	AAAGATTTCCCAAGATCTGGTTTACGCTTTACCTGATCATGTTTAATGATTTTACA	420
Db	361	AAAGATTTCCCAAGATCTGGTTTACGCTTTACCTGATCATGTTTAATGATTTTACA	420
Qy	421	TGGTACAAAAAGCGAAGAAAGCTTGGCATAAAACTGAACATCAACATGTTGGTCTT	480
Db	421	TGGTACAAAAAGCGAAGAAAGCTTGGCATAAAACTGAACATCAACATGTTGGTCTT	480

Db	421	TGGTACAAAAAGCGAAGAAAGCTTGGCATAAAACTGAACATCAACATGTTGGTCTT	480
Qy	481	TCATTATCGTTTACAACTTCAATCGACAGCAATTTTATCGATTACATTAGCTGTTTA	540
Db	481	TCATTATCGTTTACAACTTCAATCGACAGCAATTTTATCGATTACATTAGCTGTTTA	540
Qy	541	GTAACCAAAAAACACATTACCGTTTGAAGTTATCGTGACAGATGATGTTAGTTCAGGAA	600
Db	541	GTAACCAAAAAACACATTACCGTTTGAAGTTATCGTGACAGATGATGTTAGTTCAGGAA	600
Qy	601	GATCTATCACCGATCATTCGCCAATATGAAAAATAATTTGGATATTCGCTACGTGAGAA	660
Db	601	GATCTATCACCGATCATTCGCCAATATGAAAAATAATTTGGATATTCGCTACGTGAGAA	660
Qy	661	AAAGATAACCGTTTCAAGCAGTCGCGCTCGGAAATATGGAATAGCGTTAGCAGAAATAT	720
Db	661	AAAGATAACCGTTTCAAGCAGTCGCGCTCGGAAATATGGAATAGCGTTAGCAGAAATAT	720
Qy	721	GACTTTATTTGGCTTACTCGACTGATATGCGCCCAATCCATTATGGGTTTCACTTAT	780
Db	721	GACTTTATTTGGCTTACTCGACTGATATGCGCCCAATCCATTATGGGTTTCACTTAT	780
Qy	781	GTTGACAGCTATTAGAAAGATGATTTAAACAATCATTCGTCGAAGAAAAATACATCGAT	840
Db	781	GTTGACAGCTATTAGAAAGATGATTTAAACAATCATTCGTCGAAGAAAAATACATCGAT	840
Qy	841	ACACAATATTCACCCAAAGACTTCTTAAATAACGCGAGTTTGTGTAATCATTTACCA	900
Db	841	ACACAATATTCACCCAAAGACTTCTTAAATAACGCGAGTTTGTGTAATCATTTACCA	900
Qy	901	GAAGTGAACCAATATAGTGTTCGCAAAAGGGGAGGAAACAGTTTCTCTGGATTGG	960
Db	901	GAAGTGAACCAATATAGTGTTCGCAAAAGGGGAGGAAACAGTTTCTCTGGATTGG	960
Qy	961	CGTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTT	1020
Db	961	CGTTAGAACAAATTCGAAAAACAGAAAAATCTCCGCTTATCCGATTCGCTTTCCGTTT	1020
Qy	1021	TTTGGCGCGGTAAATGTTGTTTTCGTTAAAAATGCTAAATAAATCCGGTTTCTTTGAT	1080
Db	1021	TTTGGCGCGGTAAATGTTGTTTTCGTTAAAAATGCTAAATAAATCCGGTTTCTTTGAT	1080
Qy	1081	GAGGAATTTAATCACTGGGTGGAGAGATGTCGAAATTTGGATATCGCTTATCCGTTAC	1140
Db	1081	GAGGAATTTAATCACTGGGTGGAGAGATGTCGAAATTTGGATATCGCTTATCCGTTAC	1140
Qy	1141	GGTAGTTTCTTTAAAACTATTGATGCTATATGCGCTTACCATCAAGAGCCACAGGTAAA	1200
Db	1141	GGTAGTTTCTTTAAAACTATTGATGCTATATGCGCTTACCATCAAGAGCCACAGGTAAA	1200
Qy	1201	GAATAAGAAACCGATCGTGAAGCGGAAAAATAATTAACGCTCGATATATGAGAGAAAAAG	1260
Db	1201	GAATAAGAAACCGATCGTGAAGCGGAAAAATAATTAACGCTCGATATATGAGAGAAAAAG	1260
Qy	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT	1320
Db	1261	GTCCCTTATATCTATAGAAAACTTTTACCAATAGAGATTCGCATATCAATAGAGTACCT	1320
Qy	1321	TTAGTTTCAATTTATATCCAGCTTATAAATGTCGAAAACTATATTAACGTTGCGGTAGAT	1380
Db	1321	TTAGTTTCAATTTATATCCAGCTTATAAATGTCGAAAACTATATTAACGTTGCGGTAGAT	1380
Qy	1381	AGTGCACTGAATCAGACTGTTGATCTCGAGGTTGTAATTTGTAACGATGTTTCAACA	1440
Db	1381	AGTGCACTGAATCAGACTGTTGATCTCGAGGTTGTAATTTGTAACGATGTTTCAACA	1440
Qy	1441	GATTAATACCTTAGAGATCAATAGCTTTTATGCTTAATATCCTAGGTCAGCATCATG	1500
Db	1441	GATTAATACCTTAGAGATCAATAGCTTTTATGCTTAATATCCTAGGTCAGCATCATG	1500
Qy	1501	TCTAAACCAATGCGGAAATAGCCTCAGCATCAAAATGCAGCGGTTTCTTTTGTAAAGGT	1560
Db	1501	TCTAAACCAATGCGGAAATAGCCTCAGCATCAAAATGCAGCGGTTTCTTTTGTAAAGGT	1560



. Remaining prior Application data removed - See File Wrapper or PALM.

```

; REMAINING INFORMATION DATA REMOVED
; SEQ ID NO: 25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 20
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-11-172-145-20

```

Query Match	72.2%	Score 2108.8	DB 7	Length 2112
Best Local Similarity	99.5%	Pred. No.	0	
Matches 2110	Conservative	0	Mismatches	2
			Indels	0
			Gaps	0

Qy	1	ATGAATACATTTATACACGCAATAAAGCATATAACAGCAATGACTATCAATTTAGCACTC	60
Db	1	ATGAATACATTTATACAGCAATAAAGCATATAACAGCATGACTATCAATTTAGCACTC	60
Qy	61	AAATTAATTTGAAAGTCGCGGAAATCTATGGACGAAATTTGTAATTTCAAAATTTACC	120
Db	61	AAATTAATTTGAAAGTCGCGGAAATCTATGGACGAAATTTGTAATTTCAAAATTTACC	120
Qy	121	AAATGCAAGAAAACTCTCAGACATCTTTCTGTTAATTCAGCACATCTTTCTGTGAAT	180
Db	121	AAATGCAAGAAAACTCTCAGACATCTTTCTGTTAATTCAGCACATCTTTCTGTGAAT	180
Qy	181	AAAGAGAAAAAGTCAATGTTTCGCGATAGTCGGTAGATATTGCAACACAACTGTTACTTT	240
Db	181	AAAGAGAAAAAGTCAATGTTTCGCGATAGTCGGTAGATATTGCAACACAACTGTTACTTT	240
Qy	241	TCCAAAGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAAGTTAAAAAATAATGG	300
Db	241	TCCAAAGTAAAAAATTTAGTACTTTCTGACTCGGAAAAAACAAGTTAAAAAATAATGG	300
Qy	301	AAATTGCTCACTGAGAGAAATCTGAAATTCGGAGGTAGAGCGGTGCGCCTTGTAACCA	360
Db	301	AAATTGCTCACTGAGAGAAATCTGAAATTCGGAGGTAGAGCGGTGCGCCTTGTAACCA	360
Qy	361	AAAGATTTTCCCAAGATCTGGTTTTAGCGCCTTTTACCTGATCATGTTAATGATTTTACA	420
Db	361	AAAGATTTTCCCAAGATCTGGTTTTAGCGCCTTTTACCTGATCATGTTAATGATTTTACA	420
Qy	421	TGGTACAAAAAGCGAAAGAAAGACTTTGGCATAAACCTGAACATCAACATGTTGGTCTT	480
Db	421	TGGTACAAAAAGCGAAAGAAAGACTTTGGCATAAACCTGAACATCAACATGTTGGTCTT	480
Qy	481	TCATTAATTCGTACAACTTCAATTCGACAGCAATTTTATCGATTACATTTAGCCTGTTTA	540
Db	481	TCATTAATTCGTACAACTTCAATTCGACAGCAATTTTATCGATTACATTTAGCCTGTTTA	540
Qy	541	GTAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGTTAGTACAGAA	600
Db	541	GTAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACAGATGATGTTAGTACAGAA	600
Qy	601	GATCTATACCGATCATTCGCGCAATATGAAAAATAATTTGGATATTCGCTAGCTCAGACAA	660
Db	601	GATCTATACCGATCATTCGCGCAATATGAAAAATAATTTGGATATTCGCTAGCTCAGACAA	660
Qy	661	AAAGATAACGGTTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTTACGTTAGCAAAATAT	720
Db	661	AAAGATAACGGTTTTTCAAGCCAGTCGCGCTCGGAATATGGGATTTACGTTAGCAAAATAT	720
Qy	721	GACTTTTATGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGGTTTCTTTAT	780
Db	721	GACTTTTATGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGGTTTCTTTAT	780
Qy	781	GTTTCAGAGCTATTAGAAAGATGATTTAACATCATTCGTCAGAAATAATACATCGAT	840
Db	781	GTTTCAGAGCTATTAGAAAGATGATTTAACATCATTCGTCAGAAATAATACATCGAT	840
Qy	841	ACAAACAATTTGACCCAAAAGACTTTTAAATTAACCGAGTTTGGCTTTGAATCATTTACCA	900
Db	841	ACAAACAATTTGACCCAAAAGACTTTTAAATTAACCGAGTTTGGCTTTGAATCATTTACCA	900

1561	Qy	TATTACATGGGCAGTTAGATTCAGATGATTA	TCCTTGACGCTGATGCAGTTGAACTGTGT	1620
1561	Db	TATTACATGGGCAGTTAAATTCAGATGATTA	TCCTTGAGCCTGATGCAGTTGAACTGTGT	1620
1621	Qy	TTAAAGAAATTTTTTAAAGATAAAACGCTAGCTTG	TGTGTTTATACCACTAAATAGAAACGTC	1680
1621	Db	TTAAAGAAATTTTTTAAAGATAAAACGCTAGCTTG	TGTGTTTATACCACTAAATAGAAACGTC	1680
1681	Qy	AAATCCGATCGGTAGCTTAAATCGCTAAATGGT	TACAAATTGGCCAGAAATTTTCA	1740
1681	Db	AAATCCGATCGGTAGCTTAAATCGCTAAATGGT	TACAAATTGGCCAGAAATTTTCA	1740
1741	Qy	CTCACAAACGGCTATGATGTGCTACACCTTTAG	AATGTTTACAGATTAGAGCTTGGCAATTTA	1800
1741	Db	CTCACAAACGGCTATGATGTGCTACACCTTTAG	AATGTTTACAGATTAGAGCTTGGCAATTTA	1800
1801	Qy	ACTGATCGATTCAATGAAATAATGAAATGCGCT	AGACTATCAGACTGTTTCCCTCAAACCTC	1860
1801	Db	ACTGATCGATTCAATGAAATAATGAAATGCGCT	AGACTATGACATGTTTCCCTCAAACCTC	1860
1861	Qy	AGTGAAGCTTGGAAAAATTTAAACATCTTAAAT	AAAAATCTGCTATAACCGTGATTACATGGT	1920
1861	Db	AGTGAAGCTTGGAAAAATTTAAACATCTTAAAT	AAAAATCTGCTATAACCGTGATTACATGGT	1920
1921	Qy	GATAACACATCAATTAAGAAACCTGGCGATT	CAAAAGAAAAACCAATTTGTTGTAGTCAAT	1980
1921	Db	GATAACACATCAATTAAGAAACCTGGCGATT	CAAAAGAAAAACCAATTTGTTGTAGTCAAT	1980
1981	Qy	CAGTCAATTAATAGACAAAGCGATAACTTAT	TATTAATATGACGAAATTTGATGATTTAGAT	2040
1981	Db	CAGTCAATTAATAGACAAAGCGATAACTTAT	TATTAATTAATGACGAAATTTGATGATTTAGAT	2040
2041	Qy	GAAGTAGAAGTAGTATATTTTCAATATAAAAC	CGCTGAATATCAAGAAAGAGATTGATATCTTA	2100
2041	Db	GAAGTAGAAGTAGTATATTTTCAATATAAAAC	CGCTGAATATCAAGAAAGAGATTGATATCTTA	2100
2101	Qy	AAAGATATTTAA	2112	
2101	Db	AAAGATATTTAA	2112	

RESULT 9  
US-11-172-145-20  
; Sequence 20, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172,145  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/584,442  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 10/642,248  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/404,356  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/479,432  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: 60/491,362  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: 10/195,908  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/437,277  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 60/107,929  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR APPLICATION NUMBER: 09/283,402  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/080,414  
; PRIOR FILING DATE: 1998-04-02



Db 244 GATCTGGTTTGTAGCGCTTTACCTGATCACTGTAATGATTTTACATGGTACAAAAGCGA 303  
Qy 436 AAGAAAGACTTGGCATAAACCTTGAACATCAACATGTTGGTCTTTCTATTATCGTTACA 495  
Db 304 AAGAAAGACTTGGCATAAACCTTGAACATCAACATGTTGGTCTTTCTATTATCGTTACA 363  
Qy 496 ACATTTCAATGACAGCAATTTTATCGATTACATTTAGCCTGTTTGTAGTAAACCAAAAACA 555  
Db 364 ACATTTCAATGACAGCAATTTTATCGATTACATTTAGCCTGTTTGTAGTAAACCAAAAACA 423  
Qy 556 CATTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAAGATCTATCAACGATC 615  
Db 424 CATTACCGTTTGAAGTTATCGTGACAGATGATGGTAGTCAGGAAGATCTATCAACGATC 483  
Qy 616 ATTCGCCAATGAAATAAATTTGATATTCGCTACGTCAGACAAAAGATAACGGTTTT 675  
Db 484 ATTCGCCAATGAAATAAATTTGATATTCGCTACGTCAGACAAAAGATAACGGTTTT 543  
Qy 676 CAAGCAGTGGCGTTCGGAATATGGATTAGGCTTTAGCAAAATATGACTTTATTGGCTTA 735  
Db 544 CAAGCAGTGGCGTTCGGAATATGGATTAGGCTTTAGCAAAATATGACTTTATTGGCTTA 603  
Qy 736 CTCGACTGTGATATGGCCCAAAATCCATTATGGGTTCAATCTTATGTTGACAGCTATTA 795  
Db 604 CTCGACTGTGATATGGCCCAAAATCCATTATGGGTTCAATCTTATGTTGACAGCTATTA 663  
Qy 796 GAAGATGATGATTTAAACAATCATTTGGTCCAGAAAATACATCGATACACATATTCAC 855  
Db 664 GAAGATGATGATTTAAACAATCATTTGGTCCAGAAAATACATCGATACACATATTCAC 723  
Qy 856 CCBAAGACTTCTTAAATAAGCGAGTTTGTGTAATCATACCAAGAGTGAACCAAT 915  
Db 724 CCBAAGACTTCTTAAATAAGCGAGTTTGTGTAATCATACCAAGAGTGAACCAAT 783  
Qy 916 AATAGTGTGGCGCAAAAAGGGAAGAACAGTTTCTCTGGAATGGCGCTTGAACAATTC 975  
Db 784 AATAGTGTGGCGCAAAAAGGGAAGAACAGTTTCTCTGGAATGGCGCTTGAACAATTC 843  
Qy 976 GAAAAACAGAAAATCTCGCTTATCCGATTCGCCCTTTCCGTTTTCGGCGGGTAAAT 1035  
Db 844 GAAAAACAGAAAATCTCGCTTATCCGATTCGCCCTTTCCGTTTTCGGCGGGTAAAT 903  
Qy 1036 GTTGCCTTCGTAATAAATGCTTAATAATCCGGTTCTTTGTATGAGGAATTTAATCAC 1095  
Db 904 GTTGCCTTCGTAATAAATGCTTAATAATCCGGTTCTTTGTATGAGGAATTTAATCAC 963  
Qy 1096 TGGGCTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTACGGTAGTTTCTTTAAA 1155  
Db 964 TGGGCTGGAGAGATGTGGAATTTGGATATCGCTTATTCGGTTACGGTAGTTTCTTTAAA 1023  
Qy 1156 ACTATGTATGGCAATATAGCCTTACCATCAAGAGCCACAGGTAAGAAAATGAACCCGAT 1215  
Db 1024 ACTATGTATGGCAATATAGCCTTACCATCAAGAGCCACAGGTAAGAAAATGAACCCGAT 1083  
Qy 1216 CGTGAAGCGGGAATAAATTTACGCTCGATATATGAGAAAAGTCCCTTATATCTAT 1275  
Db 1084 CGTGAAGCGGGAATAAATTTACGCTCGATATATGAGAAAAGTCCCTTATATCTAT 1143  
Qy 1276 AGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGATACCTTTTATGTTTCAATTTAT 1335  
Db 1144 AGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGATACCTTTTATGTTTCAATTTAT 1203  
Qy 1336 ATCCAGCTTATTAACCTGTGCAAACTATATTCAAAGTGGTAGATGCTGCTGAATCAG 1395  
Db 1204 ATCCAGCTTATTAACCTGTGCAAACTATATTCAAAGTGGTAGATGCTGCTGAATCAG 1263  
Qy 1396 ACTGTTGTTGATCTCGAGTTTGTATTTGTAAACGATGTTTCAACAGATAACCTTAGAA 1455  
Db 1264 ACTGTTGTTGATCTCGAGTTTGTATTTGTAAACGATGTTTCAACAGATAACCTTAGAA 1323  
Qy 1456 GTGATCAATAAGCTTTATCGTAATAATCTTAGGGTACGATCATGTCTTAAACCAATGGC 1515

Db 1324 GTGATCAATAAGCTTTATGTTAATAATCTAGGTAGCATCATGTCTAAACCAATGGC 1383  
Qy 1516 GGAATAGCCTCAGCATCAAAATGAGCGGTTTCTTTTCTCTAAAGGTTATTAATTTGGGCGAG 1575  
Db 1384 GGAATAGCCTCAGCATCAAAATGAGCGGTTTCTTTTCTCTAAAGGTTATTAATTTGGGCGAG 1443  
Qy 1576 TTAGATTACAGATGATTATCTTGAGCCTGATGCGAGTTGAACCTGTTTAAAGAAATTTTAA 1635  
Db 1444 TTAGATTACAGATGATTATCTTGAGCCTGATGCGAGTTGAACCTGTTTAAAGAAATTTTAA 1503  
Qy 1636 AAAGATAAAAAGCTTAGCTTGTGTTTATACCACTAATAGAAAAGCTCAATCCGGATGGTAGC 1695  
Db 1504 AAAGATAAAAAGCTTAGCTTGTGTTTATACCACTAATAGAAAAGCTCAATCCGGATGGTAGC 1563  
Qy 1696 TTATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCAGAGAAAACCTCAACACGGCTATG 1755  
Db 1564 TTATCGCTAATGTTTACAAATTTGGCCAGAAATTTTCAGAGAAAACCTCAACACGGCTATG 1623  
Qy 1756 ATTGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTTGGCAATTTAACTGATGGATTCAAT 1815  
Db 1624 ATTGCTCACCACCTTTAGAAATGTTTACGATTTAGAGCTTTGGCAATTTAACTGATGGATTCAAT 1683  
Qy 1816 GAAAAAATTTGAAAATGCGTAGACTATGACATGTTCTCTCAAACTCAGTGAAGTTGGAAAA 1875  
Db 1684 GAAAAAATTTGAAAATGCGTAGACTATGACATGTTCTCTCAAACTCAGTGAAGTTGGAAAA 1743  
Qy 1876 TTTAAACATCTTAAATAAATCTGCTATAACCGTGTATTTACATGTTGATGATAACACATCAAT 1935  
Db 1744 TTTAAACATCTTAAATAAATCTGCTATAACCGTGTATTTACATGTTGATGATAACACATCAAT 1803  
Qy 1936 AAGAAACTTGGCATTTCAAAAAGAAAAACCAATTTTGTGTTAGTCAATCAGTCAATTAATAGA 1995  
Db 1804 AAGAAACTTGGCATTTCAAAAAGAAAAACCAATTTTGTGTTAGTCAATCAGTCAATTAATAGA 1863  
Qy 1996 CAAGCATACTTATTAATATGAGAAATTTGATGATTTAGTGAAGTAGAAAGTAT 2055  
Db 1864 CAAGCATACTTATTAATATGAGAAATTTGATGATTTAGTGAAGTAGAAAGTAT 1923  
Qy 2056 ATTTTCAATAAACCCTGTAATATCAAGAGAGATTTGATATCTTAAAAAGATTTAAA 2112  
Db 1924 ATTTTCAATAAACCCTGTAATATCAAGAGAGATTTGATATCTTAAAAAGATTTAAA 1980

## RESULT 11

US-11-172-145-14

; Sequence 14, Application US/11172145

; Publication No: US20050272696A1

; GENERAL INFORMATION:

; APPLICANT: DeAngelis, Paul

; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN POLYMERS

; FILE REFERENCE: 3554.104

; CURRENT APPLICATION NUMBER: US/11/172,145

; PRIORITY FILING DATE: 2005-06-30

; PRIORITY APPLICATION NUMBER: 60/584,442

; PRIORITY FILING DATE: 2004-06-30

; PRIORITY APPLICATION NUMBER: 10/642,248

; PRIORITY FILING DATE: 2003-08-15

; PRIORITY APPLICATION NUMBER: 60/404,356

; PRIORITY FILING DATE: 2002-08-16

; PRIORITY APPLICATION NUMBER: 60/479,432

; PRIORITY FILING DATE: 2003-06-18

; PRIORITY APPLICATION NUMBER: 60/491,362

; PRIORITY FILING DATE: 2003-07-31

; PRIORITY APPLICATION NUMBER: 10/195,908

; PRIORITY FILING DATE: 2002-07-15

; PRIORITY APPLICATION NUMBER: 09/437,277

; PRIORITY FILING DATE: 1999-11-01

; PRIORITY APPLICATION NUMBER: 60/107,929

; PRIORITY FILING DATE: 1998-11-11

; PRIORITY APPLICATION NUMBER: 09/283,402

; PRIORITY FILING DATE: 1999-04-01

; PRIORITY APPLICATION NUMBER: 60/080,414

; PRIOR FILING DATE: 1998-04-02									
; Remaining Prior Application data removed - See File Wrapper or PALM.									
; NUMBER OF SEQ ID NOS: 25									
; SOFTWARE: PatentIn version 3.3									
; SEQ ID NO 14									
; LENGTH: 1902									
; TYPE: DNA									
; ORGANISM: Pasteurella multocida									
US-11-172-145-14									
Query Match 65.0%; Score 1898.4; DB 7; Length 1902;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 1899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	213	GTATAGATATTGCAACACAACTGTTTACCTTTCCAAAGTAAATAAATAGTACTTTCTGACTC	272						
Db	3	GTATAGATATTGCAACACAACTGTTTACCTTTCCAAAGTAAATAAATAGTACTTTCTGACTC	62						
Qy	273	GGAAAAAACAACGTTAAATAATGGAATTCCTCACTGAGAGAAATCTGGAATGC	332						
Db	63	GGAAAAAACAACGTTAAATAATGGAATTCCTCACTGAGAGAAATCTGGAATGC	122						
Qy	333	GGAGGTAAAGCGGTGCGCCCTGTACCAAAAGATTTTCCAAAGATCTGGTTTTCAGCGCC	392						
Db	123	GGAGGTAAAGCGGTGCGCCCTGTACCAAAAGATTTTCCAAAGATCTGGTTTTCAGCGCC	182						
Qy	393	TTTACCTGATCATGTTTAATGATTTTACATGTTACAAAGCGAAAGAAAGACTTTGGCAT	452						
Db	183	TTTACCTGATCATGTTTAATGATTTTACATGTTACAAAGCGAAAGAAAGACTTTGGCAT	242						
Qy	453	AAAAACCTGAAACATCAACATGTTGTCCTTCTATGTTACCAATCTCAATCACCAGC	512						
Db	243	AAAAACCTGAAACATCAACATGTTGTCCTTCTATGTTACCAATCTCAATCACCAGC	302						
Qy	513	AAATTTTATCGATTACATTTAGCTGTTTGTAGTAAACCAAAACACATTAACCGTTTGAAGT	572						
Db	303	AAATTTTATCGATTACATTTAGCTGTTTGTAGTAAACCAAAACACATTAACCGTTTGAAGT	362						
Qy	573	TATCGTGACAGATGATGTTAGTCAAGGAAGATCTATACCGATCATTCGCCAATATGAAA	632						
Db	363	TATCGTGACAGATGATGTTAGTCAAGGAAGATCTATACCGATCATTCGCCAATATGAAA	422						
Qy	633	TAAATTTGGATTCGCTACGTCAGACAAAGAAATACCGTTTCAAGCCAGTCGCGCTCG	692						
Db	423	TAAATTTGGATTCGCTACGTCAGACAAAGAAATACCGTTTCAAGCCAGTCGCGCTCG	482						
Qy	693	GAAATATGGGATTACGCTTAGCAAAATATGACTTTTATGGCTTACTCGACTGTGATATGGC	752						
Db	483	GAAATATGGGATTACGCTTAGCAAAATATGACTTTTATGGCTTACTCGACTGTGATATGGC	542						
Qy	753	GCCAAATCCATTATGGGTTTCACTTATGTTTGCAGAGCTATTAGAGATGATGATTTAAC	812						
Db	543	GCCAAATCCATTATGGGTTTCACTTATGTTTGCAGAGCTATTAGAGATGATGATTTAAC	602						
Qy	813	AATCAATTTGGTCCAGAAAATACATCGATACACACATATTGACCCAAAGACTTCTTAAA	872						
Db	603	AATCAATTTGGTCCAGAAAATACATCGATACACACATATTGACCCAAAGACTTCTTAAA	662						
Qy	873	TAAACGCGAGTTTGTCTGAAATCATTTACCAAGAGTGAAGCAATTAATAGTGTTCGCGCAA	932						
Db	663	TAAACGCGAGTTTGTCTGAAATCATTTACCAAGAGTGAAGCAATTAATAGTGTTCGCGCAA	722						
Qy	933	AGGGGAAGGAAACAGTTTCTCTGATTTGGCGCTTAGAACAAATTCGAAAAAACAAGAAATCT	992						
Db	723	AGGGGAAGGAAACAGTTTCTCTGATTTGGCGCTTAGAACAAATTCGAAAAAACAAGAAATCT	782						
Qy	993	CCGCTTATCCGATTCGCTTTCCGTTTTCGCGCGGGTAAATGTTGCTTCGCTTAAAAA	1052						
Db	783	CCGCTTATCCGATTCGCTTTCCGTTTTCGCGCGGGTAAATGTTGCTTCGCTTAAAAA	842						
Qy	1053	ATGGCTAAATAAATCCCGTTTCTTTTGTATGAGAAATTTAATCACTGGGGTGGAGAGATGT	1112						
Db	843	ATGGCTAAATAAATCCCGTTTCTTTTGTATGAGAAATTTAATCACTGGGGTGGAGAGATGT	902						

RESULT 12  
US-11-172-145-15  
; Sequence 15, Application US/11172145

Qy	1113	GGAAATTTGGATATCGCTTATTCGGTTACGGTAGCTTCTTTTAAACATATTTCATGSCATTAT	1172						
Db	903	GGAAATTTGGATATCGCTTATTCGGTTACGGTAGCTTCTTTTAAACATATTTCATGSCATTAT	962						
Qy	1173	GGCTTACCATTCAAGAGCCACCAGGTAAAGAAAAAGAAACCGATCGTGAACGGGAAAAAA	1232						
Db	963	GGCTTACCATTCAAGAGCCACCAGGTAAAGAAAAAGAAACCGATCGTGAACGGGAAAAAA	1022						
Qy	1233	TATTACGCTCGATATTATAGAGAAAGGTCCTTATATCTATAGAAAACTTTTACCAAT	1292						
Db	1023	TATTACGCTCGATATTATAGAGAAAGGTCCTTATATCTATAGAAAACTTTTACCAAT	1082						
Qy	1293	AGAAGATTCGATATCAATAGACTCTTTTAGTTTCAATTTATATCCACGCTTATACTG	1352						
Db	1083	AGAAGATTCGATATCAATAGACTCTTTTAGTTTCAATTTATATCCACGCTTATACTG	1142						
Qy	1353	TGCAAACTATATTCAACGTTGCGTAGATAGTGCACCTGAATCAGACTGTTGTGATCTCGA	1412						
Db	1143	TGCAAACTATATTCAACGTTGCGTAGATAGTGCACCTGAATCAGACTGTTGTGATCTCGA	1202						
Qy	1413	GGTTTGTATTGTAACGATGGTTCAAACAGATAATACCTTTAGAAAGTGATCAATAGCTTTTA	1472						
Db	1203	GGTTTGTATTGTAACGATGGTTCAAACAGATAATACCTTTAGAAAGTGATCAATAGCTTTTA	1262						
Qy	1473	TGCTAATATCTTAGGTAGGTCAGTCACTGCTAAACCAAAATGGCGGATAGCCTCAGCATC	1532						
Db	1263	TGCTAATATCTTAGGTAGGTCAGTCACTGCTAAACCAAAATGGCGGATAGCCTCAGCATC	1322						
Qy	1533	AAATGACAGCCGTTCTTTTCTGCTAAAGGTTATTACATTTGGGCACTTAGATTCAGATGATTA	1592						
Db	1323	AAATGACAGCCGTTCTTTTCTGCTAAAGGTTATTACATTTGGGCACTTAGATTCAGATGATTA	1382						
Qy	1593	TCTTGAGCCTGATGCACTGTTGAACTGTTTAAAGAAATTTTAAAGATAAAAAGCTAGC	1652						
Db	1383	TCTTGAGCCTGATGCACTGTTGAACTGTTTAAAGAAATTTTAAAGATAAAAAGCTAGC	1442						
Qy	1653	TTGTGTTTATACCACTAAATAGAAAACTCAATCCGGATGGTAGCTTAATCGCTAATGCTTA	1712						
Db	1443	TTGTGTTTATACCACTAAATAGAAAACTCAATCCGGATGGTAGCTTAATCGCTAATGCTTA	1502						
Qy	1713	CAATTTGCCAGAAATTTTACGAGAAAACTCACAACGGCTATGATTCCTCACCACTTTTAG	1772						
Db	1503	CAATTTGCCAGAAATTTTACGAGAAAACTCACAACGGCTATGATTCCTCACCACTTTTAG	1562						
Qy	1773	AATGTTTCAAGATTAGAGCTTTGGCATTTAACTGATGGAATCAATGAAAAAATGAAAAATGC	1832						
Db	1563	AATGTTTCAAGATTAGAGCTTTGGCATTTAACTGATGGAATCAATGAAAAAATGAAAAATGC	1622						
Qy	1833	CGTAGACTATGACATGTTTCTCAACTCAGTGAAGTTGGAAAAATTTAAACATCTTAATAA	1892						
Db	1623	CGTAGACTATGACATGTTTCTCAACTCAGTGAAGTTGGAAAAATTTAAACATCTTAATAA	1682						
Qy	1893	AACTGCTATAACCGGTGATTACATGCTGATTAACACATCAATTAAGAAAACTTGGCATCA	1952						
Db	1683	AACTGCTATAACCGGTGATTACATGCTGATTAACACATCAATTAAGAAAACTTGGCATCA	1742						
Qy	1953	AAAGAAAAACCAATTTTGTGTTAGTCAATCAGTCAATTAATAAGAGGCAATTAATTA	2012						
Db	1743	AAAGAAAAACCAATTTTGTGTTAGTCAATCAGTCAATTAATAAGAGGCAATTAATTA	1802						
Qy	2013	TAATATGACGAATTTGATGATTTAGTGAAGTAGAAAGTATATTTTCAATAAAAAACGC	2072						
Db	1803	TAATATGACGAATTTGATGATTTAGTGAAGTAGAAAGTATATTTTCAATAAAAAACGC	1862						
Qy	2073	TGAATATCAAGAGAGATTCATATCTTTAAAGATATTAAA	2112						
Db	1863	TGAATATCAAGAGAGATTCATATCTTTAAAGATATTAAA	1902						







Db 1561 GACATGTTCTCAAACTCAGTGAAGTTGGAAAAATTTAAACATCTTAATAAAATCTGCTAT 1620  
Qy 1903 AACCGTGTATACATGTGTATACACATCAATTAAGAACTTGGCATTTCAAAAGAAAAC 1962  
Db 1621 AACCGTGTATACATGTGTATACACATCAATTAAGAACTTGGCATTTCAAAAGAAAAC 1680  
Qy 1963 CATTTTGTGTAGTCAATCAATCAATTAAGAACTTGGCATTTCAAAAGAAAAC 2022  
Db 1681 CATTTTGTGTAGTCAATCAATCAATTAAGAACTTGGCATTTCAAAAGAAAAC 1740  
Qy 2023 GAATTTGATGATTTAGATGAAAGTAGAAGATATATTTTCAATAAAACCGCTGAATATCAA 2082  
Db 1741 GAATTTGATGATTTAGATGAAAGTAGAAGATATATTTTCAATAAAACCGCTGAATATCAA 1800  
Qy 2083 GAAGAGATTGATATCTTAAAGATATTTAA 2112  
Db 1801 GAAGAGATTGATATCTTAAAGATATTTAA 1830

## RESULT 13

US-11-172-145-16  
; Sequence 16, Application US/11172145  
; Publication No. US20050272696A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAngelis, Paul  
; TITLE OF INVENTION: METHODS OF SELECTIVELY TREATING DISEASES WITH SPECIFIC  
; FILE REFERENCE: 3554.104  
; CURRENT APPLICATION NUMBER: US/11/172.145  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR FILING DATE: 2003-06-18  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR FILING DATE: 1998-11-11  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR FILING DATE: 1998-04-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16  
; LENGTH: 1764  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-11-172-145-16

Query Match 60.3%; Score 1759.4; DB 7; Length 1764;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1760; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 352 CTTGTACCAAAGATTTTCCAAAGATCTGGTTTGTAGCGCTTTTACCTGATCATGTTAAT 411  
Db 4 CTTGTACCAAAGATTTTCCAAAGATCTGGTTTGTAGCGCTTTTACCTGATCATGTTAAT 63  
Qy 412 GATTTTACATGGTACAAAGCGAAGAAAGACTTGGCATATAAACCTTGAACATCAACAT 471  
Db 64 GATTTTACATGGTACAAAGCGAAGAAAGACTTGGCATATAAACCTTGAACATCAACAT 123  
Qy 472 GTTGTCTTCTTATATCTTATCAACATTTCAATCGACGCAATTTTATCGATTACATTA 531

Db 124 GTTGTCTTCTTATATCTTATCAACATTTCAATCGACGCAATTTTATCGATTACATTA 183  
Qy 532 GCGTGTATAGTAAACCAAAACACATTTACCGTTTGAAGTTTATCGTACAGATGATGGT 591  
Db 184 GCGTGTATAGTAAACCAAAACACATTTACCGTTTGAAGTTTATCGTACAGATGATGGT 243  
Qy 592 AGTCAGGAAGATCTATCACCGATCATTTGCGCAATATGAAATAAATTTGGATATTCGCTAC 651  
Db 244 AGTCAGGAAGATCTATCACCGATCATTTGCGCAATATGAAATAAATTTGGATATTCGCTAC 303  
Qy 652 GTCAGACAAAGAAATAAACGTTTTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGCTTA 711  
Db 304 GTCAGACAAAGAAATAAACGTTTTTCAAGCCAGTCCGCTCGGAATATGGGATTAACGCTTA 363  
Qy 712 GCAAAATATGACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGTT 771  
Db 364 GCAAAATATGACTTTATTTGGCTTACTCGACTGTGATATGGCGCAAAATCCATTTATGGTT 423  
Qy 772 CATTTCTTATGTCAGAGCTTATTTAGAGATGATGATTTAAACAATCATTTGTCGCAAGAAA 831  
Db 424 CATTTCTTATGTCAGAGCTTATTTAGAGATGATGATTTAAACAATCATTTGTCGCAAGAAA 483  
Qy 832 TACATCGATACACAAATATTTGACCCAAAGACTTCTTAATTAACCGGAGTTTTCCTTGA 891  
Db 484 TACATCGATACACAAATATTTGACCCAAAGACTTCTTAATTAACCGGAGTTTTCCTTGA 543  
Qy 892 TCATTTACCAGAGTGAAGAAACCAATATAGTGTTCGCGCAAAAGGGGAAGAAACAGTTTCT 951  
Db 544 TCATTTACCAGAGTGAAGAAACCAATATAGTGTTCGCGCAAAAGGGGAAGAAACAGTTTCT 603  
Qy 952 CTGGATTGCGGCTTTAGAACCAATTCGAAACAAAGAAATCTCCGCTTATCCGATTCGCT 1011  
Db 604 CTGGATTGCGGCTTTAGAACCAATTCGAAACAAAGAAATCTCCGCTTATCCGATTCGCT 663  
Qy 1012 TTCCGTTTTTTTGGCGGGTAAATGTTGCTTTCGCTTAAAGAAATGCTTAATTAATCCGCT 1071  
Db 664 TTCCGTTTTTTTGGCGGGTAAATGTTGCTTTCGCTTAAAGAAATGCTTAATTAATCCGCT 723  
Qy 1072 TTCTTTGATGAGAAATTTAATCACTGGGGTGGAGAGATGGAATTTTGGATATCGCTTA 1131  
Db 724 TTCTTTGATGAGAAATTTAATCACTGGGGTGGAGAGATGGAATTTTGGATATCGCTTA 783  
Qy 1132 TTCCGTTTACGCTAGTTTCTTTAAACATTTGATGGCAATTTATGGCTTACCAATCAAGAGCA 1191  
Db 784 TTCCGTTTACGCTAGTTTCTTTAAACATTTGATGGCAATTTATGGCTTACCAATCAAGAGCA 843  
Qy 1192 CCAGGTTAAAGAAATGAAACCGATCGTGAAGCGGGAAGAAATATTTACGCTCGATATTATG 1251  
Db 844 CCAGGTTAAAGAAATGAAACCGATCGTGAAGCGGGAAGAAATATTTACGCTCGATATTATG 903  
Qy 1252 AGAGAAAGGTCCCTTATATCTATAGAAACCTTTTACCAATAGAGATTTCCGATATCAAT 1311  
Db 904 AGAGAAAGGTCCCTTATATCTATAGAAACCTTTTACCAATAGAGATTTCCGATATCAAT 963  
Qy 1312 AGAGTACCTTTAGTTTCAATTTTATATCCAGCTTATTAACCTGTGCAAACTATATTCAACGT 1371  
Db 964 AGAGTACCTTTAGTTTCAATTTTATATCCAGCTTATTAACCTGTGCAAACTATATTCAACGT 1023  
Qy 1372 TGCGTAGATAGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAACGAT 1431  
Db 1024 TGCGTAGATAGTCACTGAATCAGACTGTTGTTGATCTCGAGGTTTGTATTTGTAACGAT 1083  
Qy 1432 GGTTCACACAGATAATACCTTAGAGTGATCAATAAGCTTTTGTGTATTAATATCCCTAGGTA 1491  
Db 1084 GGTTCACACAGATAATACCTTAGAGTGATCAATAAGCTTTTGTGTATTAATATCCCTAGGTA 1143  
Qy 1492 CGCATCATGTCTAAACCAAAATGCGGAATAGCCCTCAGCATCAATGACGCGGTTCTTTT 1551  
Db 1144 CGCATCATGTCTAAACCAAAATGCGGAATAGCCCTCAGCATCAATGACGCGGTTCTTTT 1203  
Qy 1552 GCTAAAGGTTTATACATTTGGGCGAGTTAGATTCAGATGATTTATCTTTGACGCTGATGCGATT 1611



November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New). Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

**THIS PAGE BLANK (USPTO)**